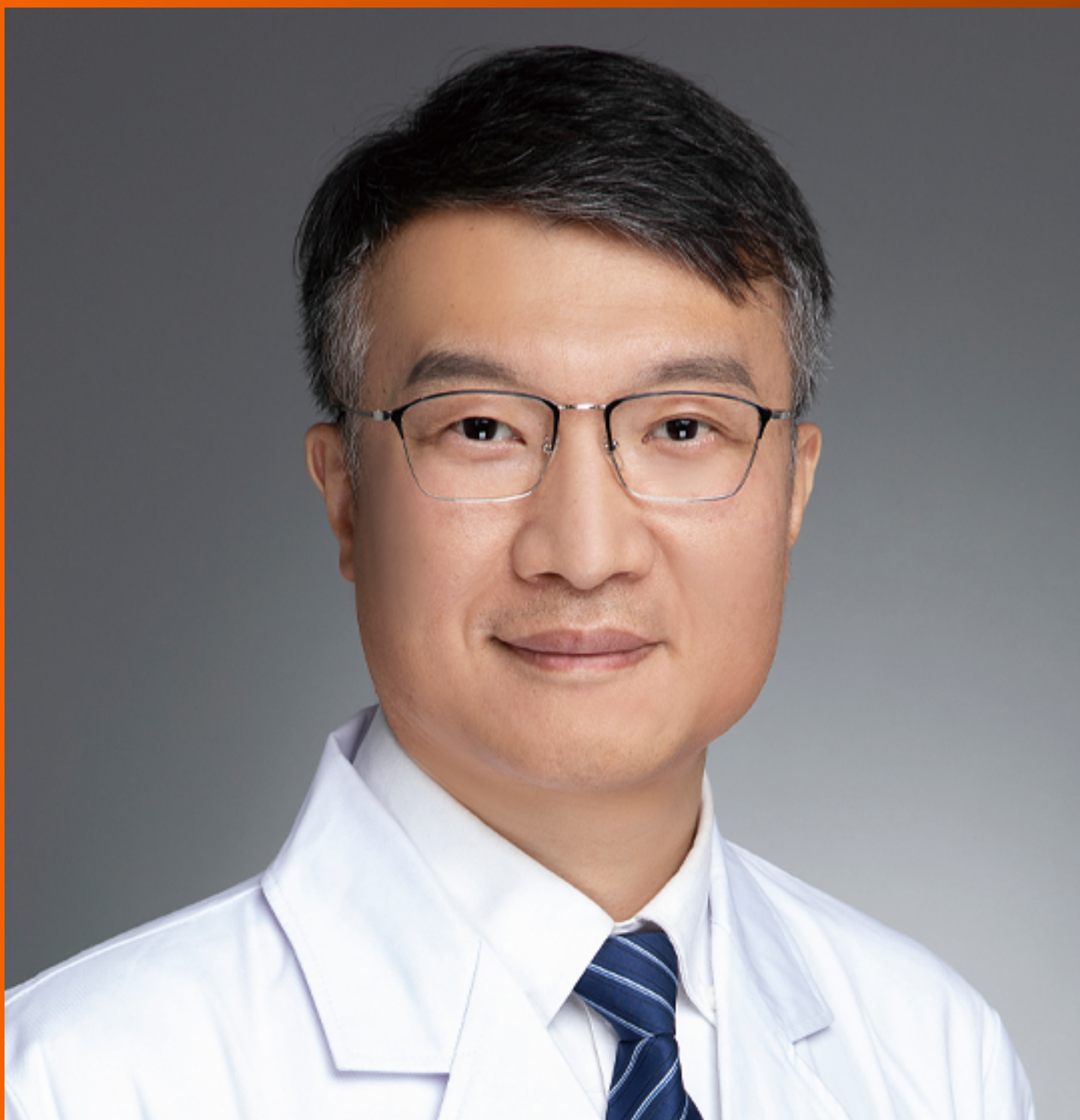


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Long-term metformin therapy and vitamin B12 deficiency: An association to bear in mind

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Abstract

To date, metformin remains the first-line oral glucose-lowering drug used for the treatment of type 2 diabetes thanks to its well-established long-term safety and efficacy profile. Indeed, metformin is the most widely used oral insulin-sensitizing agent, being prescribed to more than 100 million people worldwide, including patients with prediabetes, insulin resistance, and polycystic ovary syndrome. However, over the last decades several observational studies and meta-analyses have reported a significant association between long-term metformin therapy and an increased prevalence of vitamin B12 deficiency. Of note, evidence suggests that long-term and high-dose metformin therapy impairs vitamin B12 status. Vitamin B12 (also referred to as cobalamin) is a water-soluble vitamin that is mainly obtained from animal-sourced foods. At the cellular level, vitamin B12 acts as a cofactor for enzymes that play a critical role in DNA synthesis and neuroprotection. Thus, vitamin B12 deficiency can lead to a number of clinical consequences that include hematologic abnormalities (e.g., megaloblastic anemia and formation of hypersegmented neutrophils), progressive axonal demyelination and peripheral neuropathy. Nevertheless, no definite guidelines are currently available for vitamin B12 deficiency screening in patients on metformin therapy, and vitamin B12 deficiency remains frequently unrecognized

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in such individuals. Therefore, in this “field of vision” article we propose a list of criteria for a cost-effective vitamin B12 deficiency screening in metformin-treated patients, which could serve as a practical guide for identifying individuals at high risk for this condition. Moreover, we discuss additional relevant topics related to this field, including: (1) The lack of consensus about the exact definition of vitamin B12 deficiency; (2) The definition of reliable biomarkers of vitamin B12 status; (3) Causes of vitamin B12 deficiency other than metformin therapy that should be identified promptly in metformin-treated patients for a proper differential diagnosis; and (4) Potential pathophysiological mechanisms underlying metformin-induced vitamin B12 deficiency. Finally, we briefly review basic concepts related to vitamin B12 supplementation for the treatment of vitamin B12 deficiency, particularly when this condition is induced by metformin.

Key Words: Metformin; Vitamin B12 deficiency; Metformin-induced cobalamin deficiency; Diabetes; Type 2 diabetes; Prediabetes; Screening criteria; Neuropathy; Anemia

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Core Tip: Over the last decades, vitamin B12 deficiency has been increasingly recognized as a possible consequence of long-term metformin therapy, potentially resulting in clinical manifestations such as hematologic abnormalities and peripheral neuropathy. Metformin-induced vitamin B12 deficiency has relevant implications in light of the growing population of individuals on metformin therapy for the treatment of type 2 diabetes, prediabetes, insulin resistance and polycystic ovary syndrome on a global scale. Notwithstanding, no definite guidelines are currently available for vitamin B12 deficiency screening in metformin-treated patients. We therefore propose a list of criteria for cost-effective vitamin B12 deficiency screening in metformin-treated patients.

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INTRODUCTION

Vitamin B12, also known as cobalamin, is a water-soluble vitamin that is primarily obtained from animal-sourced foods such as red meat, poultry, shellfish, milk, eggs and other dairy products, or vitamin B12-fortified foods[1]. Once ingested, vitamin B12 is released from its food carrier proteins by proteolysis in the acidic environment of the stomach, where it binds to a glycoprotein called haptocorrin (also referred to as R-factor or R-protein). Haptocorrin is produced and secreted by the salivary glands. The haptocorrin-vitamin B12 complex protects vitamin B12 from degradation in the acidic environment of the stomach. Once the haptocorrin-vitamin B12 complex reaches the duodenum, pH change and degradation of haptocorrin by pancreatic proteases favor vitamin B12 cleavage from haptocorrin, resulting in the release of vitamin B12 in its free form. In the duodenum, the free vitamin B12 binds to intrinsic factor (IF), a glycoprotein secreted by gastric parietal cells, resulting in the formation of an IF-vitamin B12 complex. The newly formed IF-vitamin B12 complex subsequently binds, in a calcium-dependent manner, to the cubilin receptor (a protein encoded by the *CUBN* gene) on the enterocytes of the distal ileum, resulting in the absorption of vitamin B12 by receptor-mediated endocytosis. Upon internalization, the IF-vitamin B12 complex is released from its receptor, IF is degraded in lysosomes, and vitamin B12 enters the circulation *via* the multidrug resistance protein 1 (MDR1) transporter [2]. In the circulation, approximately 20%-25% of vitamin B12 is bound to its binding protein transcobalamin. The transcobalamin-vitamin B12 complex is also known as holotranscobalamin (HoloTC), which represents the biologically active form of cobalamin and allows for cellular uptake of vitamin B12 through specific cell surface

transcobalamin receptors[3]. The remaining 75%-80% of vitamin B12 is bound to haptocorrin and is stored in the liver. Some vitamin B12 is excreted in bile and undergoes enterohepatic circulation[1,4,5].

At the cellular level, vitamin B12 serves as a cofactor for the enzyme methionine synthase, which catalyzes the conversion of homocysteine into methionine. The overall reaction takes place in the cytosol and transforms 5-methyl-tetrahydrofolate (5-methyl-THF) into THF while transferring a methyl group to homocysteine to synthesize methionine. THF is then converted into intermediates that are used in the synthesis of pyrimidine bases of DNA. Therefore, vitamin B12 deficiency leads to homocysteine accumulation, impaired DNA synthesis, and hematologic abnormalities such as formation of hypersegmented neutrophils and megaloblastic anemia, a condition in which the bone marrow produces unusually large, structurally abnormal and immature red blood cells called megaloblasts as a consequence of ineffective hematopoiesis[4]. Anemia can be associated with various symptoms, including pallor, palpitations, tachycardia, and fatigue, which are frequently observed in patients with vitamin B12 deficiency. Although megaloblastic anemia is the most common hematologic abnormality, vitamin B12 deficiency can potentially affect all bone marrow cell lineages, resulting in pancytopenia[6].

Vitamin B12 also acts as a cofactor for the enzyme methylmalonyl-CoA mutase, which catalyzes the conversion of methylmalonyl-CoA to succinyl-CoA, a reaction that takes place in the mitochondria[1]. Thus, vitamin B12 deficiency results in the accumulation of methylmalonyl-CoA that is subsequently converted to methylmalonic acid (MMA), whose plasma levels are often elevated in patients with vitamin B12 deficiency. In subjects with vitamin B12 deficiency, increased levels of MMA and homocysteine have been suggested to contribute to myelin damage (myelopathy) and, as a consequence, to peripheral and autonomic neuropathy[1,4,7]. Neurologic manifestations of vitamin B12 deficiency include progressive axonal demyelination, impaired sensory and peripheral nerve function, subacute combined degeneration of the spinal cord, areflexia and loss of proprioception and vibration sensitivity[5,8,9]. The aforementioned neurologic manifestations can be erroneously interpreted as features of diabetic neuropathy in diabetic patients who are chronically treated with metformin. Failure to identify the cause of neuropathy can lead to progression of central and/or peripheral nerve damage, which may be arrested, but not completely reversed, by vitamin B12 replacement in some instances[10]. Neurocognitive manifestations such as poor memory performance, cognitive impairment, dementia, delirium, depression and episodes of psychosis are also possible in the presence of severe and chronic vitamin B12 deficiency[5,8,11]. Other symptoms that have been reported in adult patients with vitamin B12 deficiency include glossitis, skin hyperpigmentation, infertility, hearing loss, bone disease and macular degeneration[8].

BIOMARKERS OF VITAMIN B12 STATUS AND DEFINITION OF VITAMIN B12 DEFICIENCY

To date, there is no consensus about the exact definition of vitamin B12 deficiency[1]. Indeed, there is still a significant debate within the scientific community about the specific cut-off values that should be applied to define a low vitamin B12 status and about the definition of the best biomarker or combination of biomarkers to assess vitamin B12 status[1,12]. Varying cut-off values invariably lead to underestimating or overestimating the incidence of vitamin B12 deficiency. With regard to the definition of an optimal vitamin B12 status, a low vitamin B12 status (frank vitamin B12 deficiency) is generally defined as total serum vitamin B12 levels of < 148 pmol/L, with levels between 148 and 221 pmol/L being considered as “borderline” or suggestive of “marginal deficiency”[5].

As a matter of fact, there has been a debate about the clinical significance of biochemical vitamin B12 deficiency *vs* true tissue deficiency, and whether subclinical (*i.e.* mild and asymptomatic) vitamin B12 deficiency represents a public health concern [13]. Discussion of issues regarding the sensitivity and specificity of individual biomarkers of vitamin B12 status led a roundtable on NHANES monitoring of those biomarkers to agree that a comprehensive and accurate assessment of true tissue vitamin B12 deficiency should include at least one biomarker of circulating vitamin B12 (total vitamin B12 or HoloTC) coupled with one functional (metabolic) biomarker of vitamin B12 status, such as MMA or total homocysteine[13]. In fact, several studies have established that serum vitamin B12 has a limited diagnostic value as a stand-alone marker because of its low specificity and sensitivity in identifying a true tissue

vitamin B12 deficiency. Low serum levels of vitamin B12 thus may not necessarily represent a true tissue deficiency[5,12]. A major limitation of the measurement of total serum vitamin B12 is that it assesses total circulating vitamin B12, of which approximately 80% is bound to haptocorrin and is therefore not bioavailable for cellular uptake. Moreover, this assay does not reliably reflect the cellular vitamin B12 status [12]. Studies assessing serum and cellular vitamin B12 showed that serum vitamin B12 levels do not always reflect cellular vitamin B12 status[12,14]. For instance, patients with inborn errors of vitamin B12 metabolism can exhibit low or normal serum values of vitamin B12, while being deficient at the cellular level[12]. In addition, severe functional vitamin B12 deficiency has been documented in the presence of normal or even elevated levels of serum vitamin B12[12], given that serum vitamin B12 levels can be maintained at the expense of cobalamin tissue stores[15].

In light of the abovementioned remarks, measurement of functional biomarkers of vitamin B12 status (homocysteine and MMA) may be useful to confirm the diagnosis of true vitamin B12 deficiency, particularly in the presence of low-normal total serum vitamin B12 levels and/or clinical suspicion of vitamin B12 deficiency[1]. Therefore, total vitamin B12, its bioactive protein-bound form HoloTC, homocysteine and MMA are the preferred serum biomarkers to accurately assess vitamin B12 status[12]. However, it is worth noting that serum levels of homocysteine and MMA can be elevated even in the presence of folate deficiency, which can also be associated with macrocytic anemia and thereby confused with vitamin B12 deficiency. Thus, measurement of serum folate, MMA and homocysteine levels can help to distinguish vitamin B12 deficiency from folate deficiency. As discussed earlier, serum levels of both homocysteine and MMA are often elevated in the presence of true vitamin B12 deficiency. Conversely, homocysteine levels are elevated but MMA levels are normal in the presence of folate deficiency[4]. Yet, it is also worth reminding that both homocysteine and MMA levels can be elevated in the presence of renal impairment[1].

CAUSES OF VITAMIN B12 DEFICIENCY

Apart from long-term metformin therapy (discussed later in the text), several causes and conditions increase the risk of vitamin B12 deficiency (Table 1), as it has been reviewed elsewhere[5,8,16]. Those conditions should be identified promptly in metformin-treated patients with vitamin B12 deficiency for a proper differential diagnosis.

Populations at risk for vitamin B12 deficiency

Specific populations at risk for development of vitamin B12 deficiency include elderly individuals, pregnant women and selected ethnic and racial groups[5]. Vitamin B12 deficiency is more common in older individuals, particularly among those over 65 years of age, who have a prevalence of cobalamin deficiency of approximately 10%-15%[5,17,18]. The prevalence of vitamin B12 deficiency is even higher in the “oldest-old”, with reports of approximately 23% of octogenarians and 35% of centenarians [19]. Possible causes of vitamin B12 in elderly people range from malabsorption and/or poor dietary intake to a number of age-related comorbidities and underlying conditions (Table 1).

Pregnancy can also alter maternal vitamin B12 status by facilitating the transfer of cobalamin to the fetus and infant[5]. The actual prevalence of vitamin B12 deficiency during pregnancy appears to vary across geographic regions, being reported as lower than 10% in Brazil and Canada and greater than 70% in some areas of Turkey and India[5]. Total plasma vitamin B12 levels progressively decrease during pregnancy, and the reduction is often accompanied by a moderate increase in MMA levels, suggesting a functional depletion in intracellular cobalamin status[20,21]. The pregnancy-related decline in vitamin B12 levels may result from alterations in haptocorrin-bound cobalamin[22]. Nonetheless, the assessment of vitamin B12 status as well as the evaluation of the actual prevalence of vitamin B12 deficiency during pregnancy are challenging because of the profound anatomical and physiological changes that limit the use of the established reference ranges employed for determination of cobalamin status in non-pregnant women[5,20].

The prevalence of vitamin B12 deficiency has also been reported to vary across different ethnic and racial groups, probably because of genetic factors and/or cultural and religious practices that predispose different populations to diverse levels of dietary intake of animal products, especially red meat. In a study conducted in participants of the population-based multidisciplinary Georgia Centenarian Study,

Table 1 Causes of vitamin B12 deficiency and underlying mechanisms

Conditions potentially associated with vitamin B12 deficiency	Underlying mechanisms
General malnutrition, chronic alcohol abuse, and vegan or strict vegetarian diets	Low or inadequate dietary intake of foods containing vitamin B12
Older age	Vitamin B12 malabsorption and deficiency due to inadequate dietary intake are common in the elderly
Gastric bypass, partial or complete gastrectomy, gastric reduction, bariatric surgery and chronic gastritis due to <i>Helicobacter pylori</i> infection	Impaired IF secretion
Atrophic gastritis (an autoimmune disease characterized by the presence of antibodies directed against gastric parietal cells and IF)	Immune-mediated destruction of gastric parietal cells, gastric mucosal atrophy, hypochlorhydria, decreased IF production, subsequent vitamin B12 malabsorption, vitamin B12 deficiency and pernicious anemia (a type of megaloblastic anemia)
Long-term use (≥ 12 mo) of drugs altering gastric acid secretion or gastric pH (e.g., PPIs, H2RAs and antacids)	These drugs reduce the production of hydrochloric acid by gastric parietal cells; as a consequence, vitamin B12 is not adequately released from the food matrix due to insufficient hydrochloric acid and low pepsin activity
Long-term use of metformin	The underlying mechanism accounting for metformin-induced vitamin B12 deficiency is not fully understood, although it may involve one or more of the following: (1) Interference with the calcium-dependent binding of the IF-vitamin B12 complex to the cubilin receptor on enterocytes at the ileum level; (2) Interaction with the cubilin endocytic receptor; (3) Alteration in small intestine motility leading to small intestinal bacterial overgrowth and subsequent inhibition of IF-vitamin B12 complex absorption in the distal ileum; (4) Alteration in bile acid metabolism and reabsorption; (5) Increased liver accumulation of vitamin B12; and (6) Reduced IF secretion by gastric parietal cells
Use of medications that affect vitamin B12 absorption or metabolism including the bile acid resin cholestyramine (used to treat hypercholesterolemia), colchicine (used for acute gout) and many antibiotics such as neomycin and the anti-tuberculosis drug para-aminosalicylic acid ¹	Cholestyramine can chelate IF; colchicine and antibiotics can inhibit endocytosis of the IF-vitamin B12 complex
Bacterial overgrowth syndromes, ileal resection or gastrointestinal diseases such as terminal ileitis, celiac disease, inflammatory bowel disease, Crohn's disease and tropical sprue	Altered absorption of the IF-vitamin B12 complex in the terminal ileum; intestinal villous atrophy and mucosal injury (celiac disease, Crohn's disease and tropical sprue)
Intestinal parasitic infestations (often accompanied by eosinophilia) caused by the protozoan <i>Giardia lamblia</i> or the fish tapeworm <i>Diphyllobothrium latum</i>	Vitamin B12 malabsorption through vitamin B12 trapping by the parasites
Disorders of the exocrine pancreas or pancreatectomy	Insufficient pancreatic enzyme activity leads to a reduction in the proteolytic degradation of haptocorrin (mediated by pancreatic proteases in the small intestine); as a consequence, vitamin B12 remains bound to haptocorrin, cannot form the IF-vitamin B12 complex and is not available for absorption by the enterocytes in the distal ileum
Nitrous oxide anesthesia or recreational use of nitrous oxide	Irreversible oxidation and inactivation of the coenzyme form of vitamin B12 (methylcobalamin) at the active site of the vitamin B12-dependent methionine synthase reaction, resulting in increased levels of MMA and homocysteine
Inherited disorders affecting the sequential steps in the assimilation, transport and intracellular processing and metabolism of vitamin B12	Reduced expression, binding activity or affinity of receptors and proteins involved in transport, intracellular processing and metabolism of vitamin B12

¹Unlike long-term use of proton-pump inhibitors, histamine H2-receptor antagonists or metformin, the frequency or duration of use of these drugs is usually insufficient to result in clinical vitamin B12 deficiency. H2RAs: Histamine H2-receptor antagonists; IF: Intrinsic factor; PPIs: Proton-pump inhibitors; MMA: Methylmalonic acid.

Johnson *et al*[19] found that the probability of being vitamin B12-deficient was significantly increased (2 times higher) in whites compared to African Americans. Another observational study by Carmel *et al*[23] reported that vitamin B12 deficiency was most common in elderly white men and least common in black and Asian American women. A large cross-sectional survey conducted in New Zealanders aged ≥ 15 years showed that Māori/Pacific and East/South-East Asian groups had the highest vitamin B12 levels, whereas those most at risk of low vitamin B12 status were South Asians, including people with ancestral origins in the Indian subcontinent[24]. Māori and Pacific Island groups were the least likely to have inadequate vitamin B12 intakes compared with New Zealand Europeans, while the latter group was more likely to have an adequate vitamin B12 status compared with South Asians[24]. Another study confirmed a higher prevalence of vitamin B12 deficiency in South Asians compared

with the general population[25].

METFORMIN-INDUCED VITAMIN B12 DEFICIENCY: CLINICAL EVIDENCE

More than 60 years after its first clinical use, metformin is still recommended as the first-line oral glucose-lowering drug in most clinical guidelines on the management of type 2 diabetes (T2D) thanks to its well-established long-term safety and efficacy profile[26]. Possible side effects of metformin include gastrointestinal intolerance[27] and the rare occurrence of lactic acidosis, which is most likely in the presence of moderate to severe chronic kidney disease. However, moderate to severe renal impairment is a major contraindication to the clinical use of metformin[28]. Metformin is usually well tolerated and effective in maintaining glucose control in the long-term [29]. Indeed, metformin is still the most widely used oral antihyperglycemic (insulin-sensitizing) agent, being prescribed to more than 100 million people worldwide, including patients with prediabetes, insulin resistance and polycystic ovary syndrome (PCOS)[30]. Yet, in recent decades, several observational studies, systematic reviews and meta-analyses have reported an association between long-term metformin therapy and biochemical vitamin B12 deficiency, including frank deficiency or borderline vitamin B12 status[31-37]. Evidence suggests that metformin impairs vitamin B12 status primarily in a dose- and duration-dependent manner (discussed later in the text).

The reported prevalence of vitamin B12 deficiency in metformin-treated patients with diabetes varies across studies, ranging from approximately 6% to 50%[31,38-41]. The first reports documenting this association were published in the late 1960s, when annual serum vitamin B12 testing was already suggested as a valid screening measure for early detection of vitamin B12 deficiency in patients on long-term metformin therapy[42,43]. However, the exact influence of both the dose and duration of metformin therapy on vitamin B12 status is still not entirely understood. A cross-sectional study conducted by de Groot-Kamphuis *et al*[38] found that patients with T2D using metformin had a significantly higher prevalence of vitamin B12 deficiency compared with patients not using metformin (14.1% *vs* 4.4%, with a median duration of metformin use of 4.9 years). Moreover, each 100 mg step in metformin dose increased by 8% the odds of having vitamin B12 deficiency, but metformin use did not predict the chance of having anemia or neuropathy[38]. A similar cross-sectional study conducted in 550 T2D patients using metformin (mean treatment duration of 64 mo and mean daily dose of 1306 mg) found that higher daily and cumulative doses of metformin (1 mg/d increase of daily dose and 10 g increase of cumulative dose) were strongly associated with lower HoloTC and cobalamin concentrations[39]. Nevertheless, authors did not find a relationship between the duration of metformin use and cobalamin/HoloTC concentrations[39]. A nested case-control study conducted in Hong Kong also suggested that an increased risk of vitamin B12 deficiency was associated with the current dose and duration of metformin therapy in patients with diabetes[44]. Authors found that each 1 g/d metformin dose increment conferred a more than 2-fold increased risk of developing vitamin B12 deficiency (adjusted odds ratio of 2.88, 95% confidence interval: 2.15-3.87; $P < 0.001$). In patients using metformin for 3 years or more, the adjusted odds ratio was 2.39 (95% confidence interval: 1.46-3.91; $P = 0.001$) compared with those receiving metformin for less than 3 years[44].

Shivaprasad *et al*[45] recently conducted a prospective observational study to assess the combined effect of both dose and duration of metformin therapy on vitamin B12 levels in 2887 patients with T2D. They found vitamin B12 levels of < 200 pg/mL and between 200 and 300 pg/mL in 24.5% and 34.5% of metformin users, respectively. The percentages were significantly higher than those observed in non-metformin users (17.3% and 22.6%, respectively). To quantify metformin usage, authors defined a “metformin usage index” (MUI) as the product of the daily metformin dose (mg) and its duration (years) divided by 1000. Participants who were not on continuous metformin therapy for at least 6 mo prior to recruitment were included in a non-metformin user group. Interestingly, there was a significant association between a MUI value of > 5 and a high risk of vitamin B12 deficiency. Multistep logistic regression analysis adjusted for confounding variables (age, duration of T2D, body mass index, and glycated hemoglobin) found the highest risk of developing vitamin B12 deficiency in patients with a MUI value of > 15 , followed by patients with a MUI value of > 10 . The lowest risk was found in T2D patients with a MUI value of < 5 [45]. Therefore, MUI may be a valid tool to identify individuals at increased risk of vitamin B12 deficiency among T2D patients on continuous metformin therapy for at least 6 mo.

Even though definitive screening guidelines are lacking, the 2021 American Diabetes Association Standards of Medical Care in Diabetes recommend to consider a periodic assessment of vitamin B12 levels in patients with long-term metformin use, including those with prediabetes, peripheral neuropathy or anemia. This recommendation is based on a grade B level of evidence deriving from well-conducted case-control studies, prospective cohort studies and meta-analyses of cohort studies[46], including a report from the Diabetes Prevention Program Outcomes Study (DPPOS) published in *The Journal of Clinical Endocrinology & Metabolism* in 2016 by Aroda *et al* [32]. The design of the latter study consisted of a secondary analysis from the Diabetes Prevention Program (DPP)/DPPOS involving over 2000 patients across 27 centers in the United States. Participants with elevated fasting blood glucose, impaired glucose tolerance, and overweight or obesity were assigned to the placebo group ($n = 1082$) or to the metformin group (850 mg twice daily; $n = 1073$) for a mean follow-up of 3.2 years. Participants in the metformin group received open-label metformin for an additional 9 years. Authors found that low serum vitamin B12 levels (≤ 203 pg/mL) occurred with a significantly higher frequency in the metformin group than in the placebo group at 5 years (4.3% *vs* 2.3%). Furthermore, combined low and borderline-low vitamin B12 (≤ 298 pg/mL) was significantly more frequent in metformin group at 5 and 13 years. Importantly, authors reported that approximately 50% of participants with low vitamin B12 levels in their cohort had concurrently increased homocysteine levels, suggesting the presence of a true tissue deficiency of vitamin B12. Moreover, years of metformin use were associated with an increased risk of vitamin B12 deficiency. When the metformin and placebo groups were combined, the odds ratio associated with vitamin B12 deficiency per year of metformin use was 1.13 (95% confidence interval: 1.06-1.20) after adjusting for confounders such as age, sex, baseline body mass index, weight change, diabetes status, and prescription of acid suppression therapy[32]. The prevalence of anemia was higher in the metformin group, but did not differ by vitamin B12 status. The prevalence of neuropathy was significantly higher among metformin group participants with low vitamin B12 levels compared with metformin-treated participants with normal or borderline vitamin B12 levels[32]. In line with those findings, a cross-sectional study by Kim *et al*[33] found that metformin use in T2D patients for at least 6 mo and at a dose of ≥ 1500 mg/d may represent a major factor related to vitamin B12 deficiency. Of note, authors found that a metformin dose of ≥ 2000 mg was associated with the highest risk of vitamin B12 deficiency. Compared with the group taking a daily metformin dose of < 1000 mg, the adjusted odds ratios for 1000-1500 mg, 1500-2000 mg, and ≥ 2000 mg groups were 1.72 ($P = 0.080$), 3.34 ($P < 0.001$) and 8.67 ($P < 0.001$), respectively. Moreover, serum homocysteine levels were negatively correlated with vitamin B12 levels, suggesting that vitamin B12 deficiency induced by metformin may occur at the tissue level[33].

A recent retrospective study conducted in a large cohort of adult patients ($n = 13489$) who had received metformin for more than 1 year aimed to assess the appropriateness and benefits of screening recommendations for vitamin B12 deficiency[47]. The mean time between metformin initiation and incidence of vitamin B12 deficiency was 5.3 years. An older patient subgroup (> 65 years of age) had a significantly higher vitamin B12 deficiency rate compared with younger patients (4.2% *vs* 2.5%). In multivariable logistic regression models, older age was the only factor associated with vitamin B12 deficiency, while African-American ethnicity almost reached statistical significance as a protective factor. These results suggest that patients who have been using metformin for more than 5 years and patients older than 65 are at increased risk for vitamin B12 deficiency. Therefore, authors concluded that screening for vitamin B12 deficiency might be considered in such populations even if they are asymptomatic for the deficiency[47].

A prospective case-control study conducted in T2D patients with concurrent symptomatic peripheral neuropathy found that patients who had received metformin for more than 6 mo with a mean cumulative metformin exposure of 3389.5 g, compared with those without metformin exposure, had lower cobalamin levels and higher fasting MMA and homocysteine levels accompanied by more severe peripheral neuropathy (assessed by clinical and electrophysiological markers)[48]. The cumulative metformin dose was inversely correlated with serum vitamin B12 and positively correlated with fasting serum MMA and homocysteine. In addition, the median Toronto Clinical Scoring System (TCSS) and Neuropathy Impairment Score (NIS) total scores were both significantly higher in the metformin-treated group and had a strong positive correlation with increasing cumulative metformin dose[48]. In keeping with those findings, a post-hoc analysis of a randomized controlled 4.3-year trial conducted in insulin-treated T2D patients reported that addition of metformin not only reduced serum vitamin B12 levels, but also gradually increased serum MMA

levels[49]. In metformin users, the increase in MMA levels was also associated with significant worsening of symptoms of neuropathy, assessed by a validated neuropathy score[49].

A possible explanation for the delayed occurrence of biochemical or clinical vitamin B12 deficiency in patients on metformin therapy relies on the low daily requirement of vitamin B12 (approximately 2.4 µg/d) and on its substantial hepatic storage of around 2500 µg. Indeed, clinical manifestations of vitamin B12 deficiency can become evident upon depletion of the body stores to as little as 5%-10%, which may occur several years (up to 10 years) after the initial exposure to metformin or to other risk factors or conditions predisposing to vitamin B12 deficiency[50]. However, older adults may exhibit depleted vitamin B12 stores[51] and may therefore be particularly susceptible to vitamin B12 deficiency even after a short-term period of metformin therapy. For instance, Leung *et al*[52] showed that short-term (3-mo) metformin use decreased plasma levels of total cobalamin, total haptocorrin and haptocorrin-bound cobalamin in an elderly diabetic population.

Evidence also suggests that acid-suppressing medications such as histamine H2-receptor antagonists (H2RAs) and proton-pump inhibitors (PPIs) can interfere with vitamin B12 absorption by reducing the release of dietary vitamin B12 from food proteins[53]. Notably, Long *et al*[54] reported that the concomitant use of metformin and PPIs in patients with T2D may increase the risk of vitamin B12 deficiency by exerting further deleterious effects on vitamin B12 status. This has relevant clinical implications, given that approximately 40% of T2D patients are reported to experience symptomatic gastroesophageal reflux disease (GERD), and PPIs and H2RAs represent the most widely prescribed drugs for treatment of GERD in this population[53].

Metformin-induced vitamin B12 deficiency: implications for diabetic neuropathy

Metformin-induced vitamin B12 deficiency (also known as MICD or metformin-induced cobalamin deficiency) can exacerbate nerve damage in diabetic patients with preexisting neuropathy, resulting in the development of a mixed “diabetic and MICD-related neuropathy”. Hashem *et al*[55] recently conducted a case-control, prospective, observational study in 150 adults with T2D and diabetic peripheral neuropathy (DPN) to establish whether metformin represents a risk factor for DPN. The study cohort included 75 patients who received metformin for the previous 6 mo or more and 75 patients who did not receive metformin for the previous 6 mo but had received other oral antihyperglycemic drugs. Compared with the control patients, the metformin-treated patients had significantly higher homocysteine and MMA levels, along with significantly lower plasma cobalamin levels (222 pmol/L *vs* 471 pmol/L; $P < 0.001$). Moreover, metformin-treated patients had a significantly higher frequency of moderate to severe DPN and higher TCSS total scores. Spearman’s correlation revealed a significant negative correlation between plasma cobalamin levels and higher metformin doses, as well as a significant positive correlation between TCSS and increased metformin dose. Metformin-treated patients also showed significantly lower median conduction velocity and sensory nerve action potentials for superficial peroneal and sural nerves. In addition, the severity of DPN was inversely related to plasma cobalamin levels and directly related to higher levels of both homocysteine and MMA. Importantly, multivariate logistic regression analysis of independent predictors of DPN in metformin-treated patients revealed that longer duration of diabetes and metformin therapy were significantly associated with a greater incidence of DPN. Larger doses and longer duration of metformin therapy were also independent predictors of DPN[55].

In a recent 12-mo, randomized, double-blind, placebo-controlled trial, 90 adults with T2D on metformin therapy for at least 4 years and with both diabetic peripheral and autonomic neuropathy were randomized to receive vitamin B12 (1 mg of oral methylcobalamin) or placebo on a daily basis[56]. All participants had baseline vitamin B12 levels of < 400 pmol/L. Compared with placebo, vitamin B12 supplementation led to a significant increase in vitamin B12 levels (from 232.0 ± 71.8 pmol/L at baseline to 776.7 ± 242.3 pmol/L at follow-up) that was accompanied by a significant improvement in Michigan Neuropathy Screening Instrument Questionnaire, quality of life and pain scores, vibration perception threshold, electrochemical skin conductance in the feet, and sural nerve conduction velocity and amplitude[56]. Overall, these findings highlight the importance of diagnosing and correcting vitamin B12 deficiency in metformin-treated patients with diabetes and neuropathy in order to prevent or halt the exacerbation and progression of nerve damage.

POTENTIAL PATHOPHYSIOLOGICAL MECHANISMS OF METFORMIN-INDUCED VITAMIN B12 DEFICIENCY

The exact mechanisms underlying metformin-induced vitamin B12 deficiency are still not fully understood[37]. However, the mechanisms are thought to cause vitamin B12 deficiency mainly through altered vitamin B12 absorption and metabolism (Figure 1) [1,57-60]. Proposed mechanisms accounting for metformin-induced vitamin B12 deficiency include: (1) Interference with calcium-dependent binding of the IF-vitamin B12 complex to the cubilin receptor on enterocytes at the ileum level and/or interaction with the cubilin endocytic receptor; (2) Alteration in small intestine motility, leading to small intestinal bacterial overgrowth and subsequent inhibition of IF-vitamin B12 complex absorption in the distal ileum; (3) Alteration in bile acid metabolism and reabsorption, resulting in impaired enterohepatic circulation of vitamin B12; (4) Increased liver accumulation of vitamin B12, resulting in altered tissue distribution and metabolism of vitamin B12; and (5) Reduced IF secretion by gastric parietal cells. Of note, inhibition of calcium-dependent absorption of the IF-vitamin B12 complex at the terminal ileum has been increasingly recognized as the most plausible mechanism accounting for metformin-induced vitamin B12 deficiency. Indeed, the inhibitory effect is reversed by calcium supplementation[61].

VITAMIN B12 DEFICIENCY IN METFORMIN-TREATED PATIENTS: PROPOSED CRITERIA FOR A COST-EFFECTIVE SCREENING

To date, no definite guidelines are available for the screening of vitamin B12 deficiency in patients taking metformin. Thus, vitamin B12 deficiency remains frequently unrecognized in such patients. According to the British Society for Haematology guidelines for diagnosis and treatment of vitamin B12 deficiency, no definitive advice can be given on the desirable frequency of measurement of serum vitamin B12 in patients with T2D on metformin therapy. However, the same guidelines recommend to check serum vitamin B12 levels in the presence of strong clinical suspicion of deficiency[62].

Based on the current evidence, we therefore propose a list of criteria for a cost-effective vitamin B12 deficiency screening in metformin-treated patients. The criteria could serve as a practical guide for identifying individuals at high risk for vitamin B12 deficiency who may require vitamin B12 supplementation as well as a periodic assessment of their cobalamin status (Table 2). Of note, we suggest to consider screening for vitamin B12 deficiency in selected individuals even if they are asymptomatic for deficiency. The proposed screening criteria may be useful to prevent the development or worsening of the clinical consequences of vitamin B12 deficiency, particularly anemia and peripheral neuropathy, by allowing for a prompt diagnosis and treatment of vitamin B12 deficiency.

Apart from metformin-treated patients with insulin resistance, prediabetes, T2D and PCOS, another subgroup in which routine screening for vitamin B12 deficiency may be considered includes patients with type 1 diabetes (T1D) taking metformin as non-insulin adjunct therapy, especially in the presence of peripheral neuropathy or unexplained anemia. In this regard, it is also worth reminding that T1D patients are at increased risk for other autoimmune diseases such as autoimmune gastritis and pernicious anemia, which can independently lead to the development of vitamin B12 deficiency[63,64].

TREATMENT OF VITAMIN B12 DEFICIENCY

In selected individuals who are at higher risk for marginal vitamin B12 insufficiency, the goal is first of all to prevent the development of frank vitamin B12 deficiency, then to treat such deficiency by adequate repletion when it occurs[5]. This approach allows for prevention of clinical consequences of vitamin B12 deficiency, including megaloblastic anemia and neurologic manifestations such as peripheral neuropathy.

The recommended dietary allowance of vitamin B12 for subjects without malabsorption has been set at approximately 2.4 µg/d for adult men and non-pregnant women (2.6 µg/d for pregnant women)[8], even though a daily intake of 4-7 µg has been associated with lower serum MMA levels[65]. There is no defined tolerable upper intake level of vitamin B12[66]. As vitamin B12 is relatively

Table 2 Proposed criteria for cost-effective screening and subsequent intermittent periodic testing of vitamin B12 status in metformin-treated patients**Proposed criteria**

(1) A comprehensive assessment of vitamin B12 status aimed to accurately detect a true tissue vitamin B12 deficiency should include at least one biomarker of circulating vitamin B12 (total vitamin B12 or HoloTC) coupled with one functional (metabolic) biomarker of vitamin B12 status (MMA and/or total homocysteine). A recent complete blood count is also recommended

(2) Screening for vitamin B12 deficiency should be performed in the presence of one or more of the following risk factors or conditions: (a) Strong clinical suspicion of deficiency: clinical evidence of vitamin B12 deficiency, including unexplained macrocytic anemia, neurological symptoms and peripheral neuropathy¹; (b) Preexisting diabetic peripheral and/or autonomic neuropathy²; (c) Duration of metformin treatment ≥ 5 yr; (d) Older adults: age ≥ 65 yr; (e) High cumulative metformin exposure defined by a MUI value of > 5 (this criterion applies to patients with type 2 diabetes treated with metformin for at least 6 mo)³; (f) Metformin dose of ≥ 1500 mg/d for a duration of at least 6 mo (the highest risk of vitamin B12 deficiency has been observed with a daily metformin dose of ≥ 2000 mg); (g) Concomitant long-term use (≥ 12 mo) of acid-suppressing medications such as PPIs and H2RAs; and (h) Concomitant presence of risk factors or comorbidities associated with an increased risk of vitamin B12 deficiency (reviewed in Table 1) warrants screening for deficiency based on clinical judgement

¹Based on results from Diabetes Prevention Program/Diabetes Prevention Program Outcomes Study[32], peripheral neuropathy refers to monofilament-defined neuropathy (detection of an abnormal monofilament examination).

²Screening for vitamin B12 deficiency should be routinely performed in metformin-treated diabetic patients with a preexisting diabetic peripheral and/or autonomic neuropathy. Once diagnosed, metformin-induced vitamin B12 deficiency should be corrected promptly in such patients in order to counteract the exacerbation of nerve damage and prevent the development or progression of a mixed “diabetic and metformin-induced cobalamin deficiency-related neuropathy”.

³Metformin Usage Index (MUI) is defined as the product of the daily metformin dose (mg) and its duration (yr) divided by 1000. For example, 1000 mg of metformin used for a duration of 1 yr is equivalent to 1 MUI ($1000 \times 1/1000 = 1$ MUI). This criterion applies to patients with type 2 diabetes treated with metformin for at least 6 mo, based on the results from the prospective observational study conducted by Shivaprasad *et al*[45]. H2RAs: Histamine H2-receptor antagonists; HoloTC: Holotranscobalamin; MMA: Methylmalonic acid; MUI: Metformin Usage Index; PPIs: Proton-pump inhibitors.

inexpensive, easy to administer, safe and well tolerated, a personalized approach to meet the need of the individual patient is generally deemed as harmless[5].

Synthetic vitamin B12 has long been available in the form of cyanocobalamin, both for oral and injectable use. Subsequently, naturally occurring forms of vitamin B12 have become commercially available, including hydroxycobalamin, methylcobalamin and adenosylcobalamin[67]. Hydroxycobalamin is commonly used in Europe at intervals of approximately 2-3 mo, as it appears to have better retention than cyanocobalamin[5]. Oral and intramuscular routes of vitamin B12 administration are frequently used for treatment of vitamin B12 deficiency. The efficacy of alternative routes of vitamin B12 administration (*e.g.*, intranasal or sublingual administration) to treat vitamin B12 deficiency has also been reported[68,69]. Indeed, a recent 12-wk randomized intervention trial showed that sublingual administration of 50 μ g/d cyanocobalamin restored adequate serum concentrations of vitamin B12 in vegans and vegetarians with a marginal cobalamin deficiency[69]. After intramuscular injection of cyanocobalamin, about 10%-15% of the total administered dose (*e.g.*, 150 μ g of 1000 μ g) is ultimately retained in the body, primarily through storage in the liver, although a remarkable interindividual variability in vitamin B12 retention capacity has been reported[5,8]. Therefore, intramuscular injection of vitamin B12 in high doses allows for rapid replenishment of body stores of the vitamin. High-dose oral vitamin B12 supplementation is an effective alternative to parenteral treatment (*e.g.*, in patients who do not tolerate intramuscular injections). Approximately 0.5%-4% of an oral vitamin B12 dose is usually absorbed[5]; for example, an oral dose of 1000 μ g will deliver on average 5-40 μ g of vitamin B12[5], which adequately meet the recommended daily intake of vitamin B12.

However, route of administration and duration of treatment primarily depend on the underlying etiology and severity of vitamin B12 deficiency. In subjects with vitamin B12 deficiency caused by malabsorption rather than by inadequate dietary intake, high-dose vitamin B12 administration should be initiated as follows: (1) Intramuscular injection of 1000 μ g of cyanocobalamin or hydroxycobalamin daily or every other day for 1 wk, followed by weekly injections up to 8 wk, and every 3-4 wk afterward; or (2) Oral administration of cyanocobalamin in high daily doses (2000 μ g/d) until remission, and 1000-2000 μ g daily afterward[5]. Conversely, patients who are vitamin B12 deficient because of low dietary intake will require loading with high-dose vitamin B12 to restore tissue levels over 3-4 mo; subsequently, smaller doses of at least 6 μ g/d will generally suffice, as conservation of biliary vitamin B12 is possible *via* the enterohepatic recycling and the physiologically highly efficient reabsorption of biliary vitamin B12[5]. Patients lacking IF (*e.g.*, those with true pernicious anemia) cannot reabsorb the vitamin B12 lost in bile (which varies from 3 μ g/d to 9 μ g/d), and 100-300 μ g of vitamin B12 should therefore be retained monthly to maintain tissue

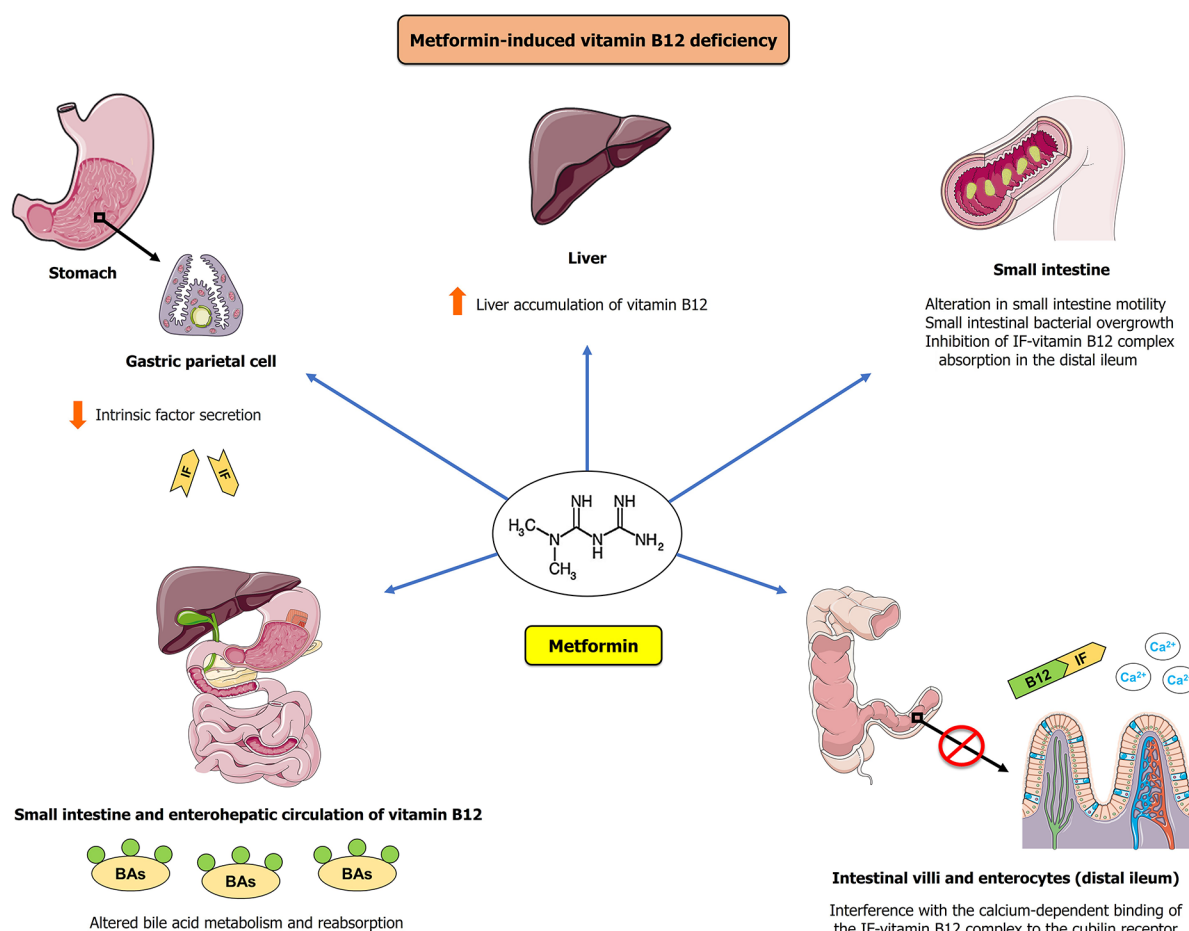


Figure 1 Postulated mechanisms accounting for metformin-induced vitamin B12 deficiency. Metformin may cause vitamin B12 deficiency through one or more of the following mechanisms: (1) Interference with the calcium-dependent binding of the intrinsic factor (IF)-vitamin B12 complex to the cubilin receptor on enterocytes at the ileum level and/or interaction with the cubilin endocytic receptor; (2) Alteration in bile acid metabolism and reabsorption, resulting in impaired enterohepatic circulation of vitamin B12; (3) Reduced IF secretion by gastric parietal cells; (4) Increased liver accumulation of vitamin B12, resulting in altered tissue distribution and metabolism of vitamin B12; and (5) Alteration in small intestine motility, resulting in small intestinal bacterial overgrowth and subsequent inhibition of IF-vitamin B12 complex absorption in the distal ileum. B12: Vitamin B12; BAs: Bile acids; IF: Intrinsic factor.

stores[5]. In this regard, it is worth mentioning that about 1% of oral vitamin B12 can be absorbed in the small intestine through a passive diffusion pathway that is independent of IF and remains unaffected in patients with pernicious anemia[70]. Thus, high oral doses of 1000-2000 µg/d vitamin B12 can meet the estimated daily requirement of 2.4 µg/d even in patients with impaired IF secretion. Notwithstanding, there are arguments against the use of oral vitamin B12 in severely deficient individuals with poor intestinal absorption (particularly in those with pernicious anemia), in whom intramuscular injection may be preferred to assure effective treatment[62]. Further-more, patients with vitamin B12 deficiency presenting with severe neurologic manifestations should be treated by intramuscular injection of 1000 µg of vitamin B12 on alternate days until no further improvement is noted[62]. With regard to the duration of vitamin B12 supplementation, patients with an irreversible cause of vitamin B12 deficiency should be treated indefinitely, and those with a reversible cause should be treated until the deficiency is corrected and the symptoms resolve[8,71]. In the presence of concomitant folate deficiency, vitamin B12 deficiency should be corrected first to prevent subacute combined degeneration of the spinal cord [8,71].

Treatment of metformin-induced vitamin B12 deficiency

According to the British Society for Haematology guidelines for diagnosis and treatment of vitamin B12 deficiency, no recommendations can be currently given on prophylactic administration with oral vitamin B12 in patients using metformin[62]. Despite the lack of definitive guidelines or recommendations on treatment of metformin-induced vitamin B12 deficiency, patients using metformin with concomitant vitamin B12 deficiency should receive cobalamin supplementation aimed to

correct this deficiency and prevent the related risk of peripheral nerve damage and/or other clinical consequences. Importantly, prompt vitamin B12 administration should be considered, particularly in metformin-treated patients with vitamin B12 deficiency accompanied by neurologic and/or hematologic manifestations such as peripheral neuropathy and megaloblastic anemia.

Although treatment of vitamin B12 deficiency in metformin-treated patients may certainly be cost-effective, an issue that still needs to be addressed relies on the fact that the most appropriate repletion method has not yet been clearly defined. As metformin appears to interfere with vitamin B12 absorption in the small intestine through different mechanisms, intramuscular or sublingual routes of administration may theoretically be superior to oral supplementation for treatment of metformin-induced vitamin B12 deficiency through bypassing the gastrointestinal tract and intestinal absorption. However, it is also plausible that high-dose oral vitamin B12 supplementation may be as effective as other routes of administration in overcoming the malabsorption caused by metformin and adequately correcting the cobalamin deficiency. Future studies are therefore warranted to establish the most effective and convenient route of administration of vitamin B12 in metformin-treated patients with concomitant vitamin B12 deficiency. As oral calcium supplementation has been shown to reverse vitamin B12 malabsorption caused by metformin[61], it would also be interesting to investigate whether this therapeutic approach may represent an alternative, safe and effective tool to treat metformin-induced vitamin B12 deficiency.

CONCLUSION

Several recent observational studies and meta-analyses have reported a significant association between long-term metformin therapy and an increased prevalence of vitamin B12 deficiency. The exact mechanisms accounting for vitamin B12 deficiency caused by metformin are still not entirely clear, although it is highly plausible that such mechanisms are related to the impaired vitamin B12 absorption in the small intestine.

Given the high global prevalence of diabetes, which affects more than 460 million people worldwide[72], the widespread use of metformin as an insulin-sensitizing agent for treatment of insulin resistance, prediabetes, T2D and PCOS, as well as the chronic nature of treatment of such conditions, it is important to recognize vitamin B12 deficiency as a potential adverse consequence of long-term and high-dose metformin therapy. As no definite guidelines are currently available for vitamin B12 deficiency screening in metformin-treated patients, this deficiency remains often unrecognized in such individuals.

Therefore, we believe that initial screening and subsequent intermittent periodic testing of vitamin B12 status in selected patients treated with metformin may be cost-effective and should be considered in order to promptly identify and correct vitamin B12 deficiency. In this regard, we have proposed a list of criteria for a cost-effective screening and subsequent intermittent periodic testing of vitamin B12 status in metformin-treated patients who are at high risk for deficiency (Table 2). The criteria include: (1) Strong clinical suspicion of vitamin B12 deficiency; (2) Preexisting diabetic peripheral and/or autonomic neuropathy; (3) Duration of metformin therapy of ≥ 5 years; (4) Age ≥ 65 years; (5) High cumulative metformin exposure defined by a MUI value of > 5 ; (6) A metformin dose of ≥ 1500 mg/d for a duration of at least 6 mo; (7) Concomitant long-term use (≥ 12 mo) of acid-suppressing medications; and (8) Concomitant presence of risk factors or comorbidities associated with an increased risk of vitamin B12 deficiency (reviewed in Table 1). Yet, we acknowledge that these criteria need to be validated in large prospective studies. Further studies are also needed to ascertain the desirable frequency of assessment of vitamin B12 status in patients receiving metformin therapy. Thus, additional research is required to develop protocols for screening, prevention and treatment of metformin-induced vitamin B12.

In patients with metformin-induced vitamin B12 deficiency, vitamin B12 supplementation offers a simple, safe and effective means of preventing the development or the worsening of peripheral nerve damage, anemia and/or other clinical manifestations of vitamin B12 deficiency. To date, there are no specific guidelines for the treatment of vitamin B12 deficiency induced by metformin therapy. Hence, clinicians should correct vitamin B12 deficiency in patients treated with metformin following the British Society for Haematology guidelines for diagnosis and treatment of vitamin B12 deficiency[62]. Likewise, these remarks apply to metformin-treated diabetic patients with preexisting diabetic peripheral and/or autonomic neuropathy who may

experience an exacerbation of nerve damage as well as a substantial deterioration of neuropathy resulting from the concomitant development of MICD. In light of the highly favorable safety and efficacy profile of metformin as an insulin-sensitizing agent, we certainly recommend against discontinuing this drug in patients with newly diagnosed vitamin B12 deficiency. However, it is prudent to periodically assess vitamin B12 status in metformin-treated patients who could remain at increased risk of vitamin B12 deficiency even after an adequate vitamin B12 supplementation.

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Figure 1 was created with images adapted from Servier Medical Art licensed under a Creative Commons Attribution 3.0 (<https://smart.servier.com/>).

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Exploring new treatment options for polycystic ovary syndrome: Review of a novel antidiabetic agent SGLT2 inhibitor

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Abstract

Polycystic ovary syndrome (PCOS) is the most common endocrinopathy in women of reproductive age associated with long-term metabolic and cardiovascular consequences. A plethora of symptoms and their severity differentiate on an individual level, giving the syndrome numerous phenotypes. Due to menstrual cycle abnormalities, women suffer from irregular menstrual bleeding, difficulty in conception, and infertility. Furthermore, the risk of pregnancy complications such as gestational diabetes mellitus, hypertensive disorders of pregnancy, and preterm birth are higher in women with PCOS than in the general population. Often, women with PCOS have comorbidities such as dyslipidemia, obesity, glucose intolerance or diabetes type 2, non-alcoholic fatty liver disease, and metabolic syndrome, which all influence the treatment plan. Historic insulin-sensitizing agents, although good for some of the metabolic derangements, do not offer long-term cardiovascular benefits; therefore, new treatment options are of

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paramount importance. Sodium-glucose co-transporter-2 (SGLT-2) inhibitors, a new class of antidiabetic agents with beneficial cardiovascular, bodyweight, and antihyperglycemic effects, although not approved for the treatment of PCOS, might be an attractive therapeutic addition in the PCOS armamentarium. Namely, recent studies with SGLT-2 inhibitors showed promising improvements in anthropometric parameters and body composition in patients with PCOS. It is important to further explore the SGLT-2 inhibitors potential as an early therapeutic option because of the PCOS-related risk of metabolic, reproductive, and psychological consequences.

Key Words: Polycystic ovary syndrome; Sodium-glucose co-transporter-2 inhibitors; Metabolic risk; Cardiovascular risk; Metabolic syndrome; Insulin resistance; Obesity; Type 2 diabetes mellitus; Dyslipidemia

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Core Tip: Sodium-glucose co-transporter-2 (SGLT-2) inhibitors are a new class of antidiabetic agents with beneficial cardiovascular, bodyweight, and antihyperglycemic effects. Although not approved for the treatment of polycystic ovary syndrome (PCOS), they might be an attractive therapeutic addition for the related metabolic, reproductive, and psychological consequences. Recent studies with SGLT-2 inhibitors in PCOS patients showed promising improvements in anthropometric parameters and body composition. Thus, it is important to explore the SGLT-2 inhibitors potential as an early therapeutic option in PCOS due to its high cardiometabolic risk.

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INTRODUCTION

Polycystic ovary syndrome (PCOS) is a complex condition defined by metabolic, fertility, and psychological consequences, with a prevalence of up to 20% among females of reproductive age[1]. It is diagnosed according to Rotterdam criteria (2 of the following): Oligo- or anovulation, clinical and/or biochemical hyperandrogenemia, or polycystic ovarian morphology on ultrasound[2]. Underlying pathologic processes create a broad spectrum of clinical and laboratory abnormalities. The underlying mechanisms are still inconclusive, however certain genetic traits[3-5], altered gonadotropin secretion[6,7], faulty ovarian follicle maturation[8], and insulin resistance (IR)[9] are considered the most important etiological factors. IR leads to hyperinsulinemia which precipitates hyperandrogenaemia by stimulating ovarian androgen secretion and inhibition of hepatic sex hormone-binding globulin (SHBG) production[10].

A plethora of symptoms and their severity differentiate on an individual level, giving the syndrome numerous phenotypes. Due to menstrual cycle abnormalities, women suffer from irregular menstrual bleeding, difficulty in conception, and infertility. Furthermore, the risk of pregnancy complications such as gestational diabetes mellitus, hypertensive disorders of pregnancy, and preterm birth are higher in women with PCOS than in the general population[11,12].

Although cardiometabolic risk factors are not part of the PCOS diagnostic criteria, they impact the treatment and prognosis[13]. Metabolic issues related to PCOS increase the risk for long-term consequences such as dyslipidemia, obesity, glucose intolerance[14], diabetes type 2[15-17], low-grade chronic inflammation[18], non-alcoholic fatty liver disease[19,20] and metabolic syndrome[21,22]. Consequently, all women with PCOS should be assessed for cardiovascular risk factors and global cardiovascular disease risk[2].

Treatment goals for PCOS include diminishing clinical hyperandrogenism, managing menstrual dysfunction, preventing endometrial hyperplasia and carcinoma, accomplishing ovulation in pursuit of pregnancy, and regulating metabolic issues in the long term. Lifestyle changes and weight loss are the cornerstones of treatment[23]. Oral contraceptives (OCs) are the first line of PCOS pharmacotherapy due to their effect on hyperandrogenism, menstrual irregularity, and endometrial carcinoma prevention[2,24]. In cases of prevalent hyperandrogenism despite OCs, antiandrogens can be added. When pursuing pregnancy, ovulation induction should be considered with clomiphene citrate, letrozole, and, rarely, gonadotropins[25]. If weight loss and ovulation induction are not successful, the next step is *in vitro* fertilization.

In the case of metabolic derangements, insulin-sensitizing agents, primarily metformin and thiazolidinediones, are widely used as an alternative or add-on to OCs [26,27]. Studies of newer glucose-lowering agents, such as glucagon-like peptide-1 receptor analogs (GLP-1RA) used for the treatment of obese women with PCOS, revealed a reduction of body weight, increase in menstrual frequency, and improvement of hyperandrogenemia and metabolic derangements even more effectively than metformin[28,29]. The down-side of the mentioned therapy might be a subcutaneous way of application.

PCOS AND CARDIOMETABOLIC RISK

One of the most important pathophysiological processes involved in PCOS development includes IR. The prevalence of IR in PCOS is high: it affects 75% of lean and 95% overweight women[30]. IR represents a link towards increased cardiometabolic risk leading to conditions such as hypertension, glucose intolerance or diabetes, dyslipidemia, and obesity[9,31].

Up to 70% of PCOS women demonstrate IR, glucose intolerance, and overt diabetes [32]. An American study on Women's Health Across the Nation showed a higher prevalence of impaired glucose tolerance (IGT) in PCOS (25%) compared to controls (9.2%)[33]. Moreover, a recent meta-analysis in women with PCOS demonstrated an increased prevalence of type 2 diabetes (T2DM) (odds ratio = 2.87, 95% CI: 1.44-5.72) [34]. Interestingly, 15%-36% of all T2DM diagnosed in women, irrespective of age, is found in association with PCOS. Women with PCOS often exhibit insulin secretory impairment, which accelerates the progression from IGT to T2DM 5 to 10-fold compared to the non-PCOS population, leading to prevalence rates of T2DM 5 to 7-fold higher than those reported in population-based studies of women aged 20-44 years[15,35].

In addition, dyslipidemia occurs in up to 70% of women with PCOS, most commonly characterized by high triglyceride, increased small dense LDL-C levels, and low HDL-C levels[36]. Obesity is also highly prevalent in PCOS; up to 60% of women with PCOS have body mass index (BMI) in the overweight or obesity range, which predisposes them to IR, gonadotropin secretion disturbances, hyperandrogenemia, and low SHBG secretion[37-39]. Consequently, metabolic syndrome is commonly found in women with PCOS (prevalence of 33%-47% in the United States, and 8%-25% in other countries)[36].

According to the recent guidelines, all women with PCOS should be screened for cardiovascular risk factors. Androgen Excess and Polycystic Ovary Syndrome (AE-PCOS) Society recommends categorizing PCOS related cardiovascular disease (CVD) risk as patients at risk (PCOS patients with obesity, cigarette smoking, hypertension, dyslipidemia, subclinical vascular disease, IGT, family history of premature CVD) or high risk (PCOS patients with metabolic syndrome, diabetes mellitus or overt vascular/renal disease)[36].

ROLE OF SGLT-2 INHIBITORS IN PCOS

Multiple metabolic disorders are well recognized among PCOS patients, so assessing the glycemic status is essential. If IGT is detected, lifestyle interventions together with insulin-sensitizing agents such as metformin and thiazolidinedione can be added to improve insulin sensitivity[31]. There are no dedicated metformin studies to confirm its effects on superior BMI reduction compared to placebo or decrease in central adiposity, a good marker for metabolic syndrome[26,27]. Incretins, primarily GLP-1RAs, have the potential to overcome metabolic derangements of PCOS and adding cardiovascular benefits. However, their use is limited by the need for subcutaneous

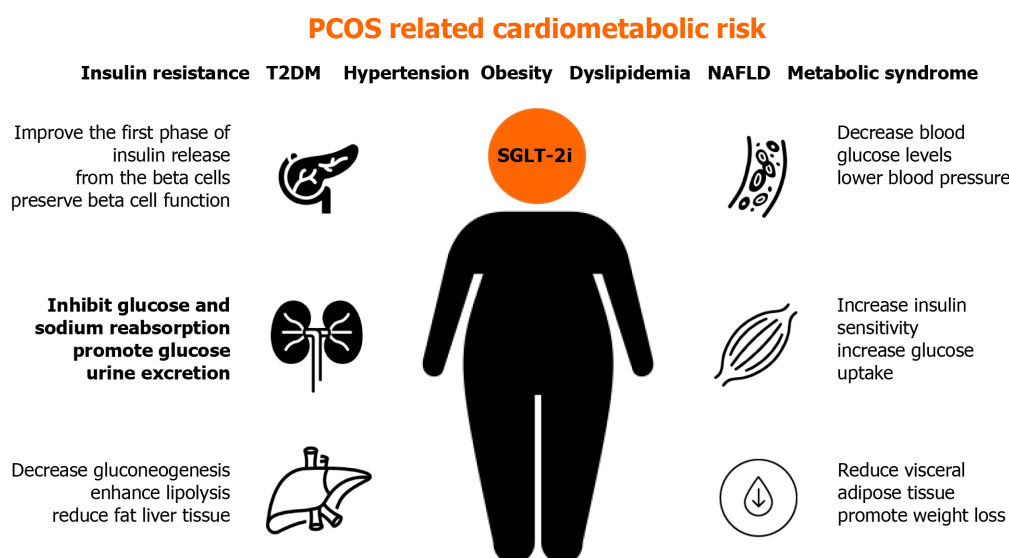


Figure 1 Potential benefits of sodium-glucose co-transporter-2 inhibitors in treatment of different metabolic and cardiovascular features of polycystic ovary syndrome. NAFLD: Non-alcoholic fatty liver disease; PCOS: Polycystic ovary syndrome; SGLT-2i: Sodium-glucose co-transporter-2 inhibitors; T2DM: Type 2 diabetes.

application, while dipeptidyl peptidase-4 inhibitors, oral incretin therapy, lack the evidence of cardiovascular protection in recently published dedicated CVOTs[40]. Therefore, there is still a considerable demand for safe and effective therapeutic agents, offering solutions against PCOS's metabolic dysregulation.

Although SGLT-2 inhibitors are not approved for PCOS treatment, this class of antidiabetic drugs could be useful for PCOS patients due to beneficial glycemic and cardiovascular effects, which are often an issue in women affected by PCOS[41] (Figure 1).

SGLT receptors are not found on ovaries, but their inhibition can indirectly improve metabolic status disrupted in certain PCOS patients. The role of SGLT-2 inhibitors in the treatment of PCOS is not yet well studied. Their mode of action can contribute to several pathophysiologic disorders in PCOS, including previously mentioned IR, hypertension, obesity, and dyslipidemia. By binding to SGLT-2 receptors in the proximal convoluted tubule of the kidney, gliflozins inhibit glucose and sodium reabsorption, causing a decrease in blood glucose levels, glucosuria, and natriuresis, which contributes to lowering blood pressure. Gliflozins promote glucose urine excretion by 60-80 g per day (approximately 240-320 kcal/d), promoting weight loss by approximately 1.7 kg. The action of SGLT-2 inhibitors does not depend on insulin secretion, beta-cell function, or IR[42,43].

SGLT-2 inhibitors achieve a further reduction in blood glucose levels by increasing insulin sensitivity, increasing glucose uptake in the muscle, decreasing gluconeogenesis in the liver, and improving the first phase of insulin release from the pancreatic beta-cells.

All mentioned processes improve metabolic profiles in diabetic patients, including lipid levels and serum uric acid levels, which could also be beneficial for PCOS patients[44]. Research also suggests the role of SGLT-2 inhibitors in preserving beta-cell function by indirectly reducing insulin secretion and promoting glucagon secretion. The latter plays a role in enhancing lipolysis and reducing the liver and visceral adipose tissue[45].

Besides the expected effect of SGLT-2 inhibitors on glycemic control, they are also shown to be cardioprotective[46], which is an important benefit regarding an increased risk of cardiovascular disease in PCOS.

So far, only one randomized controlled trial compared the effects of empagliflozin (25 mg) *vs* metformin (1500 mg) on anthropometric and body composition, hormonal and metabolic parameters in 39 women with PCOS. Group treated with empagliflozin showed beneficial effects on weight, BMI, waist circumference and hip circumference, and total body fat in overweight and obese women with PCOS compared to metformin, but no differences were seen in hormonal and metabolic parameters, including IR and androgen levels[47]. The study comparing the effects of another SGLT-2 inhibitor, canagliflozin *vs* metformin in PCOS, is still underway (Clinical Trial Gov Identifier: NCT04700839).

CONCLUSION

Until more research confirms the positive metabolic effect of SGLT-2 inhibitors in PCOS patients, the mainstream treatment option will be lifestyle intervention, metformin, and oral contraceptive pills[24]. However, this treatment strategy does not successfully address long-term cardiometabolic consequences of PCOS[48], so SGLT-2 inhibitors, due to their mode of action, emerge as a potential new treatment option for PCOS.

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Role of interferons in diabetic retinopathy

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Abstract

Diabetic retinopathy (DR) is one of the major causes of visual impairment and irreversible blindness in developed regions. Aside from abnormal angiogenesis, inflammation is the most specific and might be the initiating factor of DR. As a key participant in inflammation, interferon-gamma (IFN- γ) can be detected in different parts of the eye and is responsible for the breakdown of the blood-retina barrier and activation of inflammatory cells and other cytokines, which accelerate neovascularization and neuroglial degeneration. In addition, IFN- γ is involved in other vascular complications of diabetes mellitus and angiogenesis-dependent diseases, such as diabetic nephropathy, cerebral microbleeds, and age-related macular degeneration. Traditional treatments, such as anti-vascular endothelial growth factor agents, vitrectomy, and laser photocoagulation therapy, are more effective for angiogenesis and not tolerable for every patient. Many ongoing clinical trials are exploring effective drugs that target inflammation. For instance, IFN- α acts against viruses and angiogenesis and is commonly used to treat malignant tumors. Moreover, IFN- α has been shown to contribute to alleviating the progression of DR and other ocular diseases. In this review, we emphasize the roles that IFNs play in the pathogenesis of DR and discuss potential clinical applications of IFNs in DR, such as diagnosis, prognosis, and therapeutic treatment.

Key Words: Interferons; Cytokines; Diabetic retinopathy; Interferon-alpha; Interferon-gamma; Inflammation

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Core Tip: Diabetic retinopathy (DR) is one of the microvascular complications of diabetes mellitus and seriously threatens the eyesight of the working-age population. Inflammation and inflammatory cytokines are closely related with its pathological mechanisms. Here we discuss the roles of interferons in DR, mainly from the pathogenesis and clinical applications.

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INTRODUCTION

Diabetes mellitus has reached epidemic proportions globally and affects the health of populations in both developing and developed countries[1]. Diabetic retinopathy (DR) has been recognized as a neurovasculopathy of diabetes and is a leading cause of blindness in populations of 20-74 years old in many developed countries[2-4], accounting for 2.6% of blinding cases around the world[5]. Nearly 30% of diabetic patients develop into DR[6], and once the course of diabetes extends beyond 15 years, DR can occur in almost 98% of patients with type 1 diabetes (T1D) and more than 80% of patients with type 2 diabetes (T2D)[7]. Similarly, the chance of developing sight-threatening DR is higher in T1D patients (11%) than in T2D patients (3%)[8].

Clinically, DR is classified into two stages based on microvascular changes: Non-proliferative (also known as simple or background) DR (NPDR) and end-stage proliferative DR (PDR)[9]. The former is characterized by vascular tortuosity, retinal hemorrhages, microaneurysms, yellow-white hard exudations, and white cotton spots [10]. As the final phase of DR, PDR leads to severe and quick vision impairment, which is featured by aberrant neovascularization, preretinal or vitreous hemorrhages, epiretinal membrane, and tractional detachment of the retina[11,12]. To diagnose DR, fundus photography, optical coherence tomography (OCT), and fundus fluorescein angiography (FFA) are often used to measure vascular abnormalities in the retina, such as retinal blood vessel permeability and thickness[13].

Intensive control of related risk factors, such as blood glucose, blood pressure, smoking, and pregnancy, is the typical method to minimize the progression of lesions, especially in the early stage[14,15]. Anti-vascular endothelial growth factor (anti-VEGF) medications, laser photocoagulation therapy, intravitreal injections of corticosteroids, and vitreoretinal surgery are mainly used to treat DR, especially in the advanced stage[16-18]. These methods are effective in inhibiting pathological vascular proliferation, reducing diabetic macular edema (DME), and saving eyesight[19-21]. However, these methods are restricted by a short therapeutic half-life and the risk of attendant adverse reactions, such as injection site bleeding, increased intraocular pressure, endophthalmitis, loss of peripheral vision, accelerated cataract formation, and retinal detachment[22]. Consequently, detection during the early stage of DR (NPDR) is the most effective way to prevent further worsening of DR and improve treatment and prognosis.

It is well known that inflammation participates in the early phase of DR and plays an important role in DR pathogenesis. Thus, exploring the associated mechanisms of inflammation is essential to many aspects of DR, such as diagnosis, prognosis, and therapeutic treatment. In this review, we mainly summarize the crucial roles of interferons (such as IFN- γ and IFN- α) in DR pathogenesis and discuss the potential clinical applications for patients with DR.

INFLAMMATION IN DR PATHOGENESIS

To date, the mechanisms and pathogenesis of DR remain unclear. There is a consensus that DR is the result of the interactions of multiple pathways. Hyperglycemia, ischemia- and hypoxia-induced retinal microangiopathy, inflammation and leukocyte stasis, and retinal neurodegeneration are the main causes of DR[23-25], as well as oxidative stress, mitochondrial dysfunction, microRNAs, and other molecular mecha-

nisms[26-28]. Microvascular changes, such as the loss of pericytes, increased permeability, and vasoregression, lead to retinal ischemia/hypoxia through the upregulation of biological factors, such as hypoxia-inducible factor 1 (HIF-1), VEGF, and inducible nitric oxide synthase, which play crucial roles in aberrant neovascularization[29,30].

Although abnormal neovascularization is the most characteristic change in lesions, altered inflammation occurs before the development of microvascular lesions[31,32]. Leukocyte stasis, neutrophil and macrophage infiltration, complement and microglial activation, cytokine upregulation, and increased chemokine synthesis occur in the retina[11,33]. Studies have shown a reciprocal relationship between inflammation and angiogenesis[34]. To a certain extent, the onset of DR relies on the release of proinflammatory cytokines and the adhesion of leukocytes to retinal capillaries[35]. Moreover, accumulating evidence has shown that treatments to inhibit the inflammatory reaction, such as intravitreal steroids, interleukin-6 (IL-6) inhibitors, IL-6 receptor inhibitors, and integrin inhibitors, are effective in preventing the development and worsening of DR[6,23].

The upregulation of inflammatory cytokines, such as IFN- γ , IL-1 β , IL-6, and IL-10, is the primary contributor to persistent low-grade inflammation[36], which can increase vascular permeability, accelerate the progression of DME, and increase angiogenic responses of endothelial cells (ECs)[37,38]. As a proinflammatory cytokine, IFN- γ can be found in different parts of the eye in DR, such as tears[39], aqueous humor[40,41], vitreous fluids[42-45], and serum[46-48], even during the early stage of DR. Moreover, clinically significant differences exist between DR and diabetes without retinopathy (DNR), or between PDR and NPDR, suggesting that IFN- γ is closely related to the occurrence and development of DR. Therefore, similar to other substances, such as hemoglobin A1c (HbA1c), VEGF, complement component C3, intercellular adhesion molecule 1, and IL-6[49-51], IFN- γ may be a potential candidate biomarker of DR and greatly contribute to diagnosis, treatment, and prognosis.

According to existing studies, IFN- γ and IFN- α are involved in DR. IFN- α induces a marked effect on not only DR, but also the pathological processes of other ocular and systematic diseases, such as conjunctival papilloma, uveitis, HIV infection, central nervous system diseases, and malignant tumors, due to its important role in innate and adaptive immunity[52-56]. Moreover, IFN- α can cause associated ocular pathology-siological changes, such as endophthalmitis and neovascularization of the retina, when used to treat diseases of the eye or other systematic dysfunctions, such as serpiginous choroidopathy and hepatitis C[57,58].

IMMUNOLOGICAL REGULATION OF IFNS

As discussed above, IFNs might be involved in the inflammation and pathogenesis of DR. The activity of IFNs was first discovered in 1957 by Isaacs and Lindenmann[59]. IFNs are a group of glycoproteins that are synthesized and secreted by almost all cells in mammals and after stimulation by specific antigens[60]. IFNs are an endogenous family of cytokines with pleiotropic antiviral, antiproliferative, and immunomodulatory properties that play important roles in host defense mechanisms and maintaining homeostasis[54,61]. According to the cell surface receptors to which they bind, IFNs can be classified into three main families: Types I, II, and III[62]. There are various kinds of type I IFN, IFN- γ is the only type II IFN, and type III IFN consists of four molecules[63,64]. Clinically, IFNs are widely used, and each type has specific indications, such as the use of IFN- α for leukemia and melanoma and IFN- β for multiple sclerosis[65-67].

Regarding the molecular mechanisms, highly coordinated signaling events composed of viral sensors, adaptor proteins, kinases, and transcription factors can activate IFN transcription[61]. Currently, the mechanisms by which IFNs affect viruses, tumors, or other diseases are not completely understood. The Janus kinase signal transducer and activator of transcription (JAK/STAT) pathway is strongly associated with IFN signaling in viral infections[68]. Meantime, Gysemans *et al*[69] found that STAT-1 is a pivotal factor that controls the death of beta-cells and the accompanying immune-mediated diabetes. Once viral sensors such as pattern recognition receptors recognize viral proteins and nucleic acids and detect viral genes, adaptor proteins initiate a signal transduction cascade that leads to the formation of transcription factors and IFN I/III. The secreted IFNs act in an autocrine and paracrine manner. Then, the infected cells activate the JAK/STAT pathway and accelerate the expression of IFN-stimulated genes (ISGs)[70,71]. ISGs encode antiviral effectors or

molecules that are engaged in a wide array of cellular functions[72]. Additionally, ISGs regulate IFN signaling both positively and negatively[61]. For example, ISGs modulate viral replication (OAS/RNase L, ADAR, CD74, and GBP family members), viral entry (IFITM1/2/3, MOV10, and ZAP), protein translation (MB21D1, DDIT4, PKR, and MAP3K14), and viral egress (BST2/tetherin and RSAD2)[73]. Moreover, IFN- α can upregulate the expression of major histocompatibility complex (MHC) class I molecules as well as inflammation and endoplasmic reticulum stress markers in β cells and induce β cell apoptosis with IL-1 β [74]. IFN- γ upregulates MHC class I and MHC class II molecules, which can increase the susceptibility of infected cells to lysis by cytotoxic T lymphocytes[75,76].

In this review, we highlight the relationship between DR and IFN- α or IFN- γ , elaborating on their key roles in DR.

IFN- γ IN DR

IFN- γ is the only type II IFN and is released by T helper 1 lymphocytes, natural killer cells, natural killer T lymphocytes, and CD8+ T cells[77]. IFN- γ can inhibit cell proliferation, modulate the activity of cytotoxic T cells, stimulate the biosynthesis of other cytokines, and is closely associated with innate and adaptive immunity[78-80]. In addition, IFN- γ and IFN- α can upregulate the expression of programmed death-ligand 1 in pancreatic β cells in the context of T1D, which may exert protective effects to resist T cell-mediated β cell apoptosis[81].

It is well documented that inflammation is a central driver of capillary occlusion and hypoxia, which can maximize the expression of VEGF[82]. IFN- γ plays a role in the etiology of DR due to its inflammatory functions. Numerous studies have improved the understanding of the relationship between IFN- γ and DR: (1) The concentration of IFN- γ is increased in tears in DR compared with those in DNR and the ratios of anti-angiogenic and angiogenic cytokines, such as IFN- γ /MCP and IFN- γ /IL-8 are decreased[39], suggesting the formation of an angiogenic environment; (2) The level of IFN- γ is higher in the aqueous humor in DR than in DNR[40,41]; and (3) The concentrations of IFN- γ in serum and vitreous fluids in DR are significantly higher than those in DNR or DM[42,45-47] (Tables 1 and 2). These studies all provide evidence that IFN- γ promotes and sustains chronic inflammation in the diabetic retina, which can result in neuro-glial degeneration, activation of inflammatory cells, vascular dysfunction, and breakdown of the blood-retina barrier (BRB)[50,83]. In addition, IFN- γ seems to be correlated with blood glucose. It has been found that IFN- γ was significantly increased in uncontrolled T2D or patients diagnosed with T2D recently but without treatment compared with patients who received effective glucose-lowering treatment[84,85]. IFN- γ is closely correlated with systolic blood pressure, platelets, mean platelet volume (MPV), and platelet distribution width (PDW)[85], which can be used to predict microvascular complications in diabetes[85,86]. The pathological changes mediated by IFN- γ not only exist in the retina, but also occur in the cornea and vitreous.

As essential parts of innate immunity, macrophages have two primary phenotypes: M1 and M2. The balance between these two phenotypes is controlled by macrophage phenotypic plasticity, inflammatory modulators, and the activity of intracellular signaling mediators and transcription factors[87]. M1 macrophages release inflammatory cytokines, such as tumor necrosis factor alpha (TNF- α), IL-1, IL-6, IL-12, type I IFN, and proteases and perform phagocytosis, while M2 macrophages perform phagocytosis and tissue repair and remodeling, and generate chemokines and anti-inflammatory cytokines such as transforming growth factor- β (TGF- β) and IL-10[76,88,89]. In DR, M1 macrophages inhibit angiogenesis and mediate inflammation, while M2 macrophages are involved in abnormal neovascularization. M1 polarization can be induced by IFN- γ [90]. Hence, IFN- γ may mediate the pathogenesis of DR by modulating the polarization of macrophages. Moreover, we know that IL-12 participates in the process of anti-angiogenesis in many diseases, such as corneal neovascularization and tumors[91,92]. Zhou *et al*[93] showed that IL-12 could mediate and inhibit pathological neovascularization in a mouse model of oxygen-induced retinopathy through the downstream molecules IP-10 (CXCL10) and MIG (CXCL9), which are mainly induced by IFN- γ . Importantly, the study demonstrated that the intravitreal injection of recombinant IL-12 did not significantly decrease the expression of VEGFA or fibroblast growth factor-2 (FGF2), which suggests that the mechanisms of IL-12 are independent of VEGFA and FGF2[93].

Table 1 Expression of interferons in samples

Source	Condition of disease	Expression
Tears	DR	(IFN- γ) $\uparrow\uparrow$, (IFN- γ /MCP-1) \downarrow , (IFN- γ /IL-8) \downarrow [39]
	DNR	(IFN- γ) \uparrow [39]
Aqueous humor	PDR	(IFN- γ) $\uparrow\uparrow$ [40]
	NPDR	(IFN- γ) \uparrow [40]
	DR	(IFN- γ) $\uparrow\uparrow$ [41], (IFN- α) $\downarrow\downarrow$ [117,118]
	DNR	(IFN- γ) \uparrow [41], (IFN- α) \downarrow [117,118]
Vitreous fluids	DR	(IFN- γ) \uparrow [42]
	DM	(IFN- γ) \uparrow [45]
Serum	DR	(IFN- γ) $\uparrow\uparrow$ [46]
	DNR	(IFN- γ) \uparrow [46]
	DM	(IFN- γ) \uparrow [47,48]
Plasma	DM	(IFN- α) \uparrow , (IFN- β) \uparrow [113]
Retina	DR	(IFN- β) \uparrow [115]

DR: Diabetic retinopathy; DNR: Diabetes without retinopathy; PDR: Proliferative diabetic retinopathy; NPDR: Non-proliferative diabetic retinopathy; DM: Diabetes mellitus; IFN: Interferons.

Table 2 Concentration of interferons in patient samples

IIFNs	Source	Condition of disease	Concentration
IFN- γ	Tears (multiplex bead analysis)	Controls	1463.0 \pm 158.8 (pg/mL)[39]
		DNR	1612.8 \pm 228.2 (pg/mL)[39]
		DR	1957.50 \pm 166.1 (pg/mL)[39]
	Aqueous humor (CBA)	Controls	60.29 \pm 14.17 (pg/L)[40]
		DNR	54.96 \pm 16.29 (pg/L)[40]
		NPDR	114.26 \pm 50.76 (pg/L)[40]
		PDR	136.36 \pm 35.55 (pg/L)[40]
	Vitreous fluids (ELISA)	Controls	3.83 \pm 0.80 (pg/mL)[42]
		DR	6.25 \pm 0.84 (pg/mL)[42]
	Serum (ELISA)	Controls	2.9 (pg/mL)[46]
		DNR	27.8 (pg/mL)[46]
		DR	56.8 (pg/mL)[46]
IFN- α	Aqueous humor (Bio-Plex pro tm magnetic color-bead-based multiplex assay)	Controls	26.2 (0-84) (pg/mL)[117]
		DNR	0 (0-20) (pg/mL)[117]
		DR	0 (0-18) (pg/mL)[117]

Data are expressed as the mean \pm SEM or median (range). DNR: Diabetes without retinopathy; DR: Diabetic retinopathy; NPDR: Non-proliferative diabetic retinopathy; PDR: Proliferative diabetic retinopathy; CBA: Cytometric bead array technique; ELISA: Enzyme linked immunosorbent assay; IFN: Interferons.

In addition, IFN- γ is involved in other microcirculatory damage in diabetes. Taylor *et al*[94] showed that the proinflammatory cytokine IFN- γ and abnormal IFN- γ signaling were responsible for microglial repair of microvascular injuries and cerebral microbleeds (CMBs) in T1D through the downregulation of *P2ry12* gene expression, which decreased the accumulation and polarization of microglia. In addition, many other studies have shown that overexpressed IFN- γ was blood-derived, and entered

the brain through the injured blood-brain barrier to bind to highly-expressed IFN- γ receptors 1 and 2 on microglia[95,96]. Du *et al*[97,98] reported that IFN- γ played a protective role in the kidney in type II diabetes and could inhibit the excessive accumulation of mesangial matrix by activating the JAK2/STAT pathway, which could suppress the high glucose-induced increase in TGF- β 1 and collagen IV. In addition, IFN- γ can impair renal fibrosis by inhibiting fibroblast activation and proliferation and reducing collagen synthesis[99].

Additionally, IFN- γ is involved in other neovascularization diseases, such as ischemia, clearance of malignant tumors, and age-related macular degeneration (AMD). IFN- γ plays a central role in the pathogenesis and development of AMD, which is characterized by retinal cell atrophy and choroidal neovascularization in the macula[100]. On the one hand, IFN- γ accelerates pathological progression: (1) IFN- γ selectively promotes M1 macrophage polarization through increased secretion of IFN-regulatory factors (IRFs), such as IRF-1, IRF-5, and IRF-8[101,102], and the activation of nuclear factor- κ B and STAT-1[87], which can increase the secretion of inflammatory cytokines, such as IL-1 β , IL-6, and TNF- α [89,103]; and (2) IFN- γ independently upregulates VEGF in retinal pigment epithelial cells through the activation of the PI-3K/Akt/mTOR/p70 S6 kinase pathway[104]. On the other hand, IFN- γ mediates protective effects in AMD: It downregulates the functions of VEGF in ECs by inhibiting necessary genes that are indispensable for VEGF bioprocessing and upregulates IL-1 receptor antagonist[105-107].

The role of IFN- γ in angiogenic diseases is inconsistent. On the one hand, IFN- γ can prevent and slow the development of vascular proliferation by increasing the proportion of M1 macrophages, and recombinant IFN- γ can reduce pathological choroidal neovascularization in a dose-dependent manner[108]. On the other hand, IFN- γ accelerates angiogenic process by increasing the expression of VEGF and upregulating other inflammatory cells and cytokines. Further studies are needed to investigate the mechanisms by which IFN- γ affects DR pathogenesis.

IFN- α IN DR

For many years, approaches to cure DR primarily included anti-VEGF agents, anti-inflammatory therapy, photocoagulation, vitrectomy, and controlling related risk factors[23,109]. With further research on DR, many novel discoveries of new targets and methods are constantly occurring, such as neuroprotective substances (somatostatin and brimonidine), polyphenols, the Tie-2 activator AKB 9778, small interfering RNAs (bevasiranib and PF04523655), encapsulated cell technology, and small intraocular pumps[109,110]. These new interventions can be applied to patients who are resistant to traditional therapies or have severe side effects.

As a type I IFN, IFN- α functions against infection, neoplasms, and immunity[111]. IFN- α is involved in the early stage of β cell death in T1D for its autoimmune ability[112], because IFN- α is markedly increased in the plasma of individuals with T1D, and inhibition of IFN- α / β receptor 1 and antibody against IFN- α can reduce the occurrence of T1D[113,114] (Table 1). Additionally, IFN- β is highly expressed in the retina of DR rats[115] (Table 1). Gerber *et al*[116] showed that IFN- α increased the expression of HIF-1 α in a dose- and time-dependent manner by activating JAK1, tyrosine kinase 2, and IFN-stimulated gene factor 3, which inhibit the proliferation of vascular ECs. Priming with IFN- γ followed by IFN- α can enhance the magnitude and duration of HIF-1 α . Among 13 human IFN- α subtypes[55], IFN- α 2 has been shown to have a therapeutic effect in a wide range of ophthalmological dysfunctions involving both the anterior and posterior segments of the eye[57] (Table 3). Moreover, it has been reported that IFN- α in the aqueous humor was more unmeasurable in diabetic patients than in non-diabetic patients, and its median level was decreased in turn among nondiabetic patients, DNR patients, and DR patients, suggesting that an imbalance in immune function may be involved in the pathogenesis of DR[117,118] (Table 2).

IFN- α 2a can suppress intraocular inflammation, possibly by helping regulatory T cells restore their inhibitory functions[119]. After subcutaneous injection of 6 million/IU IFN- α 2a 3 times/wk for an average of 10 mo, patients with PDR were found to have obvious improvements in visual acuity, decreased leakage of vessels, and regression of neovascularization after complete laser panretinal photocoagulation (PRP)[120]. Chronic drug use of recombinant IFN- α 2a for PDR presented certain clinical value because regression of capillary tufts and no new hemorrhage or neovascularization were found in patients during treatment[121]. Refractory DME was cured

Table 3 Applications of interferon- α in ocular disorders

IFN	Clinical applications
IFN- α -2a	Ocular surface diseases: Tumors (such as limbal conjunctival melanoma, squamous neoplasias, and conjunctival MALT lymphoma)[134, 137]; Mooren's ulcers[138]; herpes simplex keratitis[139] Uveal disease: Behcet's uveitis[131]; serpiginous choroiditis[140]; choroidal neovascularization[141]; HHV-8-associated uveitis[142]; chronic noninfectious posterior uveitis[143] Macular and retinal disorders: Uveitic CME; angiogenesis after PRP; refractory non-infectious inflammatory macular edema[144]
IFN- α -2b	Ocular surface diseases: Tumors (such as squamous cell carcinoma[145], melanocytic tumors[145], CIN[146], conjunctival papillomatosis [147], and MALT lymphoma[57]); LSCD[135]; vernal keratoconjunctivitis[132] Uveal disease: Metastatic uveal melanoma[148]; Behcet's uveitis[149] Macular and retinal disorders: CME caused by intraocular infection[150]; refractory diabetic macular edema[133]
IFN- α -2	Dendritic keratitis[151]

MALT: Mucosa-associated lymphoid tissue; HHV-8: Human herpes virus 8; CME: Cystoid macular edema; PRP: Panretinal photocoagulation; CIN: Conjunctival and corneal intraepithelial neoplasia; LSCD: Limbal stem cell deficiency; IFN: Interferons.

by IFN- α 2a at a dose of 1 million IU/mL 3 times/wk through posterior subtenon injections, and IFN- α 2a could be effective in reducing central macular thickness and improving visual acuity[122]. There are few cases of clinical use of IFN- α 2a in the treatment of DR, thus criterion of when and how to implement and evaluate the therapeutic effect of IFN- α 2a is not unified now, which needs further exploration. Based on clinical experience, clinicians can choose appropriate intervals to review the progression of the disease, such as glucose metabolism index, vision, visual field, neovascularization, and fundus examination. There is hardly any evidence that IFN- α 2b is able to treat DR. Moreover, the susceptibility to and risk for retinopathy are increased after clinicians use IFN- α as a therapeutic method for chronic hepatitis C [123,124], which is known as IFN-associated retinopathy (IAR). Recent guidelines indicate IFN-based therapy (pegylated IFN plus ribavirin) as a first-line method in treating chronic HCV patients[125]. Although this therapeutic plan is effective for most patients, it inevitably has some side effects, including adverse ophthalmological effects. Cotton-wool spots and retinal hemorrhage are the most common symptoms in patients with IAR[126], but these patients rarely exhibit decreased visual acuity and subjective symptoms[58,127]. The potential mechanism of IAR involves IFN- α -induced deposition of immune complexes in the retinal vasculature, which can lead to ischemic changes in the retina, such as occlusion of retinal capillaries, cotton-wool spots, and retinal hemorrhage[128]. Furthermore, another study explained that glucose tolerance was obviously improved by treatment with recombinant IFN- α in both nondiabetic and diabetic HCV patients[129].

IFN- α 2a is a promising treatment for DME and DR, because it can assist in preventing vision deterioration, inhibiting active neovascularization, and promoting the barrier function of ECs in the retina[64]. According to existing clinical records, the clinical effect of IFN- α 2a was only observed in patients after PRP and those with active neovascularization but not meeting the criteria of PRP treatment[120-122]. However, the therapeutic effect of IFN- α is not widely demonstrated by clinical trials and studies, and there are side effects and risks of using IFN- α , such as flu-like symptoms and increased liver enzymes[130]. In addition, the functions of IFN- α in DM and DR seem to be contradictory. On the one hand, the overexpression of IFN- α can result in the onset of T1D; on the other hand, IFN- α has the potential to treat DR and DME and help pancreatic β cells resist T cell-mediated apoptosis. Hence, more studies are needed to estimate the therapeutic effect of IFN- α .

IFN- α is also used in many other ocular disorders, such as uveitis[131], vernal keratoconjunctivitis[132], and refractory DME[133]. In cases of conjunctival melanomas and ocular surface squamous neoplasia (OSSN), intralesional IFN- α 2a injection before surgery exhibited excellent results in reducing size and vascularity, defining tumor margins, and improving prognosis[134]. The combined use of IFN- α 2b and all-trans retinoic acid is effective in patients with partial limbal stem cell deficiency (LSCD)[135]. Topical and subconjunctival administration of IFN- α 2b exhibits good effects in controlling and preventing the recurrence of OSSN, and the adverse effects of IFN- α 2b are less severe than those of 5-fluorouracil and mitomycin C[136]. To date, there have been few reports about the role and expression of other IFNs in DR, which

deserves to be further investigated.

POTENTIAL APPLICATIONS OF IFNS IN DR

So far, DR diagnosis mainly depends on clinical manifestations. Many types of technologies are utilized to observe specific pathological changes, such as funduscopy, FFA, and OCT. Besides, some indexes, such as HbA1c and VEGF, have also been suggested for the diagnosis, treatment, or prognosis of DR.

Inflammation is thought to be an initial event in DR. IFN- γ contributes to inflammation and is involved in the early stage of DR and other microvascular lesions associated with mellitus, such as those in kidney and brain tissues. IFN- γ is tied to indices like MPV, PDW, and blood sugar, which can predict microvascular complications of DM. And a positive correlation exists between IFN- γ and HbA1c% [48,85] and inflammatory cytokines, such as IL-1 β and IL-3 [47]. Besides, compared with blood glucose and hemoglobin, IFN- γ has the advantage of being less susceptible to dietary changes and better reflecting inflammation of the eye. Hence, we presume that IFN- γ might be a biomarker of DR, indicating the incidence of retinopathy once diabetes has happened, the speed of progression towards PDR, and the possibility of a poor prognosis.

For early-stage patients, the control of relevant risk factors, such as blood pressure, blood sugar, smoking, and blood lipids, is recommended. Anti-VEGF is recommended as the first-line therapy for PDR, but this treatment is restricted by its short half-life, high cost, and adverse effects. Importantly, blocking VEGF is unable to attenuate disease progression completely or reverse damage to the retina, and merely delays the rate of development and alleviates symptoms, but cannot affect a permanent cure. Currently, with the expansion of medications targeting inflammatory pathogenesis, mediators of angiopoietin signaling axes, immunosuppressants, and nonsteroidal anti-inflammatory drugs, such as tocilizumab, EBI-031, and luminate, have been shown to be effective in clinical trials and need to be further verified [23,82]. Therefore, whether there is clinical effectiveness when antibodies against IFN- γ are applied locally or intrasessionally is worth being further investigated. However, the findings are controversial because IFN- γ has protective effects against renal fibrosis and inhibits vascular proliferation. Consequently, this therapeutic application for DR requires additional consideration and experimental verification.

IFN- α 2 is effective in multiple ocular diseases, such as uveitis and cystoid macular edema. Clinical effectiveness has only been observed in PDR after PRP, DME, and continued neovascularization in some reports, although this factor is effective on angiogenesis and EC proliferation. And clinicians need to closely observe the progression of patients during the use of IFN- α through a series of physical examination, fundus examination, FFA, *etc.* Moreover, IFN- α enhances glucose tolerance and may improve prognosis. Hence, IFN- α may be a potential therapeutic treatment for DR in the future.

CONCLUSION

As a retinal neovascularization disease, DR is a frequent and serious microangiopathy associated with diabetes, and is the principal cause of vision loss in the working-age population [5,51]. Inflammation is a major pathological mechanism associated with the occurrence and development of DR, through the effects of many inflammatory cells and cytokines, such as IFN- γ , IL-1 β , and IL-6, macrophages, and microglia. IFNs are a group of glycoproteins that are responsible for antiviral activity, inhibiting cell proliferation, and regulating immunity and malignant tumors. Every subset has corresponding functions, and they are broadly applied to malignant tumors and viral infections, such as hepatitis type C, herpes zoster, hairy cell leukemia, T cell lymphoma, and melanoma. IFN- α and IFN- γ are tightly linked with DR in the context of inflammatory pathogenesis and treatment. As a proinflammatory cytokine, IFN- γ can be detected in tears, aqueous humor, the vitreous body, and the retina, indicating that it plays a role in the breakdown of the BRB, inflammatory injuries, abnormal angiogenesis, and other processes. IFN- γ also participates in the pathogenesis of other diabetic vascular complications, such as DN and CMBs. In addition, the presence of IFN- γ results in macrophage polarization to proinflammatory M1 phenotype, which produces inflammatory cytokines, such as TNF- α , IL-8, and IL-12, and exacerbates the inflammation. Meanwhile, IFN- γ is associated with the changes and control of blood

glucose and presents a positive correlation with HbA1c%, IL-1 β , and IL-3. Consequently, IFN- γ can be a prospective biomarker of DR. Based on its immunomodulatory effect, IFN- α helps to improve visual acuity, reduce uncommon vascular proliferation, and improve glucose tolerance. However, IFN- α contributes to the occurrence of T1D. IFN- α and IFN- γ also play important roles in other diseases characterized by abnormal angiogenesis, such as AMD, hepatocellular carcinoma, cervical neoplasia, and IAR by proinflammatory and immunoregulatory functions.

Therefore, we believe that IFN- γ has the potential to be a biomarker in the diagnosis and prognosis of DR, as well as to be a key regulator in treating DR. Additionally, the applications of IFN- α still need to be further explored.

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Ejaculatory dysfunction in men with diabetes mellitus

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Abstract

Diabetes mellitus (DM) is a metabolic disorder that is characterized by elevated blood glucose levels due to absolute or relative insulin deficiency, in the background of β -cell dysfunction, insulin resistance, or both. Such chronic hyperglycemia is linked to long-term damage to blood vessels, nerves, and various organs. Currently, the worldwide burden of DM and its complications is in increase. Male sexual dysfunction is one of the famous complications of DM, including abnormal orgasmic/ejaculatory functions, desire/libido, and erection. Ejaculatory dysfunction encompasses several disorders related to DM and its complications, such as premature ejaculation, anejaculation (AE), delayed ejaculation, retrograde ejaculation (RE), ejaculatory pain, anesthetic ejaculation, decreased ejaculate volume, and decreased force of ejaculation. The problems linked to ejaculatory dysfunction may extend beyond the poor quality of life in diabetics as both AE and RE are alleged to alter the fertility potential of these patients. However, although both diabetes patients and their physicians are increasingly aware of diabetic ejaculatory dysfunction, this awareness still lags behind that of other diabetes complications. Therefore, all these disorders should be looked for thoroughly during the clinical evaluation of diabetic men. Besides, introducing the suitable option and/or maneuvers to treat these disorders should be tailored according to each case. This review aimed to explore the most important findings regarding ejaculatory dysfunction in diabetes from pre-clinical and clinical perspectives.

Key Words: Diabetes mellitus; Ejaculation; Anejaculation; Retrograde ejaculation; Semen

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Core Tip: Male sexual dysfunction is a famous complication of diabetes mellitus (DM),

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including abnormal orgasmic/ejaculatory function, desire/libido, and erection. DM-related ejaculatory dysfunction encompasses several disorders such as premature ejaculation, anejaculation (AE), delayed ejaculation, retrograde ejaculation (RE), ejaculatory pain, anesthetic ejaculation, decreased ejaculate volume, and decreased force of ejaculation. The problems linked to ejaculatory dysfunction may lead to poor quality of life as both AE and RE are alleged to alter their fertility potential. All these disorders should be looked for thoroughly during the clinical evaluation of diabetic men.

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INTRODUCTION

Ejaculation is a complex, coordinated sequence of mechanisms and reflexes compared to erection. It requires coordinated innervation of the sympathetic and parasympathetic systems in addition to somatic innervation. In essence, it is intermediated by a multifaceted neural control system including sensory receptors, afferent pathways, cerebral sensory areas, cerebral motor centers, spinal motor centers, and efferent pathways. Likewise, this process comprises complex neurochemical interplay between central serotonergic and dopaminergic neurons, with involvement of cholinergic, adrenergic, oxytocinergic, and gamma-aminobutyric acidergic neurons[1]. However, ejaculation entails two diverse sequential coordinated phases, seminal emission and ejaculation proper, each of them involving diverse anatomic structures[2].

The sympathetic nervous system is accountable for bladder neck closure and emission, whereas the somatic nervous system is accountable for the contraction of the pelvic muscles and the bulbourethral and ischiocavernosus muscles[3]. Additionally, the external urinary bladder sphincter as well as the perineal periurethral muscles are under somatic control[4]. Emission process is characterized by closure of the bladder neck and contraction of smooth muscles across the seminal tract aiming of propulsion of the ejaculate constituents into the posterior urethra where they are mixed with spermatozoa to form seminal fluid[5]. This phase is activated by augmented sexual arousal and the peripheral sex-related stimuli. The sympathetic centers, found within the intermediolateral and the intermediomedial cell columns in lamina VII of segments T₁₂-L₂, supply the smooth muscles of the male accessory glands, seminal tract, and urinary bladder neck[6]. Before emission, there are secretions from the distal epididymis, seminal vesicles (SVs), and the prostate supporting emission. Neural control of those secretions is mediated by the cholinergic post-ganglionic, sympathetic, and parasympathetic fibers, derived from the pelvic plexus[6-8]. The emission phase is under the cerebral control and can be affected by the physical or visual erotic stimulation[9].

The ejaculation proper phase follows emission and refers to the relaxation of the external urinary sphincter followed by repetitive contractions of the bulbospongiosus, ischiocavernosus, and the pelvic striated muscles leading to expulsion of seminal fluid out of the urethra[10]. Motor neurons controlling the pelvic and perineal striated muscles are situated in the ventral horn of segments S₂-S₄ in Onuf's nucleus[11]. Both emission and ejaculation proper occur in coherence to bring normal antegrade ejaculation. Although the precise trigger for the ejection phase is not yet known, it is believed that the filling of the posterior urethra urges the urethral-muscular reflex boosted by sensory inputs-somatosensory, visceral sensory, or proprioceptive-to the spinal control center might trigger the onset of ejection. Harmonization between autonomic and somatic neurons for emission as well as ejection is supposed to be controlled by a group of lumbar spinothalamic interneurons called "spinal ejaculation generator (SEG)"[12]. In rats, these interneurons are situated in lamina X and the medial part of lamina VII of the gray matter in the L₃-L₄[13]. In humans, neurohistologic data, in addition to the clinical observations, have established the existence of SEG in L₃-L₅ segments[14].

Exact knowledge on hormonal control of ejaculation is still lacking. Studies have shown an oxytocin surge during male sexual activity, peaking during or soon after ejaculation[15]. Additionally, oxytocin's contractile effect concerning the seminal tract in humans appears to be weaker than in the animal models[16]. Moreover, estrogens have been demonstrated to take part in the peripheral regulation of epididymal contractility[17]. Furthermore, prolactin was also noted to increase around orgasm with oxytocin suggesting that it may serve as a neuroendocrine reproductive reflex for peripheral reproductive organs[18,19]. Androgens are deeply elaborated in the ejaculation process[20]. The effects of androgens are not limited to the fact that the development of the epididymis, vas deferens, and SVs is dependent on androgens, but also, spinal nuclei elaborated in the control of ejaculation, such as the nucleus of the bulbocavernosus nerve, are androgen-dependent[21], as are the muscles of the pelvic floor[22,23]. However, the dynamic and complex interplay among androgens, growth factors, and genes in the ejaculatory process is less well understood.

Diabetes mellitus (DM) is a metabolic disorder characterized by chronic hyperglycemia due to defects in insulin secretion and/or action[24]. The worldwide burden of DM and its complications are presently in an increase. DM is usually associated with long-term dysfunction of blood vessels, nerves, and several organs including the epididymis, vas deferens (VD), SV, prostate, and urethra[25-29]. Although both diabetes patients and their physicians are increasingly aware of diabetic ejaculatory dysfunction, this awareness still lags behind that of other diabetes complications. The problems linked to the ejaculatory dysfunction may extend beyond the poor quality of life in diabetics. Because anejaculation (AE) and retrograde ejaculation (RE) are believed to alter the fertility potential of patients[25,30]. Thus, the careful diagnosis and timely management of these cases together are of extreme importance. Therefore, this narrative review aims to explore the most important findings regarding ejaculatory dysfunction in diabetes from pre-clinical and clinical perspectives.

METHODS

We searched the PUBMED/MEDLINE, Scopus, Academic Search Complete database, Google Scholar, Cochrane Library, EMBASE, ProQuest, and CINAHL databases from inception to December 2020, for relevant studies. The literature search included these terms (with synonyms and closely related words): type 1 and type 2 diabetes mellitus; or hyperglycemia; or insulin resistance; and ejaculatory dysfunction; or premature ejaculation (PE); or delayed ejaculation (DE); or AE; or RE; or ejaculatory pain (EP); or anesthetic ejaculation; or spontaneous ejaculation (SE); or sexual dysfunction; or male sexual function; or epididymis; or VD; or SVs; or prostate; bladder neck; or urethra. The search was not limited by study design but restricted to English-language periodicals. Further studies were recognized by examining the reference lists of all retrieved articles.

ANIMAL STUDIES

In an attempt to understand the influence of DM on ejaculatory function, we have identified 18 studies (Table 1) reporting on the association between experimental DM and ejaculatory dysfunction. Generally, it seems that ejaculatory dysfunction after experimental DM is inexplicable because it ranges from PE, normal ejaculatory performance, to AE. Although the duration of the diabetic state seems to be the major determinant of the development of ejaculatory dysfunction, other factors such as dissimilar animal species and strains, with a diversity of metabolic pathways, different models for inducing DM, small experimental groups, nuances in laboratory technique that may affect the results, and selection of outcome measures of the ejaculatory function. Nonetheless, the following different observations were noted: (1) 3 studies showed no sexual performance difference between diabetic and control rats[31-33]; (2) prolonged ejaculation latency (EL) was reported in 9 studies suggesting DE[34-42]. Notably, in 1 study diabetic rats showed a significantly decreased amount of secretions stored in the seminal vesicle indicating that streptozotocin (STZ)-induced diabetic might affect the cholinergic nerve endings that are situated at the rich glandular epithelium[38]; (3) 0% ejaculations (rats did not achieve ejaculation) was noted in 4 reports suggesting AE[43-46]; and (4) reduced EL was reported in 2 reports suggesting PE[47,48]. These findings suggest not only that ejaculatory dysfunction in diabetic

Table 1 Ejaculatory behavior in diabetic animals

Ref.	Animal model	Effects observed on ejaculatory function	Type of treatment and response
Sach <i>et al</i> [31], 1982	STZ-induced diabetic rats	No sexual performance difference between diabetic and control rats.	
Clark[32], 1995	STZ-induced diabetic rats	No sexual performance difference between diabetic and control rats.	
Scarano <i>et al</i> [33], 2006	STZ-induced diabetic rats	No sexual performance differences in EL after 15 d.	
Steger <i>et al</i> [34], 1990	STZ-induced diabetic rats	Prolonged EL (DE or AE)	Delayed insulin replacement (4 wk) cannot prevent ejaculatory dysfunction.
Murray <i>et al</i> [35], 1992	Diabetic BB/WOR rats	Prolonged EL (DE or AE) after 28 wk	
McVary <i>et al</i> [36], 1997	Diabetic BB/WOR rats	Prolonged EL (DE or AE) after 40 wk, reduced number of ejaculations. No differences regarding serum testosterone, FSH, and LH.	
Ebiko <i>et al</i> [37], 2006	STZ-induced diabetic rats	Deteriorated spontaneous seminal emission after 5 wk. In 15 and 30 wk, occurrence of SSE was almost completely suppressed.	Early insulin replacement can prevent ejaculatory dysfunction.
Yonezawa <i>et al</i> [38], 2009	Streptozotocin (STZ)-induced diabetic rats	Deteriorated spontaneous seminal emission after 5 wk. Decreased ejaculated semen and decreased seminal vesicle fluid.	Early insulin replacement can prevent ejaculatory dysfunction. Once dysfunction occurs, insulin cannot restore it.
Suresh <i>et al</i> [39], 2012	STZ-induced diabetic rats	Prolonged EL suggesting DE. -Low serum testosterone.	Mucuna pruriens showed recovery of EL.
De <i>et al</i> [40], 2016	STZ-induced diabetic rats	Prolonged EL suggesting DE. -Low serum testosterone.	l-Norvaline (arginase inhibitor) reduced EL.
Shi <i>et al</i> [41], 2017	STZ-induced diabetic rats	Prolonged EL suggesting DE.	Lycium barbarum polysaccharide reduced EL.
Li <i>et al</i> [42], 2019	STZ-induced diabetic rats	Prolonged EL at 62 d suggesting DE.	No effect of vitexin (herb) on EL.
Lert-Amornpat <i>et al</i> [43], 2016	STZ-induced diabetic rats	Lack of copulatory behavior suggesting AE.	<i>Kaempferia parviflora</i> (herb) showed recovery of EL.
Fernández-Collazo <i>et al</i> [44], 1970	Rats with subtotal pancreatectomy	They did not AE.	
Hassan <i>et al</i> [45], 1993	STZ-induced diabetic rats	Rats exhibited AE in diabetics. -Low serum testosterone.	Sabeluzole treatment was beneficial to correct dysfunction.
Pontes <i>et al</i> [46], 2011	STZ-induced diabetic rats	Lack of the sperms ejaculated into the uterus. -Low serum testosterone.	Testosterone supplement did not restore ejaculatory function.
Ghaheri <i>et al</i> [47], 2018	STZ-induced diabetic rats	Shorten EL after 28 d suggesting PE.	Stevia Bertoni extract improved EL.
Minaz <i>et al</i> [48], 2019	STZ-induced diabetic rats	Shorten EL after 8 wk suggesting PE. - Low serum testosterone.	Inhibition of soluble epoxide hydrolase prolonged EL.

AE: Anejaculation; DE: Delayed ejaculation; EL: Ejaculation latency; FSH: Follicle stimulating hormone; LH: Luteinizing hormone; PE: Premature ejaculation; STZ: Streptozotocin.

animals is variable but also may indicate that the dysfunction may occur during the early stage following experimental diabetes and becomes poorer as it progresses[34, 38]. Additionally, early insulin replacement had been demonstrated to prevent ejaculatory dysfunction suggesting that insulin may play a role in controlling of seminal emission[34,37,38]. However, once the dysfunction occurs; delayed insulin replacement cannot restore normal ejaculatory function suggesting that long-term exposure to the hyperglycemia may lead to an irreversible ejaculatory dysfunction[34, 38]. In this respect, it appears that insulin replacement may only delay rather than prevent changes in copulatory behavior[34].

The development of ejaculatory dysfunctions in animals is not limited to STZ-induced diabetic rats[34,37-40,43,45-48] but also have been demonstrated in STZ-induced diabetic mice[42,43], subtotal pancreatectomy-induced diabetic rats[44], and Bio Breeding Wistar Strain (BB/WOR) rats with spontaneous DM[35,36]. The major attributes of this latter strain (BB/WOR) are not only limited to the fact that its pathophysiology closely look like the development as well as the clinical features of type 1 diabetes in humans but also it lacks the artefactual end-organ changes seen with STZ such as angiopathy[36]. In other words, diabetic neuropathy is a prevailing feature of this model[49]. EL, the time of the first intromission until ejaculation, was the most frequently employed outcome measure to assess the ejaculatory function in these animal studies[34-36,39-43,47,48]. Other tools include spontaneous seminal emission test[37,38], measurement of seminal vesicle fluid[38], failure to recover spermatozoa in the female uterus[46], and numbers of ejaculations[36,43-45].

In the context of ejaculatory dysfunction associated with experimental DM, it would be of interest to review the potential effects of different therapeutic compounds to restore the ejaculatory function in STZ-induced diabetic mice. Nine studies were identified[39-43,45-48]. Animal studies have demonstrated that *Mucuna pruriens*[39], L-Norvaline (arginase inhibitor)[40], and Lycium barbarum polysaccharide[41] showed a reduction in the EL in those showing prolonged EL during the diabetic state. Additionally, both *Kaempferia parviflora*[43], and sabeluzole (benzothiazole derivative)[45], were found to be beneficial in correcting an ejaculatory condition. Moreover, Stevia Bertoni extracts and the soluble epoxide hydrolase inhibitor “trans-4-{4-[3-(4-trifluoromethoxyphenyl)-ureido] cyclohexyloxy} benzoic acid/t-TUCB”[47,48] showed prolongation of EL in those animals showing a reduction in EL. Unfortunately, both vitexin (bioactive flavonoids) and testosterone did not restore ejaculatory function in STZ-induced diabetic and mice, respectively. Finally, further experiments are needed to delineate better the effects of experimental diabetes on the ejaculatory function using a unified generally accepted easily measurable outcome measure.

ETIOPATHOPHOGENESIS OF DIABETIC EJACULATORY DYSFUNCTION

Animal studies assessed the effects of experimental diabetes on the end-organs of a seminal emission (epididymis, VD, SV, prostate, bladder neck, and urethra) have revealed that hyperglycemia is capable of altering the contractility of these organs either by modulating neurotransmitters release or by modifying the basal tone of the smooth muscle layers[50-52]. Interference with the normal function of these organs may therefore include central or peripheral mechanisms. Besides, these diabetes-associated changes may have general pathophysiological interest since ejaculatory dysfunction such as PE, DE, AE; or RE has been proven to be one of the complications of DM[25,27,28]. Moreover, animal models can deliver an important method to assess neural circuitry and molecular and cellular pathways in an organized setting. The following summarizes the major observations regarding the effects of experimental diabetes on the end-organs of seminal emission to understand the pathogenesis of diabetes-associated ejaculatory dysfunction: (1) Chronically STZ-diabetic rats and mice showed degenerative changes in the sympathetic supply of the VD leading to a decreased reaction to stimulation of their noradrenergic nerves and a supersensitivity to exogenous noradrenaline[50-54]. These findings suggest that a significant proportion of animals may have developed sympathetic neuropathy that may explain the prolongation of EL, reduction of the numbers of ejaculations, and the occurrence of AE; (2) The paravertebral thoracic ganglion cells of spontaneously diabetic BB rats exhibited a decreased number of synapses and the postganglionic fibers demonstrated increased glycogenosomes, axonal sequestration, and reduced axonal size suggesting an axonopathy in sympathetic nerves[49,53]. Additionally, this model showed a peripheral neuropathic change in both the hypogastric and motor pudendal nerve fibers suggesting that diabetic neuropathy is not only disturbed the emission phase but also may disrupt the ejection phase of the ejaculatory process[36]; (3) Reactive oxygen species (ROS) may be accountable for impaired sympathetic neurotransmission and the abnormal function of diabetic vas deferens in STZ-diabetic rats[54,55]; (4) There is evidence to suggest the presence of Ca channel hyperactivity in the smooth muscle of VD of STZ-induced diabetic rats possibly due to increased phosphatidylinositol turnover mediated by alpha 1-adrenoceptors[56,57]. These findings may reduce EL and explain the occurrence of PE; (5) Noradrenaline is the principal excitatory neurotransmitter in the internal urethral sphincter and augments closure of the bladder neck during ejaculation[58,59]. By principle, the combination of long-term

diabetic sympathetic neuropathy in animals[37,38,49] and external urethral sphincter relaxation dysfunction[60] may result in RE; (6) It has been demonstrated that long-term diabetes is associated with changes in serotonergic transmission in the rat brain including changes in several types of 5-HT receptors[61,62]. Theoretically, 3, 5-HT receptor subtypes (5-HT_{1A}, 5-HT_{1B}, and 5-HT_{2C}) were assumed to mediate 5-HT's modulating activity on the ejaculation process. PE is associated with decreased neurotransmission of serotonin, 5-HT_{2C} receptor hyposensitivity, and 5-HT_{1A} receptor hypersensitivity[63]. Accordingly, ejaculatory dysfunction due to changes in serotonergic transmission among diabetic animals could be anticipated; (7) There is adequate evidence to suggest that experimental diabetes in different animal models (STZ rats, spontaneously diabetic BB rats, BB/WOR diabetic rats, and spontaneously diabetic Torii rats) is associated with low testosterone levels[64-70]. The pathogenesis of hypogonadism in diabetic animal models may include impaired hypothalamic or pituitary signaling[34,71,72], deficiency of gonadotropic hormones, or blockade of their actions[73,74], and/or primary Leydig cell defect in steroidogenesis due to lack of stimulating effect of insulin[74-76]. In the light of the foregoing, it might be assumed that there is a link between low testosterone levels and ejaculatory dysfunction. However, it has been shown that testosterone supplement is not able to bring back ejaculatory function in induced diabetic rats[46,77] suggesting that the deficiency of testosterone was not related directly to the diabetes-induced ejaculatory dysfunction in this experimental model. Although expression of androgen receptors are demonstrated at different levels of the ejaculatory process such as the medial preoptic area of the hypothalamus[78], smooth muscles of the male genital tract[79], and in the spinal nucleus of the bulbocavernosus muscle[80], it is thought that testosterone plays a much superior role in libido than the ejaculatory process and the physiological capacity for ejaculation is less sensitive to testosterone reduction than that for the desire[81,82]. In support of this notion, it has been shown that testosterone levels as low as 0.2 ng/mL, can support ejaculatory behavior in rats[83]; (8) It is possible that diabetic ejaculatory dysfunction might be a reflection of decreased sexual desire[36, 48]. Although the classic description of diabetic erectile dysfunction showed preserved desire[84], it has been shown that sexual desire (mount frequency) is notably decreased in diabetic rats[34,45,85-87], but this possibility was unlikely because of the absence of improved ejaculation behavior among diabetic rats after testosterone therapy despite the improvement of their libido (mount behavior)[77]; and (9) Lastly other factors that may participate in the pathogenesis of ejaculatory dysfunction in experimental diabetes may include decreased body and reproductive organs weight [45,77]. However, the relationship between these variables and diabetic ejaculatory dysfunction remains incompletely understood.

Ejaculatory dysfunctions are established complications found with variable prevalence in men with diabetes. There is also a substantial contribution of human studies to the pathogenesis of diabetic ejaculatory dysfunction. The factors that have been postulated to influence the development of ejaculatory dysfunctions in DM are summarized (Tables 2 and 3). However, there are limited data regarding the weight of each mechanism in participating in the pathogenesis of different ejaculatory dysfunctions in diabetes patients.

DIABETES-RELATED EJACULATORY DYSFUNCTIONS

Ejaculatory dysfunctions encompass several disorders related to DM and its complications, such as PE, DE, AE, RE, ejaculatory pain, anesthetic ejaculation, decreased ejaculate volume, and decreased force of ejaculation. Up to 40% of men with diabetes may complain of ejaculatory dysfunction[99]. Of these PE, DE, AE, and RE are the most common and the focus of this discussion[100-113].

PE

There is contradictory evidence concerning the prevalence of PE in diabetics, with one study reporting increased PE prevalence in diabetic men compared to healthy controls (78.8% *vs* 47.5%, $P = 0.001$)[92]. On the other hand, a study by the Italian Society of Andrology pointed out to a protecting effect of diabetes on PE (6.2% *vs* 8.4%, adjusted odds ratio = 0.6, $P = 0.001$)[114]. This low prevalence was endorsed to delayed emission caused by diabetic sympathetic neuropathy of nerve fibers innervating the organs of emission (VD, SV, prostate). However, with the well-known relation between erectile dysfunction (ED) and PE that recognizes ED as the significant comorbidity of PE[115] and a higher prevalence of ED among diabetics, we could

Table 2 Possible pathophysiological mechanisms underlying ejaculatory dysfunctions in diabetes mellitus (animal studies)

Ref.	Postulated mechanisms	Possible ejaculatory dysfunction
McVary <i>et al</i> [36], Yagihashi <i>et al</i> [49]	Pathologic changes in the nerve supply of seminal tract due to accumulation of AGE increased ROS (sympathetic neuropathy)	Prolongation of EL
Tomlinson <i>et al</i> [50], Longhurst <i>et al</i> [51]	Decreased number of synapses in thoracic ganglia	Reduction of the numbers of ejaculations
Kaschube <i>et al</i> [52], Kamata <i>et al</i> [53]	Axonopathy in postganglionic sympathetic fibers	Disturbed the emission phase
Güneş <i>et al</i> [54], Tsounapi <i>et al</i> [55]	Neuropathic changes in hypogastric nerve and motor pudendal nerve fibers	Disruption of the ejection phase
Tomlinson <i>et al</i> [50], Longhurst <i>et al</i> [51], Kaschube <i>et al</i> [52], Kamata <i>et al</i> [53], Güneş <i>et al</i> [54]	Hypersensitivity (supersensitivity) of seminal tract smooth muscles to exogenous noradrenaline	Reduction of EL
Sakai <i>et al</i> [56], Sakai <i>et al</i> [57]	Hyperactivity of Ca channels in smooth muscles	Reduction of EL
Ebiko <i>et al</i> [37], Yonezawa <i>et al</i> [38], Yagihashi <i>et al</i> [49], Torimoto <i>et al</i> [60]	Sympathetic neuropathy and external urethral sphincter relaxation dysfunction	Disruption of bladder neck closure Disruption of AE
Sandrini <i>et al</i> [61], Abraham <i>et al</i> [62]	Changes in serotonergic transmission	Reduction or prolongation of EL
Seethalakshmi <i>et al</i> [71], Wolfe <i>et al</i> [72]	Impaired hypothalamic or pituitary signaling	Decreased sexual performance
Oksanen <i>et al</i> [73], Sudha <i>et al</i> [74]	Deficiency of gonadotropic hormones or blockade of their actions	Decreased sexual performance
Ballester <i>et al</i> [75], Neirijnck <i>et al</i> [76]	Decrease in number and function of Leydig cells	Decreased sexual performance
Neirijnck <i>et al</i> [76]	Defective testicular steroidogenesis	Decreased sexual performance
Kühn-Velten <i>et al</i> [64], Anderson <i>et al</i> [65], Ricci <i>et al</i> [66], Murray <i>et al</i> [67], Cameron <i>et al</i> [68], Ohta <i>et al</i> [69], Nakane <i>et al</i> [70]	Reduced serum levels of LH and testosterone (T)	Decreased sexual performance
McVary <i>et al</i> [36], Minaz <i>et al</i> [48], Steger <i>et al</i> [85], Al-Roujayee <i>et al</i> [86], Kashif <i>et al</i> [87]	Reduced libido	Decreased sexual performance, decreased mount frequency, and reduced EL
Hassan <i>et al</i> [45], Steger <i>et al</i> [77]	Reduced reproductive organ weight	Exact Effects on ejaculation still unknown

AGE: Advanced glycation end products; Ca: Calcium; DE: Delayed ejaculation; EL: Ejaculation latency; FSH: Follicle stimulating hormone; LH: Luteinizing hormone; PE: Premature ejaculation; ROS: Reactive oxygen species; STZ: Streptozotocin; T: Testosterone.

speculate that diabetes might be considered a risk factor for PE. Anyway, most of the studies showed comparable prevalence between diabetic and non-diabetic persons[90, 91,95,96]. Theoretically, diabetes-related PE is recognized to have a multi-factorial etiology (Tables 2 and 3). The lack of a significant difference in the prevalence of PE among men with/without diabetes might be attributed to socio-demographic factors, a multiplicity of different tools for measurement of PE such as self-reported PE, PE diagnostic tool (PEDT) score, self-reported, and stopwatch-recorded intravaginal ejaculation latency time (IELT) or to the presumed balance between the protective and detrimental factors inside the diabetes patients. Therefore, the true prevalence of PE in DM has not been firmly established. However, the PE subjects diagnosed with PEDT score or stopwatch IELT showed significant prevalence of diabetes[88,116] suggesting that DM is an important etiologic factor in acquired PE. Studies assessing whether PE in DM can be related to glycometabolic control and associated morbidities have also produced mixed results. While El-Sakka[91] and Malavige *et al*[93] have demonstrated that elongated duration of diabetes, poor metabolic control, and presence of cardiovascular disease are linked to increased risk of PE in type 2 DM, Other studies have found no such evidence in type 2 DM[92,97]. Additionally, in the subgroup of type 1 DM patients assessed for glucose variability, the PEDT score was associated with low blood glucose indices ($r = 0.43$; $P = 0.01$), but not with a standard deviation of blood glucose ($r = 0.1$, $P = 0.6$), mean amplitude of glycemic excursions ($r = -0.1$; $P = 0.4$), or high blood glucose indices ($r = 0.1$; $P = 0.6$) suggesting a link between glycemic excursions and PE[96]. This association between hypoglycemia and PE might be linked to increased adrenergic activity[117] or reduced serotonergic activity[118]. Moreover, PE is known to be associated with diabetes-related ED as shown in different studies[91-93,97]. Likewise, one study suggests that 95% of Type 2 diabetes patients

Table 3 Possible pathophysiological mechanisms underlying ejaculatory dysfunctions in diabetes mellitus (human studies)

Ref.	Possible cause	Outcome
Premature ejaculation		
Culha <i>et al</i> [88]	Anxiety	Among PE patients with DM, 15% had anxiety
Culha <i>et al</i> [88], Khan <i>et al</i> [89]	Depression	Among PE patients with DM, 16.9% had depression Depression score Significantly higher among diabetic-related PE patients
Khan <i>et al</i> [89], Malavige <i>et al</i> [90]	Genetic and racial factors	Long tri-nucleotide repeats of the androgen receptor are related to the lowest IELT (PE) Asian men reported higher diabetic PE than European counterparts
El-Sakka[91]	Diabetic condition, duration of MD	> 10 yr of diabetes were 2.7 times as likely to report diabetic-related PE
	Poor glycemic control	Poor glycemic control were 9.6 times as likely to report PE
El-Sakka[91], Majzoub <i>et al</i> [92]	Having diabetic-related -erectile dysfunction (ED) and Cardiovascular diseases	Significant association between PE and cardiovascular diseases
Malavige <i>et al</i> [93], Malavige <i>et al</i> [90]		ED showed a significantly higher incidence of PE
Olamoyegun <i>et al</i> [94]		ED was strongly associated with PE odds ratio = 4.4
El-Sakka[91]	Having diabetic -related neuropathy	It is not associated with PE
Khan <i>et al</i> [89]	Total serum testosterone	Significantly higher among type 2 diabetic-related PE patients
Owiredun <i>et al</i> [95]		It correlates negatively with short IELT among type 2 DM
Bellastella <i>et al</i> [96]		No significant difference in type 1 diabetes
Delayed ejaculation and anejaculation		
Corona <i>et al</i> [97]	Depression	Severe depressive symptoms are associated with ejaculatory problems in DM
Ellenberg <i>et al</i> [25], La Vignera <i>et al</i> [27], Dinulovic <i>et al</i> [98]	Progressive autonomic neuropathy of the sympathetic nerves	Denervation leads to weak or loss of VD and SV peristaltic movements
Dunsmuir <i>et al</i> [99], Condorelli <i>et al</i> [100]		Abnormal inflammatory responses lead to alteration of the VD and SV peristaltic movements
La Vignera <i>et al</i> [101], Pop-Busui <i>et al</i> [102]		Delayed /poor emission Absent emission
Haddad <i>et al</i> [26], Culver <i>et al</i> [103]	Calcification of vas deferens and seminal vesicles	Loss of their ability to contract as the smooth muscle is replaced by fibrotic, calcified tissue
Tsuno <i>et al</i> [104]		Delayed/poor emission
Hylmarova <i>et al</i> [29], Corona <i>et al</i> [81]	Hypogonadism	No association between serum testosterone levels and ejaculation time in men self-reporting DE including diabetic patients
Paduch <i>et al</i> [82], Gianatti <i>et al</i> [105]		
Morgentaler <i>et al</i> [106]		T replacement is not associated with improvement in DE or AE
Burke <i>et al</i> [107], Corona <i>et al</i> [108]	Low sexual desire	DM is significantly associated with low sexual desire
Corona <i>et al</i> [109]		DE and AE are associated with low sexual desire
Retrograde ejaculation		
Klebanow <i>et al</i> [110]	Diabetic neuropathy (T10-L3)	Intact vasal and seminal vesicle contraction but incomplete simultaneous bladder neck closure leads to partial RE
Greene <i>et al</i> [111]		Intact vasal and seminal vesicle contraction and simultaneous complete lack of bladder neck closure leads to complete RE

Koyanagi[112]	External urethral sphincter relaxation dysfunction (triple parasympathetic-sympathetic-somatic innervation)	Lack of active external urethral sphincter relaxation leads to disruption of antegrade ejaculation
Cao <i>et al</i> [113]		

AE: Anejaculation; DE: Delayed ejaculation; DM: Diabetes Mellitus; EL: Ejaculation latency; ED: Erectile dysfunction; PE: Premature ejaculation; SV: Seminal vesicle; VD: Vas deferens.

with PE also reported ED[91] indicating that ED is the principal risk factor of PE in type 2 DM. A vicious cycle probably exists between ED and PE with each condition being deteriorated by the other[93]. However, Culha *et al*[88] disputed these findings and have shown that simultaneously occurring different etiologic factors may be responsible for the development of DM-related PE. These factors include ED (20.75%), chronic prostatitis (18.87%), depression (16.98%), anxiety (15.09%), FSH-LH abnormality (7.55%), hyperprolactinemia (7.55%), and hyperthyroidism (1.89%). These latter findings still await confirmation.

According to the consensus of the International Society for Sexual Medicine, acquired PE (*e.g.*, diabetes-related PE) is an ejaculation that always or nearly always occurs before or within about 3 min of vaginal penetration or, a significant and bothersome reduction in the latency time, associated with the incapability to delay ejaculation on all/nearly all vaginal penetrations, and negative personal consequences, as; distress, bother, frustration and/or avoidance of sexual intimacy[119]. Evaluation of diabetes-related PE includes a clinical history and careful physical examination focusing on all related symptoms, signs, and risk factors. A list of assessment steps that could be helpful in evaluating DM-related ejaculatory dysfunction is presented (Table 4). The most important dimensions in history taking include assessment of self-estimated IELT, subjective perceived control over ejaculation, existed distress by the condition, and the existence of an interpersonal difficulty owing to PE. Routine laboratory tests or neuro-physiological tests should merely directed by precise findings from either the history taking or physical examination[120].

In principle, scarce data are assessing the treatment of DM-related PE. Additionally, one should know that DM-related PE may be a heterogeneous group of patients. Hence, it is important to diagnose any associated comorbidity such as ED, depression, prostatitis, or hyperthyroidism as they should be treated first or at the same time as PE [120]. Therefore, the treatment may involve numerous interventions as per the kind of mechanism that would cause such condition: (1) The initial management for PE is controlling the patient's blood glucose that in some cases may allow recover the normal ejaculatory function[91,93]; (2) Amelioration of glycemic variability would improve PE in type 1 diabetes patients[96]; (3) In cases of concomitant ED and PE, ED should receive phosphodiesterase type 5 inhibitors before, or at least at the same time as, PE[91,93,94]. The efficacy of the combined use of phosphodiesterase type 5 inhibitors and dapoxetine in males with comorbid PE and ED are supported by some studies[121-123]; (4) DM-related PE patients had a worse response to 30-60 mg oral dapoxetine treatment compared to non-diabetic PE patients. Poor treatment outcomes in diabetes patients may be attributed to DM-associated complications[123]; and (5) Various behavioral techniques (such as 'squeeze' technique or 'stop-start' program) may be beneficial in those associated with psychological factors or those patients uncomfortable with pharmacological therapy. However, the long-term success of these maneuvers is limited[120].

DE and AE

DE (also termed retarded ejaculation, inhibited ejaculation (IE), inadequate ejaculation, male orgasmic disorder, or primary impotentia ejaculationis), was used to describe "a marked delay in or inability to achieve ejaculation"[124]. Current diagnostic criteria from the Diagnostic and Statistical Manual of Mental Disorders, 5th edition, defines DE as either a marked delay in or a marked infrequency or absence of ejaculation on 75% to 100% of occasions for at least 6 mo of partnered sexual activity without the individual desiring delay and causing significant distress to the individual[125]. Therefore, the terminology DE aimed to describe all ejaculatory disorders that lead to a delay or absence of ejaculation (AE)[1]. Furthermore, the severity of DE was classified according to Kaplan criteria into mild and moderate forms and the most severe ones (AE or severe DE)[126]. For these reasons, both DE and AE will be discussed together in this section.

Overall, DE is the rarest and the least understood male sexual dysfunction. Its incidence in the general population rarely exceeds 3%[127,128]. There have been few

Table 4 Assessment steps in the evaluation of diabetes mellitus-related ejaculatory dysfunctions**History**

Asking about the period from vaginal intromission to ejaculation (intravaginal ejaculatory latency time).

Is the patient unable to advance his ejaculatory response?

Is the patient or his partner distressed or bothered by the situation?

Is the symptom occurring since the first sexual experience or occurring after a period of normal ejaculatory performance?

Onset and duration of the symptom.

Is the symptom occurring on every/almost every attempt and with every partner?

Presence or absence of premonitory ejaculatory sensation.

The duration of thrusting before the suspension of intercourse.

Reasons for delay of intercourse (*e.g.*, fatigue, loss of erection, a sense of ejaculatory futility, or partner request).

Presence of post-coital self- or partner-assisted masturbation.

Psychogenic anejaculation/anorgasmia can be suspected when there is a history of nocturnal emission.

Patient's ability to get an erection, relax, sustain, and heighten sexual arousal.

Exclude anorgasmia by asking about lack of orgasm.

Whether orgasm is present but there is a lack of external ejaculation that may indicate retrograde ejaculate.

Feeling before ejaculation/orgasm: The inadequate combination of "friction and fantasy" may exacerbate DE.

Intercourse frequency.

Presence of other sexual dysfunctions such as ED (ability to initiate or maintain an erection), low libido.

Other symptoms of hypogonadism (such as lack of energy, depressed mood).

Masturbation habits

The life events/circumstances related to the complaint.

Sexual communication abilities.

Paraphilic inclinations/interests (may be related to DE and anejaculation).

Cultural or religious beliefs (if any).

History of a psychiatric disorder (may be the etiologic factor).

History of previous treatment for this symptom.

History of neurologic disorders, spinal cord injury, medical diseases, trauma, abdominal/pelvic operations, drug intake, or pelvic radiotherapy.

History of pelvic or testicular pain (may indicate inflammation).

History of dysuria, burning micturition, or any urinary symptom (indicate inflammation).

Clinical examination

Signs of diabetic complications and co-morbidities.

Signs of hypogonadism.

Rule out systemic disorders that contribute to ejaculation dysfunction as neurological impairment, endocrine/ urological diseases.

Examination for secondary sexual characteristics, penile and testicular abnormalities.

Examination of the epididymis, and vas deferens on each side.

PR examination to determine the prostate size, anal sphincter tone, and quality of the bulbocavernosus reflex.

The cremasteric reflex: measures intact L1-2 spinal segments, also mediating emission and psychogenic erection.

Perineal reflexes (bulbocavernosus and anal reflex) mediated by sacral segments, also mediating reflex erection (for intact S2-4 pathway).

Examination of pinprick and temperature sensations in the saddle area (perineal) and glans penis for healthy sacral cord segments.

Inability to feel testicular squeeze: measures the integrity of T11 to T12 spinal nerves *via* the sympathetic nervous system.

Examination of lower abdominal cutaneous reflex: measures intact Th11-12.

Penile biothesiometry.

Investigations

Blood levels of glucose, HbA1c, serum testosterone, thyrotropin, and prolactin to exclude other endocrine disorders.

Post-masturbation first-void urine if we suspect retrograde ejaculation to search for spermatozoa and fructose content to confirm retrograde ejaculate

Microbiological examination of expressed prostatic secretion and urine to verify or exclude associated genital infections.

Urine cytology to exclude bladder cancer

Serum prostate-specific antigen to exclude prostate cancer

Neurophysiologic investigations (bulbocavernosus evoked response and dorsal nerve somatosensory evoked-potentials): If there is clinical evidence of neurologic lesions. These tests are little used in clinical practice and usually do not affect management.

Trans-rectal ultrasound examination if we suspect ejaculatory duct obstruction, prostatic or seminal vesicle abnormalities or stones.

CT or MRI scans to assess pelvic anatomy if we suspect major pelvic lesions.

CT: Computed tomography; MRI: Magnetic resonance imaging.

attempts to study the prevalence of DE and AE in DM. While one study showed 0% prevalence among a series of 54 diabetes patients[129], another research demonstrated self-reported absent ejaculation and DE in 7.2 % and 0.36 % respectively among a total series of 276 diabetes patients[130]. However, sporadic cases were reported in literature either in the context of fertility evaluation[110,131] or as a sexual complaint [132]. It is thought that several pathophysiological factors may contribute to the development of DE and AE such as depression, progressive autonomic neuropathy, calcification of VD and SV, hypogonadism, or low sexual desire (Table 3).

Unfortunately, careful history is still the key there is no test to diagnose DE/AE [133]. It starts by excluding RE, genital tract obstruction, anorgasmia, and other sexual dysfunctions that may be misdiagnosed as DE/AE, such as ED, a subtly decreased libido, ejaculatory pain, the partner's sexual dysfunction, sexual orientation conflicts, or paraphilic inclinations/interests (Table 4). A focused psychosexual evaluation is critical and typically begins by differentiating whether the complaint concerns DE/AE, the sensation of orgasm, or both. Attention should be given to identifying reversible factors such as poor glycemic control, hypogonadism low sexual desire, psychological factors, and genital infections. A focused clinical examination, laboratory tests, as well as radiologic imaging may help to diagnose these risk factors (Table 4). Sometimes the diagnosis of those risk factor(s) unfolds over time many clinical visits[134].

In this context, defining solid approaches for the treatment of DM-related DE/AE is difficult for a condition that the literature is restricted to case reports, case series, or small studies. It is assumed that intensive glycemic control may reduce the prevalence of diabetic autonomic dysfunction and might slow the deterioration of DM-related DE/AE; unfortunately, no article studying this effect has been published. If organic and iatrogenic reasons have been let off in DM-related DE/AE behavioral therapy may be considered[1]. Several drugs are recognized for the possible use in DE/AE. Those agents include; testosterone, amantadine, cyproheptadine, cabergoline, bupropion, yohimbine, buspirone, bethanechol, and others. Yet, no drug was approved for this indication[125]. Testosterone replacement therapy may be an appropriate option for DM-related DE/AE with decreased testosterone levels. However, in a clinical trial, in which diabetes is not an exclusion criterion, Paduch *et al*[82] reported that treatment of testosterone-deficient DE patients with a 2% solution of testosterone is not linked to improved perceived delay of ejaculation suggesting that testosterone deficiency is not the sole contributor to DE. Mechanistically, diabetic autonomic neuropathy is an important factor in the development of DM-related DE/AE that may affect neural systems at all levels of emission and ejection. Once diabetic autonomic neuropathy becomes clinically evident, there is no treatment to reverse it[135]. In the most severe cases, there may be a total lack of seminal emission leading to male infertility. If infertility is an issue, several approaches can be employed: (1) Assisted ejaculation by penile vibratory stimulation (PVS) is an option for sperm retrieval[136] because it is noninvasive and inexpensive[137]. However, DM patients frequently fail to obtain sperms by this method because it requires intact lumbosacral pathways[136,137]; (2) In cases in whom PVS fails, electroejaculation (EEJ) may be effective to retrieve spermatozoa[99,138]; and (3) If these procedures fail, surgical sperm retrieval can be tried through VD aspiration[139], percutaneous epididymal sperm aspiration (PESA) [140], or testicular sperm extraction (TESA)[141]. Using spermatozoa obtained by any of these procedures and utilizing intracytoplasmic sperm injection (ICSI), one can

attain clinical pregnancy and live birth rates in DM-related AE. However, the fertilization rate and high-quality embryo rate in diabetic PE patients are lower than in non-diabetic PE patients[140].

RE

RE is unique in that it is almost exclusively organic in origin. Despite being a common type of ejaculatory dysfunction, it is responsible for only 0.3%-2% of infertility[142, 143]. Specifically, young men with type 1 diabetes have a higher incidence of ejaculatory dysfunction estimated to be 5%-18% of cases due to diabetic neuropathy, which has been shown to cause male infertility[29,144,145].

RE is an ejaculation that is deposited into the posterior urethra but propelled backward into the urinary bladder. In the normal state, the bladder neck closes with high pressure under the sympathetic control during orgasm and the seminal bolus takes the route of least resistance, being antegrade. Diabetic neuropathy can interfere with the sympathetic fibers that provide for normal high-pressure bladder neck closure, causing a comparatively low-pressure route into the urinary bladder for semen[146].

Impairment of sympathetic innervation of the urinary bladder neck was supposed to be a cause of diabetic RE. Ibragimov *et al*[147] used the liquid profilometric technique to examine 3 groups of men: 8 patients with RE; 5 patients with DM without ejaculatory disorders; and 7 healthy subjects. Diabetic RE patients showed no elevation of the intraureteral pressure in the area of the inner sphincter of the urinary bladder, which evidenced its atony. In health the elevation of vesical pressure is usually accompanied by increased ureteral resistance, thus maintaining the stability of the positive pressure gradient and preventing the escape of urine. Correlation analysis revealed alterations of the interrelations between both intravesical and sphincter pressures in diabetes patients evidencing the disorders of somatic innervation of the outer ureteral sphincter being more pronounced in these patients.

DIAGNOSIS

RE can be partial or complete and the diagnosis is frequently suggested by the patient's report of cloudy urine following orgasm confirmed by a post-ejaculatory urine analysis that reveals sperm, seminal fluid, or fructose[148]. McMahon[149] endorsed that the post-orgasmic urine should be centrifuged and visualizing of 10-15 sperm/high-power field could confirm RE diagnosis whereas Fedder *et al*[150] defined RE as > 1 million sperms in a post-ejaculatory urine sample.

TREATMENT STRATEGIES

Infertility is usually the main concern in RE patients as the combination of dry orgasm and infertility makes the condition upsetting to the patient and his partner[151]. Therefore, many lines of therapeutic approaches were advocated, either medical or surgical, with limited success rates.

Medical treatment

It is based either on increasing the sympathetic tone of the urinary bladder or on decreasing the parasympathetic activity but the onset of side effects and the lack of response should be considered. Several treatments were proposed with varied results [152-161] (Table 5).

Endourethral collagen injection

Kurbatov *et al*[145] analyzed the long-term outcome of endourethral injection of volume-forming material (VFM) of collagen type 2 into the bladder neck submucosa in 23 patients with RE secondary to type 1 DM with complete RE refractory to imipramine. These patients were randomized with a 1: 1 ratio into 2 groups; group A (endourethral collagen type 2 injection) and group B (endourethral saline water injection). This technique included an endoscopic injection of VFM such as collagen into bladder neck submucosa. In group A, significant differences from baseline to 12 mo were detected relative to antegrade volume (mean difference: 0.71 mL), antegrade count (mean difference: 45.6 million/mL), antegrade total sperm motility (mean difference: 15.4%), and antegrade progressive sperm motility (mean difference: 8.4%).

Table 5 Studies involving medical treatment for reversal of diabetic retrograde ejaculation

Ref.	Dosage	Ejaculation after	n	No. of successes	Ejaculate volume (ml)	Sperm count (10 ⁶ /m)	Sperm motility (%)
Brompheniramine							
Andaloro <i>et al</i> [152]	16 mg/ d p.o.	12 h	1	1	Unclear	Unclear	Unclear
Budd[153]	16 mg/ d p.o.	3 d	1	1	Unclear	Unclear	Unclear
Chlorpheniramine + phenylpropanalamine							
Stewart <i>et al</i> [154]	50 mg/ d p.o.	Unclear	1	1	4.5	Normal	Normal
Ephedrine							
Gilja <i>et al</i> [155]	50 mg/ d p.o.	4 wk	17	3	Unclear	Unclear	Unclear
Arafa <i>et al</i> [156]	120 mg twice/ d	14 d	23	11	Unclear	Unclear	Unclear
Shoshany <i>et al</i> [157]	60 mg/6 h the day before test + 2 doses on test day	At the test	6	4	1.5	Unclear	17.8
Imipramine							
Brooks <i>et al</i> [158]	75 mg/ d p.o.	1 wk	2	2	3	1.72	33
Okada <i>et al</i> [159]	25-150 mg/ d	Unclear	7	3	Unclear	Unclear	Unclear
Gilja <i>et al</i> [155]	75 mg/ d p.o.	4 wk	14	2	Unclear	Unclear	Unclear
Eppel <i>et al</i> [160]	50 mg/ d p.o.	5 d	3	3	8	20	50
Arafa <i>et al</i> [156]	50 mg/ d p.o	14 d	23	10	Unclear	Unclear	Unclear
Imramine + pseudoephedrine							
Arafa <i>et al</i> [156]	50 + 120 mg/ d	14 d	23	16	Unclear	Unclear	Unclear
Amoxapine							
Hibi <i>et al</i> [161]	50 mg/ d	1 mo	1	1	0.2	213	53

It was concluded that correcting RE in type 1 DM patients could be accomplished with the endourethral injection of collagen type 2.

SPERM RETRIEVAL

Beyond using standard sperm retrieval techniques such as; TESE and PESA, 3 methods of sperm retrieval were recognized for managing infertility in RE patients. These techniques include; centrifugation and resuspension of post-ejaculatory urine specimens, the Hotchkiss (or modified Hotchkiss) technique, as well as ejaculation on a full urinary bladder.

Centrifugation and resuspension: To improve the conditions for the sperm, the patient is asked to either increase their fluid intake or to take sodium bicarbonate to dilute or alkalize the urine. A post-orgasmic urine sample is collected by either introducing a catheter or spontaneous voiding. This sample is centrifuged and suspended in a medium such as bovine serum albumin, human serum albumin, Earle's/Hank's, phosphate-buffered medium. The resultant modified sperm mixture can be used in assisted reproductive techniques (ART) (Table 6)[162-165]. In their meta-analysis in couples with the male partner with RE, Jefferys *et al*[142] reported a 15% pregnancy rate/cycle (0%–100%) after using the centrifugation and resuspension method.

Hotchkiss method: It involves emptying the urinary bladder before ejaculation by a catheter, washing out and instilling a small quantity of lactated Ringers to improve the ambient conditions of the bladder. The patient then ejaculates and the semen is retrieved by catheterization or voiding[166].

Modified Hotchkiss method: It involves a variance in the instillation medium. Pregnancy rates were 24%/cycle (0%–100%)[142]. Philippon *et al*[167] reported the largest series of births using frozen-thawed sperms retrieved from post-ejaculatory urine by a this technique that allows for successful association with sperm cryopreser-

Table 6 Semen parameters of studies recovering sperms from alkalized urine in diabetic premature ejaculation patients

Ref.	Medium installed	Post-masturbatory retrieval	No. of patients	Total sperm count (10 ⁶)	Total sperm motility (%)	Pregnancies
Brassco <i>et al</i> [163]	NaHCO ₃ 4 g	Voiding	3	91	28	3
Templeton <i>et al</i> [162]	NaHCO ₃	Voiding	1	Unclear	2-21	0
Shangold <i>et al</i> [164]	NaHCO ₃ 1.6 g	Voiding	1	30-240	0	5

vation, leading to efficient management of couples with refractory RE with an average live birth rate/transfer of 28%.

Ejaculation on a full bladder: The patient is encouraged to ejaculate on a full urinary bladder and semen is suspended in Baker's buffer [162].

EEJ

EEJ has been used to a restricted degree in diabetic men who have developed ejaculatory failure as a consequence of diabetic neuropathy. Gerig *et al* [131] described the experience of 2 male fertility programs using EEJ in managing men with ejaculatory failure secondary to DM. Overall, 29 EEJ procedures were performed in seven diabetic men with ejaculatory failure. Following EEJ, retrograde semen specimens retrieved from the urinary bladder contained a mean of 3444.5 million sperm (range 269.2-4996 million), mean sperm motility was 4% (range 0%-11%). Semen specimens were used for intrauterine insemination. It was concluded that EEJ can be successfully used to retrieve sperms from men with ejaculatory failure due to DM. That procedure requires general anesthesia, and the pregnancy rates after intrauterine insemination with the processed sperm were low. Therefore, AET could offer a practicable alternate, yielding higher success rates.

ICSI

ICSI-ART can greatly reduce the impact of sperm factors of infertility [167]. In cases of diabetic RE, TESA is combined with ICSI to treat infertility. Liu *et al* [168] assessed the effect of TESA-ICSI on first cycle ICSI-embryo transfer for type 2 diabetic patients in 1219 azoospermic patients or RE who were treated with TESA-ICSI classified into 2 groups; type 2 DM group ($n = 54$) and non-diabetic controls ($n = 1165$). There were no significant differences in clinical pregnancy, implantation, normal fertilization, or cleavage rates between these groups.

CONCLUSION

Ejaculatory dysfunction encompasses several disorders related to DM and its complications, such as PE, DE, AE, RE, ejaculatory pain, anesthetic ejaculation, decreased ejaculate volume, and decreased force of ejaculation. All these disorders should be looked for thoroughly during the clinical evaluation of diabetic men. Besides, introducing the suitable option and/or maneuvers to treat these disorders should be tailored according to each case.

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Diabetic patients with chronic kidney disease: Non-invasive assessment of cardiovascular risk

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Abstract

The prevalence and burden of diabetes mellitus and chronic kidney disease on global health and socioeconomic development is already heavy and still rising. Diabetes mellitus by itself is linked to adverse cardiovascular events, and the presence of concomitant chronic kidney disease further amplifies cardiovascular risk. The culmination of traditional (male gender, smoking, advanced age, obesity, arterial hypertension and dyslipidemia) and non-traditional risk factors (anemia, inflammation, proteinuria, volume overload, mineral metabolism abnormalities, oxidative stress, *etc.*) contributes to advanced atherosclerosis and increased cardiovascular risk. To decrease the morbidity and mortality of these patients due to cardiovascular causes, timely and efficient cardiovascular risk assessment is of huge importance. Cardiovascular risk assessment can be based on laboratory parameters, imaging techniques, arterial stiffness parameters, ankle-brachial index and 24 h blood pressure measurements. Newer methods include epigenetic markers, soluble adhesion molecules, cytokines and markers of oxidative stress. In this review, the authors present several non-invasive methods of cardiovascular risk assessment in patients with diabetes mellitus and chronic kidney disease.

Key Words: Diabetes mellitus; Diabetes complications; Chronic kidney disease; Atherogenesis; Atherosclerosis; Cardiovascular risk

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Core Tip: The culmination of traditional and non-traditional atherosclerosis risk factors in patients with diabetes mellitus and chronic kidney disease leads to fulminant and advanced atherosclerosis, consequently resulting in cardiovascular morbidity and mortality. Non-invasive cardiovascular risk assessment should therefore be performed in all these patients and can be based on standard laboratory parameters, cytokines and markers of oxidative stress, 24 h blood pressure measurements, ankle-brachial index, arterial stiffness parameters, imaging techniques and epigenetic markers. In this review article, we present different methods of non-invasive cardiovascular risk assessment in patients with diabetes mellitus and chronic kidney disease.

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INTRODUCTION

The burden of diabetes mellitus (DM) on global public health and socioeconomic development is heavy and is escalating. The International Diabetes Foundation has stated that in 2017, 451 million people worldwide have lived with DM and that this number would soar in the next couple of years and decades[1].

DM is the number one cause of chronic kidney disease (CKD) worldwide and is inherently linked with increased mortality mostly due to cardiovascular causes[2]. CKD is another major public concern with rising prevalence, which is now estimated at 9.1%[3]. In 2017, CKD resulted in 1.2 million deaths and was the 12th leading cause of death globally. Additionally, 7.6% of all cardiovascular deaths were due to CKD[4].

Cardiovascular disease in patients with DM and CKD is attributed to advanced and fulminant atherosclerosis, due to the presence and interplay of traditional [male gender, smoking, advanced age, obesity, arterial hypertension (AH), dyslipidemia] and non-traditional, CKD-specific risk factors (anemia, inflammation, proteinuria, volume overload, mineral metabolism abnormalities, oxidative stress, etc.)[5].

Due to the increased rate of cardiovascular events, prompt and timely cardiovascular risk assessment is crucial in reducing the morbidity and mortality of these patients[6]. In this review article, the authors present non-invasive methods of assessing cardiovascular risk in patients with DM and CKD (Figure 1).

STANDARD LABORATORY PARAMETERS

Estimated glomerular filtration rate

The diagnosis of CKD is based on functional and structural changes of the kidneys, with the former assessed by estimating or measuring the glomerular filtration rate (GFR) and albuminuria/proteinuria and the latter by using different imaging techniques and/or kidney biopsy. Multiple creatinine and/or cystatin C based equations are only an assessment of kidney function and have several limitations, but the alternative (measurements of GFR) is usually not available in routine clinical practice[7].

Reduced estimated GFR is an important marker of cardiovascular risk. Go *et al*[8] performed a study in which they estimated the longitudinal GFR among 1120295 adults in whom serum creatinine had been measured between 1996-2000 and who had not undergone dialysis or kidney transplantation. Of the included patients, 9.6% had concomitant DM. They found an independent, graded increase in cardiovascular deaths, events and hospitalization rates in those with reduced estimated GFR. The authors postulated that the relationship between reduced GFR and cardiovascular disease is partly due to the presence of several traditional atherosclerosis risk factors and partly due to the presence of several CKD-specific risk factors, such as increased levels of inflammation markers, hyperhomocysteinemia, abnormal apolipoprotein levels, enhanced coagulability, anemia, left ventricular hypertrophy (LVH), increased

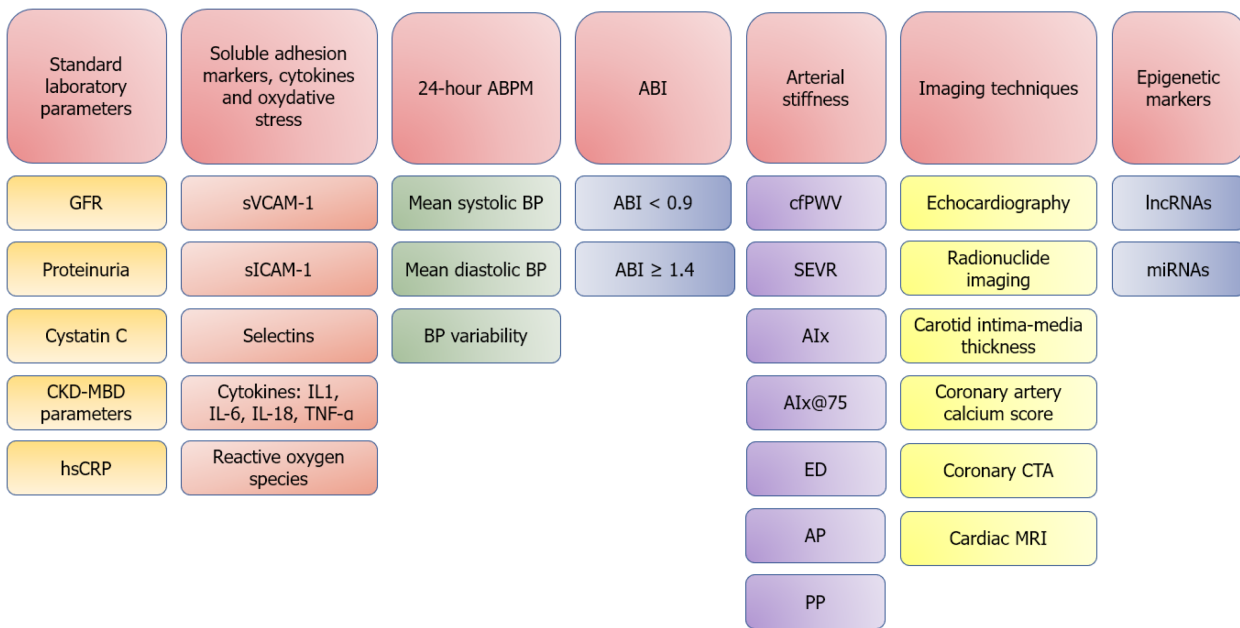


Figure 1 Non-invasive assessment of cardiovascular risk in patients with diabetes mellitus and chronic kidney disease. GFR: Glomerular filtration rate; CKD-MBD: Chronic kidney disease mineral bone disorder; hsCRP: High sensitivity C-reactive protein; sVCAM-1: Soluble vascular cell adhesion molecule-1; sICAM-1: Soluble intercellular adhesion molecule-1; IL-1: Interleukin-1; IL-6: Interleukin-6; IL-18: Interleukin-18; TNF-α: Tumor necrosis factor-α; ABPM: Ambulatory blood pressure measurements; BP: Blood pressure; ABI: Ankle-brachial index; cFPWV: Carotid-femoral pulse wave velocity; SEVR: Subendocardial viability ratio; AIx: Augmentation index; AIx@75: AIx adjusted for heart rate 75/min; ED: Ejection duration; AP: Augmentation pressure; PP: Pulse pressure; CTA: Computed tomography angiography; MRI: Magnetic resonance imaging; lncRNAs: Long non-coding ribonucleic acids; miRNAs: Micro-ribonucleic acids.

endothelial dysfunction, increased arterial stiffness and augmented arterial calcifications.

In a study by Wu *et al*[9], the authors found that reduced estimated GFR was an important hallmark of diabetic retinopathy, which is commonly associated with advanced diabetic nephropathy and increased cardiovascular risk as well. In a 1-year cross-sectional study by Babaliche *et al*[10], the authors found that reduced GFR in type 2 DM patients was significantly associated with a higher incidence of microvascular complications, such as diabetic neuropathy, retinopathy and nephropathy.

DM exerts its negative effects on kidney function through negative glomerular hemodynamic effects, especially through glomerular hyperfiltration, which is defined as an estimated GFR more than two standard deviations above the mean estimated GFR of healthy individuals. In a study performed on healthy, middle-aged individuals by Dupuis *et al*[11], the authors found that glomerular hyperfiltration is independently associated with higher cardiovascular risk, similar to the risk observed in patients with CKD stage 3A. Similar findings have been observed in several studies on patients with type 1 and type 2 DM, with and without previous cardiovascular disease[12-14]. Glomerular hyperfiltration was also associated with an increased incidence of coronary artery calcification and LVH, both important cardiovascular risk markers[15].

Proteinuria

Proteinuria (defined as urine protein excretion greater than 300 mg over 24 h) and moderately increased albuminuria (defined as urinary albumin excretion of 30-300 mg over 24 h) are usually signs of renal injury and can often be detected earlier than any tangible fall in GFR[16]. Both are strong and independent predictors of increased risk for all-cause and cardiovascular mortality in patients with and without DM. Additionally, both are risk factors for faster CKD progression as well and are therefore included in the KDIGO (kidney disease: Improving global outcomes) CKD staging system[16].

In a post-hoc analysis of the Reduction in Endpoint in Non-insulin dependent DM with the angiotensin II antagonist losartan trial, the authors found that proteinuria of 3 g or more per day was associated with a renal endpoint of doubling of creatinine or end-stage renal disease (ESRD) in 85% of patients and with a cardiovascular endpoint (defined as the composite of myocardial infarction, stroke, first hospitalization for heart failure or unstable angina, coronary or peripheral revascularization or cardiovascular death) in 44% of patients. In the same study, moderately increased

albuminuria was associated with an increased likelihood of kidney disease progression and cardiovascular risk as well, even after adjusting for estimated GFR and comorbidities[17].

The Strong Heart Study showed that patients with type 2 DM and proteinuria had worse left ventricular function and impaired diastolic left ventricular filling compared with patients without proteinuria[18]. According to studies, diabetic patients with proteinuria are at increased risk for peripheral artery disease (PAD)[19] and incident stroke as well[20].

In a Heart Outcome Prevention Evaluation (HOPE) substudy, a linear relationship between moderately increased albuminuria and cardiovascular events, especially in patients aged 55 years or more with previous cardiovascular disease or DM, was proven. In the same study, a higher incidence of systolic and diastolic dysfunction was found in patients with moderately increased albuminuria[21]. A study of 308 patients showed that patients with angiographic evidence of coronary artery disease (CAD) had higher urinary albumin levels than disease-free individuals and that urinary albumin excretion increased progressively with CAD severity[22].

All the above-stated studies confirm the fact that the detection and early recognition of moderately increased albuminuria and proteinuria is crucial in managing cardiovascular risk and the rate of CKD progression[23,24].

The exact pathophysiologic pathways that would explain the mechanism behind increased cardiovascular risk and proteinuria are still not known. It is postulated that the proteins that leak through damaged glomerular capillary endothelium cause tubulointerstitial injury and inflammation and subsequently lead to parenchymal damage, renal fibrosis and progressive decline in renal function[25]. The steno hypothesis suggests that urinary protein excretion signals a subclinical renal disease and systemic endothelial dysfunction and systemic inflammation[26]. Additionally, several thrombogenic factors, for example, von Willebrand factor, fibrinogen, cell adhesion molecules and tissue plasminogen activator have also been connected with proteinuria. It has been suggested that high platelet adhesiveness and erythrocyte aggregation demonstrated in diabetic patients with proteinuria could indicate increased thrombosis risk. Insulin resistance has been proven in patients with proteinuria, implying the role of hyperinsulinism in explaining the increased cardiovascular risk in these patients[26].

Cystatin C

Serum cystatin C is a low-molecular-weight, non-glycosylated protein from the family of cysteine protease inhibitors that closely approximates what could be considered an ideal marker of renal function because it is freely filtered by the glomerulus, reabsorbed and degraded completely by proximal tubule and is not secreted by the tubules. It is more sensitive than usual endogenous markers (serum creatinine and urea) used in kidney function assessment, especially in the early stages of CKD[27]. However, cystatin C can also be used as a cardiovascular risk marker having important prognostic implications in patients with different degrees of CKD[28].

According to a cross-sectional epidemiological study by Cepeda *et al*[29], elevated cystatin C was associated with an increased presence of several cardiovascular risk factors, such as DM, AH and CKD, along with higher levels of C-reactive protein (CRP), homocysteine and fibrinogen. Correa *et al*[30] performed a study on 4965 individuals after acute coronary syndrome in which they found a higher likelihood of adverse cardiovascular events in those with increased cystatin C, opening up a potential new role of cystatin C in risk stratification. Madero *et al*[31] performed an arterial stiffness study on 2468 individuals (24% diabetic) and found an association between cystatin C and increased arterial stiffness, especially in older patients. In two mortality studies, elevated cystatin C levels were associated with increased all-cause mortality, even in patients with normal renal function[32,33].

It has been suggested that cystatin C exerts its function through inhibition of lysosomal cathepsins, which leads to a reduction in atherosclerotic plaque degradation and increased risk of cardiovascular events[34].

Calcium, phosphate, parathyroid hormone, fibroblast growth factor-23 and vitamin D homeostasis

CKD mineral and bone disorder (CKD-MBD) refers to the clinical syndrome of laboratory abnormalities, bone disease and extraskeletal calcification, including the arterial system. Among the earliest manifestations of CKD-MBD are vitamin D deficiency, disordered calcium and phosphate homeostasis, elevated levels of parathyroid hormone and fibroblast growth factor-23 (FGF-23). These alterations lead

to an increased risk of ESRD, cardiovascular disease and mortality[35]. The amount of evidence is especially strong for elevated serum phosphate and FGF-23, both of which have direct negative cardiovascular effects through promoting LVH and consequent left ventricular dysfunction[36,37]. Several cross-sectional studies have demonstrated that vitamin D deficiency also increases the risk of developing AH, heart failure and sudden cardiac death, all through downregulation of the renin-angiotensin-aldosterone system, impaired insulin sensitivity, direct effects on the heart and vasculature and through worsened glycemic control[38,39].

The difference in CKD-MBD according to diabetes status has also been noticed. In a large descriptive study of patients with CKD stages 2-4, participants with DM had higher levels of serum phosphate, parathyroid hormone and FGF-23 and lower levels of vitamin D compared to patients without DM. Moreover, the elements of CKD-MBD evolved earlier in the course of CKD in diabetic patients, partly explaining the higher cardiovascular risk in diabetic CKD patients. An inverse relationship between the level of proteinuria and vitamin D was also observed, further confirming the importance of surveillance of mineral metabolism in diabetic CKD patients[40].

High-sensitivity CRP

Chronic, low-grade inflammation plays a grand role in the initiation and progression of atherothrombosis, metabolic disorders, AH, DM and renal disease[41]. High-sensitivity CRP (hsCRP) is an established inflammatory biomarker and is one of the most widely used markers associated with risk of cardiovascular events[42]. In the study by Ridker *et al*[43], 27939 presumed healthy American women were followed up for a mean of 8 years for incident myocardial infarction, ischemic stroke, coronary revascularization or death from cardiovascular causes. The authors found that cardiovascular events were more common in those with higher hsCRP levels, independent of traditional atherosclerosis risk factors. In the Cardiovascular Health Study, nearly 6000 subjects were followed up for 3-4 years, and their inflammatory markers were measured before and after completed follow-up. The results of the study showed that those with higher baseline hsCRP values were more likely to develop DM in the follow-up period[44]. An association has also been found between higher values of glycated hemoglobin and hsCRP, suggesting the role of systemic inflammation in diminished insulin sensitivity and suboptimal glycemic control[45].

Interestingly, studies have not shown uniform results regarding the role of hsCRP as a marker of cardiovascular risk in diabetic patients. In a pooled analysis of 25797 patients from four different United Kingdom prospective cohort studies, hsCRP was linked to increased risk of cardiovascular events and mortality only in patients without DM[46]. Similar results were found in the Jager *et al*[47] study and in the Strong Heart Study as well[48]. In the Diabetes Heart Study, hsCRP was analyzed in 846 type 2 DM patients who had follow-ups for a mean period of 7.3 years. On the contrary to other studies, baseline hsCRP was a strong predictor of mortality in this group of patients[49].

Elevated hsCRP has been found to be an important marker of acute kidney injury, subclinical kidney injury, incident CKD and CKD progression[50,51]. Sinha *et al*[52] found that higher baseline hsCRP is associated with incident diabetic nephropathy. In a study by Jalal *et al*[53] in which 3166 elderly subjects were included (18% diabetics), high hsCRP was associated with a higher likelihood of major adverse cardiovascular events. In a meta-analysis by Li *et al*[54] on CKD and ESRD patients, hsCRP was associated with a significantly higher risk of cardiovascular morbidity and mortality. Besides being an important biomarker of cardiovascular risk, a change in hsCRP can be a sign of changed renal and consequently cardiovascular risk profile. Liu *et al*[55] found that a reduction in hsCRP favored kidney outcomes in patients with impaired glucose metabolism or DM, showing that serial measurements of hsCRP can be indicative of change in systemic inflammation and atherogenesis.

SOLUBLE ADHESION MOLECULES, CYTOKINES AND OXIDATIVE STRESS

Inflammation underlies all stages of atherosclerotic plaque formation, even in the early stages where inflammatory cells adhere and infiltrate the subendothelium. The two most important adhesion molecules that play a major role in atherosclerosis are vascular cell adhesion molecule-1 (VCAM-1) and intercellular adhesion molecule-1 (ICAM-1). Selectins are another group of adhesion molecules and are found on leukocytes, endothelial cells and thrombocytes[56]. Cell adhesion molecules and

selectins can be broken off into the circulation and can be measured in the serum. Soluble adhesion molecules have shown potential as biomarkers of cardiovascular risk [57].

Increased levels of soluble VCAM-1 (sVCAM-1) and soluble ICAM-1 (sICAM-1) have been found in diabetics with increased stages of CKD [57,58]. In a study by Bavbek *et al* [56], increased serum levels of selectins were associated with microvascular complications of DM, including proteinuria and decreased estimated GFR. Becker *et al* [59] demonstrated increased 10-year cardiovascular mortality in diabetic patients with increased sICAM-1 levels, independent of other known traditional cardiovascular risks. Both sICAM-1 and sVCAM-1 were higher in elderly patients with type 2 DM with cerebrovascular and cardiovascular disease [60,61].

Another important component of the inflammatory process in atherosclerosis are cytokines and their receptors. Interleukin (IL)-2 receptor has been associated with increased carotid intima-media thickness (IMT) and advanced atherosclerosis in hemodialysis patients [62]. Population-based studies have shown that inflammatory cytokines are strong predictors of the development of DM and are also important in the development of micro- and macrovascular complications in diabetic patients [63]. IL-1, IL-6, IL-18 and tumor necrosis factor- α enhance the expression of ICAM-1, VCAM-1 and selectins, affect the dynamics of the mesangial matrix, lead to glomerular basal membrane thickening, alter glomerular hemodynamics and lead to renal toxicity [64,65]. Cytokines can also lead to dysregulation between antioxidative mechanisms and the formation of reactive oxygen species, such as superoxide anions, hydrogen peroxide and hydroxyl radicals. Ineffective antioxidant capacity or excess reactive oxygen species is implicated in the development and progression of renal and cardiovascular disease through several pathophysiologic mechanisms, including through direct tissue toxicity and promotion of further inflammation [66-68].

TWENTY-FOUR HOUR AMBULATORY BLOOD PRESSURE MEASUREMENTS

In patients with AH, multiple blood pressure measurements during longer periods of time [for example 24 h ambulatory blood pressure measurements (ABPM)] are more likely to predict cardiovascular risk and are therefore superior to those obtained in the doctor's office for estimating the risk of future cardiovascular morbidity and mortality [69].

In a population-based prospective study on 1700 Danish people by Hansen *et al* [70], the authors found that 24 h ABPM was an important prognostic tool in assessing subjects' cardiovascular risks and that isolated ambulatory systolic hypertension as well as blunted decrease in blood pressure during the night were both prognostically unfavorable. The percentage of DM was higher in the sustained high blood pressure group (4.3%) compared to the isolated ambulatory hypertension group (2.8%), isolated office hypertension group (1.3%) and normotensive group (1.2%).

In a cohort study by Grezzana *et al* [71] that included 569 hypertensive patients, the 24 h ABPM showed a predictive result for new cases of atrial fibrillation and a combination of cardiovascular outcomes, mortality and hospital admissions. In a study by Iqbal *et al* [72] in which 1187 individuals were included, significant associations were found between cerebrovascular events and absent nocturnal drop in blood pressure ($\leq 10\%$), between high day time diastolic blood pressure, PAD and morning surge $\geq 20/15$ mmHg and between cardiac arrhythmias, high day time and nighttime diastolic blood pressure.

In patients with and without DM, 24 h ABPM is superior to office recordings in terms of recognizing masked and white coat hypertension [73]. A lack of nocturnal dip in blood pressure is suggestive of autonomic neuropathy and is commonly observed in diabetic patients and can very commonly be a sign of concomitant obstructive sleep apnea, which is a known cardiovascular risk factor [74]. In a study by Eguchi [75] performed on patients with type 2 DM, 24 h systolic blood pressure was significantly correlated with silent cerebral infarcts and LVH, even more so than the values of glycosylated hemoglobin, indicating that perhaps uncontrolled hypertension is the main cause of accelerated atherosclerosis and increased cardiovascular risk in this population.

Like DM, CKD is also associated with a distinctive blood pressure profile, resulting in undiagnosed hypertension, which is a major factor in a continuing decline in kidney function. Manios *et al* [76] demonstrated that short-term blood pressure variability is more pronounced in CKD patients, rendering office measurements obsolete and

imprecise in this population. Similar studies have confirmed these findings and additionally showed a larger presence of non-dippers and patients with masked hypertension in the CKD group as well[77]. Decreased diurnal blood pressure variation is independently associated with a faster decline in kidney function[78] and with increased cardiovascular mortality in CKD patients[79]. In the prospective African American study of kidney disease and hypertension cohort study of 617 CKD patients, Gabbai *et al*[80] demonstrated that 24 h systolic blood pressure predicted both kidney and cardiovascular outcomes. Wang *et al*[81] studied a large ($n = 1219$) cohort of diabetic and non-diabetic CKD patients and found that blood pressure load and ABPM levels were independently correlated with left ventricle mass index, estimated GFR and proteinuria in all groups of CKD patients. Besides CKD stages 2-4, studies have shown an adverse cardiovascular profile in ESRD patients with elevated 24 h systolic blood pressure and a non-dipping ABPM profile as well[82-84].

ANKLE-BRACHIAL INDEX

PAD is usually diagnosed by ankle-brachial index (ABI) < 0.9 and can be considered a clinical model for atherosclerosis. It is the result of structural and functional vessel wall aberrations, resulting in limb ischemia and changes in pulse wave propagation, ultimately impacting the myocardium as well[85]. PAD is an independent risk factor for stroke, myocardial infarction and cardiovascular death, and the risk is even more apparent in diabetic patients[86]. In a study by Li *et al*[87] that was performed on 1647 patients with type 2 DM, low ABI (≤ 0.9) was independently associated with a high risk of all-cause and cardiovascular mortality. In a retrospective study by Alves-Cabrato *et al*[88] in which 34689 patients with type 2 DM were included, the authors found that even ABI in the lower normal range (0.91-1.00) was associated with significantly increased risk for nephropathy, retinopathy, acute myocardial infarction and mortality. In the same study, high ABI (> 1.3) was a marker of increased medial calcinosis and was associated with cardiovascular complications, most likely due to increased arterial stiffness, directly leading to increased cardiac workload, left ventricular hypertrophy, myocardial fibrosis, ischemia and arrhythmias[89].

CKD patients are especially prone to complications of atherosclerosis, PAD, calcifications of arterial walls and increased arterial stiffness[90]. According to the Cardiovascular Health Study, in which 4.513 community-living subjects aged 65 years or more were enrolled (15.3% diabetics), CKD was associated with both high (> 1.4) and low (< 0.9) extremes of ABI, which was explained by advanced atherosclerosis and increased vessel wall calcifications in this subgroup[90]. The prevalence of medial calcinosis has been shown to be even higher in patients on hemodialysis[91]. The results of the prospective NEFRONA study, in which 2445 CKD and 559 non-CKD subjects were included, showed higher prevalence of PAD in CKD patients and a rising prevalence of ABI > 1.4 in advanced stages of CKD. DM was the only factor predicting both pathological values of ABI in all CKD stages[92].

Both high and low ABI measurements play a role in assessing cardiovascular risk and renal outcome. According to a study by Chen *et al*[93] in which 436 CKD patients were enrolled (36.9% with DM type 2), reduced ABI (< 0.9) was associated with a more rapid decline in renal function and with a higher incidence of cardiovascular events. Similar association was found between renal function, cardiovascular events and high ABI[94]. In a study on 52 hemodialysis patients by Bevc *et al*[95], survival analysis showed higher risk for cardiovascular death in patients with ABI > 1.4 . It appears that the systemic nature of atherosclerosis is only partly responsible for these effects of changed ABI and that increased arterial stiffness and consequent hemodynamic changes play an integral role as well[96].

ARTERIAL STIFFNESS PARAMETERS

Increased arterial stiffness is recognized as a surrogate endpoint for cardiovascular disease and is the result of several structural alterations in the arterial walls, leading to reduced distensibility and decreased buffering capacity of arteries to pulsatile cardiac ejection[97].

Applanation tonometry is a non-invasive, easily reproducible technique often used for measuring arterial stiffness. It enables us to perform pulse wave analysis on the radial artery, giving us information on indirect parameters of central arterial stiffness and blood supply to the endocardium of the heart[98]. It also allows us to measure

carotid-femoral pulse wave velocity (cfPWV) on the carotid and femoral arteries, which is the most precise way to non-invasively determine central arterial stiffness [99]. All the applanation tonometry-derived arterial stiffness parameters are presented in Table 1.

Increased arterial stiffness is a well-known risk factor for major cardiovascular events. Weber *et al*[100] performed a prospective study on 465 male patients undergoing coronary angiography and found that augmentation pressure, augmentation index (AIx), and AIx@75 (AIx adjusted for heart rate 75/min) were strong predictors of obstructive CAD. Prskalo *et al*[101] performed a study on 160 patients with CAD undergoing elective coronary angiography and found that increased values of PWV and AIx were associated with a more advanced CAD, a higher likelihood of in-stent restenosis and left main CAD. An association between PAD and increased arterial stiffness has also been described[96]. A prospective Rotterdam study involving 2835 volunteers aged 55 years or more reported that subjects with higher values of cfPWV had a higher risk of coronary and cerebrovascular events[102]. A population Hoorn study included 261 healthy subjects and 358 patients with prediabetes or diabetes and found that the latter group had significantly higher values of cfPWV and AIx, indicating increased arterial stiffness in patients with impaired glucose metabolism[103]. In a 2015 meta-analysis by Prentner *et al*[104], increased arterial stiffness (in most studies determined with cfPWV and AIx) correlated with higher mortality and a more advanced target organ damage (nephropathy, neuropathy and retinopathy) in diabetic patients. Laugesen *et al*[105] demonstrated that female patients with DM have the lowest values of subendocardial viability ratio (SEVR) compared to men with and without DM, indicating impaired subendocardial perfusion and endothelial dysfunction in this population.

Briet *et al*[106] performed a study on 95 patients with CKD (GFR measured with ⁵¹Cr-EDTA clearance; 11% diabetics) and 121 hypertensive patients without CKD (GFR estimated with the use of Modification Diet in Renal Disease equation; 5% diabetics). They found that patients with CKD presented with increased arterial stiffness, determined by higher values of cfPWV. They explained their findings by the higher presence of DM and other traditional and non-traditional atherosclerosis risk factors in the CKD group. According to Sedaghat *et al*[107], the correlation between CKD and arterial stiffness is reciprocal, suggesting that besides being the result of CKD, increased arterial stiffness can lead to a faster CKD progression as well. A similar finding was found in a study by Fountoulakis *et al*[108], which was performed on diabetic patients with CKD. Proteinuria has also been linked to higher cfPWV and reduced SEVR and ejection duration[109,110].

Di Micco *et al*[111] performed a prospective, 3-year study involving 212 patients with CKD stages 3 and 4. During the study period, 34 patients died, 29 of them due to cardiovascular causes. Patients with lower SEVR had higher mortality. Post-mortem evaluation showed a higher degree of coronary artery calcification and a larger myocardial mass in patients with previously lower values of SEVR. Ekart *et al*[112] performed a study on non-dialysis CKD patients (27% diabetics) and found that SEVR < 130% predicted fatal and non-fatal cardiovascular events.

In a study by Kimoto *et al*[113], the authors found that the degree of CKD-associated increase in arterial stiffness varies among arterial regions in type 2 DM and is predominantly increased in the aorta. This has clinical implications because aortic stiffness is a strong and independent predictor of cardiovascular death, as shown in ESRD, DM, hypertensive and elderly patients.

IMAGING TECHNIQUES

Echocardiography

Structural and functional changes of the heart muscle are pivotal in understanding the increased cardiovascular risk in patients with DM and CKD. Both entities are related to macrovascular and microvascular pathology, resulting in increased myocardial fibrosis and subsequently in systolic and diastolic dysfunction[114,115]. It appears as though these changes are even more pronounced in the uremic milieu and are most likely intensified through myocardial calcifications in CKD patients[116]. Several studies have shown an independent association between DM, LVH and reduced systolic function of the left ventricle, both of which are commonly linked to an increased likelihood of sudden cardiac death, mostly due to arrhythmias[114,117,118]. LVH is especially common in CKD patients as it is linked to common comorbidities in these patients (AH, DM) and to CKD-specific factors, for example, volume overload,

Table 1 Arterial stiffness parameters and their definitions[98,99]

Arterial stiffness parameter	Definition
cfPWV (m/s)	Pulse wave distance between two measuring sites (carotid and femoral artery) divided by pulse transit time (measured by electrocardiographic monitoring)
PP (mmHg)	Difference between systolic and diastolic pressure
AP (mmHg)	Difference between systolic and inflection pressure
AIx (%)	AP divided by PP
AIx@75 (%)	AIx adjusted for heart rate at 75 beats per minute
ED (ms)	Duration of left ventricular systolic ejection
EDI (%)	The ratio of the duration of systolic ejection to the total duration of the heart cycle
SEVR (%)	The diastolic area under the curve divided by the systolic area under the curve, derived from the pulse wave curve

cfPWV: Carotid-femoral pulse wave velocity; PP: Pulse pressure; AP: Augmentation pressure; AIx: Augmentation index; AIx@75: AIx adjusted for heart rate 75/min; ED: Ejection duration; EDI: Ejection duration index; SEVR: Subendocardial viability ratio.

hyperphosphatemia and elevated levels of FGF-23. The clinical significance of LVH is prognostically unfavorable and is linked to increased cardiovascular mortality in patients with different degrees of CKD, including those on hemodialysis[119,120]. An additional strength of echocardiography is shown in a study by Di Cori *et al*[121], in which the authors found important subclinical dysfunction in asymptomatic type 1 DM patients aged under 40 years by using strain, strain rate and integrated backscatter. A similar finding was demonstrated in a study by Ha *et al*[122], in which the authors presented the importance of tissue Doppler indexes for unmasking subclinical myocardial ischemia. The prevalence of diastolic dysfunction, left atrial fibrosis and left atrial enlargement is also higher in patients with DM and CKD. All of the mentioned changes are a reflection of structural myocardial disease and are markers of increased cardiovascular risk as well[123].

Radionuclide imaging

Regadenoson-stress single-photon emission computed tomography (SPECT) is particularly appealing for cardiovascular risk assessment in asymptomatic diabetic patients [124]. The cause of concern in this population is silent myocardial ischemia and the data on the prevalence of this condition have been disparate. In the prospective detection of ischemia in asymptomatic diabetics study, which included asymptomatic patients with type 2 DM, a 22% prevalence of any perfusion defect or left ventricle dysfunction by SPECT was detected, and in 6% of patients, a moderate to large myocardial ischemia was found[125]. In a more recent analysis of 1354 asymptomatic patients (302 without DM) a lower prevalence of myocardial ischemia was found (7.2%). An important finding of the study was a much higher prevalence of silent ischemia observed in diabetic patients (12.5% *vs* 5.6%)[126]. The Basel asymptomatic high-risk diabetes outcome trial prospectively recruited 400 asymptomatic patients with type 2 DM. In the study, nearly a quarter of asymptomatic patients had silent myocardial ischemia, which was associated with a worse outcome and a higher likelihood of major adverse cardiovascular events[127]. The yield of SPECT can be further improved by choosing patients with higher basal cardiovascular risk, especially patients with certain other comorbidities, such as CKD. According to studies, abnormal SPECT is a good indicator of future acute coronary events and cardiovascular disease in diabetic and non-diabetic CKD patients[128]. Conversely, a normal SPECT is associated with a fairly good cardiovascular outcome in CKD patients, but it should be noted that due to accelerated coronary atherosclerosis in patients with CKD stages 4 and 5, a normal SPECT testing is still linked to higher cardiovascular risk compared to patients with better renal function[129]. In these patients, continuous follow-up is pivotal in preventing major adverse cardiovascular events[130].

Carotid intima-media thickness

Carotid IMT is an ultrasound-based, non-invasive measurement of atherosclerosis burden. It is used to investigate the determinants and consequents of atherosclerosis

and has been used as a surrogate end-point and a therapeutic target in some clinical trials as well[131,132].

Several clinical studies have demonstrated the association between the presence of atherosclerotic plaques in the carotid arteries, increased carotid IMT and atherosclerosis in other vascular territories[133]. Bots *et al*[134] have shown that patients with an increased carotid IMT have a higher likelihood of having advanced atherosclerotic plaques in the abdominal aorta. In a study by Ogata *et al*[135], a significant correlation between left main coronary atherosclerosis (determined by intravascular coronary ultrasound) and increased carotid IMT was observed. A positive association was also found for patients with symptomatic CAD, cerebrovascular disease and patients with PAD[136]. A descriptive, cross-sectional study was performed by Gómez-Marcos *et al* [137] in which they found an increased carotid IMT in patients with DM compared to patients without DM, and the difference was even greater in patients with advanced age. Signs of carotid damage were found in 23% of patients with DM. In a study by Matsagoura *et al*[138] that included patients with type 2 DM, an increased carotid IMT was observed in patients with moderately increased albuminuria or proteinuria compared to patients without proteinuria.

Kota *et al*[139] demonstrated a higher risk for ischemic stroke in type 2 DM patients with increased thickness of carotid intima-media. Sunil Kumar *et al*[140] performed a study on 30 patients with ESRD in which they found increased carotid IMT in these patients. They found the measurements to be an easy, non-invasive, easily-reproducible and cost-effective investigation in assessing cardiovascular risk in patients with chronic kidney failure. According to a study by Ekart *et al*[141], carotid IMT correlated with higher blood pressure in hemodialysis patients. In a study by Lawal *et al*[142], carotid IMT correlated with many cardiovascular risk factors among CKD patients, serving as a potential surrogate marker for cardiovascular disease in these patients. Roumeliotis *et al*[143] performed a study on 142 diabetic patients with different stages of CKD. Patients with increased carotid IMT had higher all-cause and cardiovascular mortality and had a higher degree of atherosclerosis in other vascular territories, further confirming the important role of carotid IMT measurements in recognizing patients with higher cardiovascular risk.

Coronary artery calcium score

High coronary artery calcium (CAC) score is associated with advanced atherosclerosis and with a 4-10-fold increase in the incidence of cardiovascular disease, independent of other risk factors[144]. Diabetic patients harbor larger amounts of CAC than non-diabetic patients of similar age[145]. Additionally, asymptomatic diabetic patients have a similar CAC than non-diabetic patients with known CAD[146]. In the coronary artery calcification in type 1 diabetes study, 656 adult patients with type 1 DM had higher CAC compared to 764 age- and sex-matched individuals without DM, with no differences between genders. Extensive vascular calcifications were registered even in younger patients with type 1 DM (17-28-years-old)[147]. The extent of CAC has also shown an important positive association with SPECT-registered myocardial ischemia, cardiovascular events and mortality[148,149]. Anand *et al*[150] followed 392 patients with type 2 DM and found that CAC progression was among the best predictors of increased cardiovascular risk.

Patients with CKD exhibit a higher prevalence of vascular calcification than the general population. In a 10-year prospective study on 137 CKD patients, the authors found that severe CAC was an important predictor of cardiovascular mortality[151]. Krajnc *et al*[152] compared CAC score between patients on hemodialysis and diabetic patients without renal involvement and found higher CAC score in the hemodialysis group, with the difference between both groups especially evident in the very high risk CAC score category. Besides being an adverse prognostic sign, higher CAC has been associated with faster progression of CKD to ESRD[153]. According to a study by Cano-Megias *et al*[154], the synergistic effect of DM and CKD leads to an even higher CAC score, increased inflammation and higher mortality compared to patients without DM, showing the importance of higher CAC in cardiovascular risk assessment of diabetic CKD patients.

Coronary computed tomography angiography

Coronary computed tomography angiography (CTA) is a non-invasive imaging modality that provides a detailed and comprehensive evaluation of the presence and the extent of CAD. According to a study by de Araújo Gonçalves *et al*[155], DM is an independent predictor of CAD and is associated with a more advanced CAD and a higher prevalence of atherosclerotic plaques in every anatomical subset of coronary arteries, all evaluated with the use of coronary CTA. An important obstructive CAD

was observed even in asymptomatic diabetic patients[156]. An additional important advantage of coronary CTA was found in a study by Madaj *et al*[157] in which they studied the presence of CAD in younger patients with type 1 and 2 DM. They found that coronary CTA detects CAD even in patients with a normal CAC score, which can be explained by a higher percentage of non-calcified plaques in younger patients with diabetes, rendering the CAC score less useful in this context. In diabetic CKD patients, coronary CTA is useful in determining the extent of CAD and atherosclerotic plaque characteristics; in CKD patients, a trend towards non-obstructive calcified plaques has been noticed[158]. There is, however, a reason for cautious use of coronary CTA in patients with advanced stages of CKD because of the risk of contrast-induced nephropathy[159].

Cardiac magnetic resonance imaging

Cardiac magnetic resonance imaging (CMRI) provides important prognostic information and aids in risk stratification in most cardiovascular diseases. It is a non-invasive imaging modality that can visualize myocardial scarring, myocardial steatosis and triglyceride content, interstitial fibrosis and interstitial myocardial edema. It is also useful in the evaluation of coronary arteries, valvular pathology, and in the differentiation of cardiomyopathies[160]. Diabetic patients are at risk of developing severe cardiomyopathy, partly due to CAD and partly due to metabolic derangements. The presence of late gadolinium hyperenhancement as a marker of prior myocardial infarction is associated with a 4-fold increased risk of a major adverse cardiovascular event and with a 7-fold increased risk of mortality[161]. Late gadolinium hyperenhancement was demonstrated in 4.3% of asymptomatic type 1 DM patients in the diabetes control and complications trial/epidemiology of diabetes interventions and complications trial[162] and 17% of asymptomatic diabetic older patients in a community-based study in Iceland[163].

T1 mapping is useful in assessing the amount of extracellular volume and interstitial fibrosis. Wong *et al*[164] demonstrated high short-term mortality in non-diabetic patients with increased extracellular volume. Some studies have shown increased extracellular volume and diastolic dysfunction in diabetic patients as well[165,166]. By using spectroscopy, myocardial lipid content can be assessed, which is an important pathophysiological step in understanding left ventricular dysfunction in diabetic patients[167]. Adenosine stress MRI test has excellent characteristics for the detection of obstructive CAD and microvascular dysfunction in patients with DM[168] and CKD patients as well[169]. Myocardial fibrosis is a hallmark of progressive CKD, uremic cardiomyopathy and is a crucial cause of increased cardiovascular risk in these patients[170]. Concerns relating to an association between gadolinium contrast agents and nephrogenic systemic fibrosis have led to the use of lower doses, lower risk gadolinium agents and even native CMRI in CKD patients, which is an important step forward in the wider use of CMRI in this subgroup of patients[171]. In the Graham-Brown *et al*[172] study on hemodialysis patients, a native CMRI was performed. The authors found an increase in myocardial fibrosis and interstitial edema, mostly in the septal region of the heart. By applying a similar methodology, Rutherford *et al*[170] showed that these findings were independent of patient's fluid status. In a study by Edwards *et al*[173] on CKD patients stages 2-4, a low dose gadolinium method was used. They found increased interstitial fibrosis and myocardial dysfunction in these patients, and the finding was not dependent on blood pressure. CMRI has a proven role in the understanding of uremic cardiomyopathy, ventricular dysfunction, myocardial fibrosis and cardiovascular risk assessment in patients with early and advanced CKD[171].

EPIGENETIC MARKERS

Epigenetics is the study of gene expression and involves phenotypic changes without changes in genotype. Several studies have confirmed that epigenetic regulations are crucial in the pathogenesis of atherosclerotic plaque formation, vessel wall inflammation and plaque rupture, in a cell-type and stage-specific manner[174,175]. Three epigenetic mechanisms are important in atherosclerosis: DNA methylation, post-translational modification of histones and the activity of non-coding ribonucleic acids (RNAs), most commonly long non-coding RNAs and micro RNAs (miR)[176]. The expression of non-coding RNAs can be measured in peripheral blood, urine and saliva using microarrays, indicating the potential of these markers as diagnostic tools and future therapeutic targets[177,178].

Several long non-coding RNAs are linked to LVH, myocardial infarction, heart failure and mortality[179]. Polymorphisms and increased expression of miR-124a, miR-375 and miR-146a are associated with obesity, insulin resistance and increased incidence of type 2 DM[180,181]. miR-27 exerts negative effects on adipogenesis and is associated with decreased incidence of DM[182]. In a study by Buraczynska *et al*[183], miR-196a2 has been linked to an increased likelihood of cardiovascular events in diabetic patients. miR-4513 is overly expressed in patients with metabolic syndrome and DM and is associated with major cardiovascular events, especially acute coronary syndrome[184]. Endothelial dysfunction is an important factor in CKD patients and according to a study by Kétszeri *et al*[178], miR-142-3p expression is linked to preventing endothelial dysfunction.

Non-coding RNAs are a marker of increased cardiovascular risk and can be employed to determine the risk of developing and/or progressing CKD in patients with DM. According to studies, several long non-coding RNAs (ERBB4-IR, MGC, ENSMUST00000147869) are centrally involved in the development and progression of CKD in patients with DM, either *via* direct pathogenic roles or as indirect mediators of different nephropathic and profibrotic pathways[185]. The upregulation of profibrotic miR-192 and miR-21 was confirmed to be linked to renal fibrosis, development and progression of CKD in diabetic patients[186]. Vice versa, reduced expression of anti-fibrotic miR-29 and miR-200 was also associated with more advanced kidney disease [187,188]. The downregulation of miR-30s, miR-124 and miR-93 has been shown to lead to increased podocyte injury and proteinuria[186]. In a study by Abdelsalam *et al* [189], miR-451 is a highly specific marker of CKD chronicity in patients with DM. In a study by Fourdinier *et al*[190], decreased serum levels of miR-126 and miR-223 were found in patients with advanced CKD with DM and were linked to increased mortality due to cardiovascular causes. It appears that the potential of non-coding RNAs is vast but currently of limited clinical importance due to high cost, limited availability and non-specificity of different molecules[176].

CONCLUSION

Due to the increasing burden of DM and CKD, the prevalence of the cardiovascular disease will continue to rise. To reduce morbidity, mortality and socioeconomic burden of these patients, immediate cardiovascular risk assessment is pivotal. Fulminant atherosclerosis, a hallmark of diabetic patients with CKD is a complex process, involving the interplay between traditional and non-traditional, CKD-specific risk factors, culminating in endothelial dysfunction, inflammation, plaque formation and ultimately target organ ischemia and damage. Due to the multifaceted process, it appears that a multimarker approach should be used to recognize patients with the highest risk for cardiovascular events. In the future, more attention should be given to the decrease in prevalence of DM and prevention of CKD development in diabetic patients.

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Mechanisms of altered bone remodeling in children with type 1 diabetes

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Abstract

Bone loss associated with type 1 diabetes mellitus (T1DM) begins at the onset of the disease, already in childhood, determining a lower bone mass peak and hence a greater risk of osteoporosis and fractures later in life. The mechanisms underlying diabetic bone fragility are not yet completely understood. Hyperglycemia and insulin deficiency can affect the bone cells functions, as well as the bone marrow fat, thus impairing the bone strength, geometry, and microarchitecture. Several factors, like insulin and growth hormone/insulin-like growth factor 1, can control bone marrow mesenchymal stem cell commitment, and the receptor activator of nuclear factor- κ B ligand/osteoprotegerin and Wnt- β catenin pathways can impair bone turnover. Some myokines may have a key role in regulating metabolic control and improving bone mass in T1DM subjects. The aim of this review is to provide an overview of the current knowledge of the mechanisms underlying altered bone remodeling in children affected by T1DM.

Key Words: Type 1 diabetes; Children; Bone remodeling; Osteoclasts; Osteoblasts

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Core Tip: Bone fragility is a well-known complication related to type 1 diabetes mellitus, and it can manifest from the disease onset, already in childhood. The mechanisms underlying this relationship, and the precise role of metabolic control in preventing bone impairment, are not yet fully understood. Future studies are needed to clarify better the factors responsible for bone damage in diabetic subjects, and to identify strategies for avoiding and managing osteopenia/osteoporosis in these subjects.

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INTRODUCTION

Type 1 diabetes mellitus (T1DM) is a common endocrine disease that affects approximately 500000 children and adolescents worldwide. Moreover, in the last decade the incidence has been rising and the age at onset dropping[1]. Micro and macrovascular T1DM-related complications may already have developed a few years after disease onset[2] and are correlated with the age at onset, diabetes duration, body mass index, and pubertal development[3-5]. Hyperglycemia is the main systemic risk factor for diabetic complications, although multiple biochemical pathways, such as the formation of advanced glycation end products, oxidative stress, endoplasmic reticulum stress, inflammatory cytokines, and kallikrein-bradykinin activation, link the adverse effects of hyperglycemia with the microvascular dysfunction[6]. Consequently, long-term glycemic control is considered the most important modifiable factor to delay the onset, as well as the progression of microvascular complications, as clearly demonstrated by The Diabetes Control and Complications Trial[7]. In addition, beyond the effect of glycemic control, the impairment of some protective factors, such as insulin and insulin-like growth factor-1 (IGF1), may contribute to the vascular damage over time[8].

Recently, it was recognized that autoimmune diabetic disease also affects the skeleton[9-11]. In T1DM, a reduced bone mass may be present at an early stage after diagnosis[11], but it is unclear whether it is the duration of diabetes or degree of glycemic control that may induce a lifelong increased risk of fractures[12]. The association between glucose metabolism and bone-fat tissue interactions[13,14], as well as muscle-bone crosstalk, has been clearly demonstrated[15]. In particular, the skeleton acts as an endocrine organ, by modulating glucose tolerance through the secretion of bone-specific proteins, in particular osteocalcin (OCN). Furthermore, proteins involved in bone remodeling, like osteoprotegerin (OPG), are associated with an impaired insulin function[16].

The aim of this review is to provide an overview of current knowledge of the mechanisms underlying altered bone remodeling in children affected by T1DM.

FACTORS INFLUENCING BONE MASS ACCRUAL IN T1DM CHILDREN AND ADOLESCENTS

Childhood and adolescence are the critical ages for linear growth, bone mineral accrual, and the attainment of the peak bone mass, which is a key determinant of the lifelong risk of osteoporosis[17,18]. Therefore, osteoporosis prevention begins by improving bone mineral gains during an individual's years of growth[19]. During peripuberty, the bone mineral content and bone mineral density (BMD) in the lumbar spine and proximal femur increase by four-fold to six-fold. Furthermore, puberty is also the time when the main gender differences in bone growth emerge, particularly in terms of bone size and bone mass content. At the same time, the peak T1DM onset time ranges between the ages of 9 and 14 years[20], so children and adolescents affected by T1DM may be particularly predisposed to bone impairment.

Among the risk factors for osteoporosis, some factors are modifiable, such as a balanced diet and exercise, which have an important role already in childhood,

whereas obvious non-modifiable factors include gender, age, genetic factors, diseases, and drugs[21,22].

Impaired bone mass accrual (density and quality) in T1DM children has been attributed to multiple local factors in the bone marrow, as well as to systemic factors, which affect osteoblast (OB) differentiation and function (Figure 1).

Local factors in the bone marrow

Several studies have suggested that hyperglycemia impairs the biology and function of multipotent bone marrow-derived mesenchymal stem cells (BMSCs), which generate mesodermal tissues including cartilage, bone, muscle, tendon, ligament, and fat[23]. In particular, hyperglycemia both reduces the proliferation and increases the senescence of BMSCs *in vitro*[24,25] and also inhibits OB activities[26] (Figure 1). In addition, runt-related transcription factor 2 (*RUNX2*) and *RUNX2*-related osteogenic genes are downregulated in T1DM[27], suggesting that diabetic conditions may affect the BMSC fate commitment. Chronic hyperglycemia increases the expression of peroxisome proliferator-activated receptors (*PPAR*) genes, which also stimulate BMSCs differentiation in bone marrow adipocytes[28] (Figure 1). In addition to this, thiazolidinediones, antidiabetic *PPAR γ* agonists, promote marrow adipogenesis, thus increasing the fracture risk[29]. The bone marrow adipose tissue (BMAT) is considered to be a single anatomical entity with a different distribution in the various skeletal sites. In an animal T1DM model, BMAT was significantly augmented, and bone formation was inversely associated with the adipocytes in the bone marrow[30]. BMAT also directly regulates osteoclastogenesis by producing receptor activator of nuclear factor- κ B ligand (*RANKL*)[31]. Bone morphogenetic protein-6 (*BMP6*) is known to induce bone formation (Figure 1), and adipose-derived BMSCs overexpressing *BMP6* have been shown to be capable of repairing bone defects in an animal model[32]. In addition, *BMP6* can probably mitigate T1DM-associated bone loss by directing BMSC differentiation towards the osteogenic lineage. Recently, *BMP6* supplementation in streptozotocin-induced diabetic mice has been demonstrated to directly restore BMD without influencing glucose levels[33], although a possible indirect role of *BMP6* exerted through the modulation of glucose concentrations was observed[34].

This finding suggests that hyperglycemia may not be the main determinant of bone loss in T1DM patients, since other factors, like insulin and the growth hormone/insulin-like growth factor 1 (GH/IGF-1) axis, could modulate BMSCs osteogenesis *via* *BMP6* or other pathways.

Insulin and GH/IGF-1 axis

Insulin, GH, and IGF-1 are anabolic hormones that directly affect bone cells (Figure 1). Insulin stimulates both osteoclast (OC) formation and OB proliferation, achieving a steady state in favor of bone formation[35]. Insulin signaling is essential for normal bone acquisition, as demonstrated in insulin receptor (IR) knockout mice[36], likely due to the role of insulin in the regulation of bone energy metabolism. Moreover, IR activation in the growth plate of mice fed with a hypercaloric diet stimulates skeletal growth as well as growth plate chondrogenesis[37]. OBs also express the IGF-1 receptor (IGF1R), and IGF-1 binds both to IGF1R and, with a lower affinity, to IR, thus triggering the insulin signaling pathway and exerting osteoanabolic activities.

Linear growth as well as BMD are critically affected by the GH/IGF-1 axis. Moreover, GH and IGF-1 play a key role at the growth plate, acting on chondrocyte proliferation, differentiation, and hypertrophy. Abnormalities in this axis have been reported in T1DM subjects, especially during puberty because of the increased insulin requirements due to physiological insulin resistance. In particular, T1DM patients exhibit GH hypersecretion, resulting from portal insulinopenia associated with a decreased hepatic output of IGF-1 together with pituitary hypersecretion of GH. The low IGF-1 serum levels are also related to increased levels of the inflammatory cytokines interleukin-6 and interleukin-8, which inhibit IGF-1 transcription[38] (Figure 1).

Several studies have established correlations between a low BMD, low IGF-1, and glycemic control in T1DM children and adolescents, also providing evidence of low BMD in subjects with poor glycemic control[39-42]. These data are correlated with reduced IGF1, IGF1R and transforming growth factor β 1 gene expression in peripheral blood mononuclear cells in T1DM patients[43]. In addition, changes in the levels of the IGF-1 binding proteins that modulate IGF-1 bioactivity in serum and tissues have been observed in T1DM subjects[44].

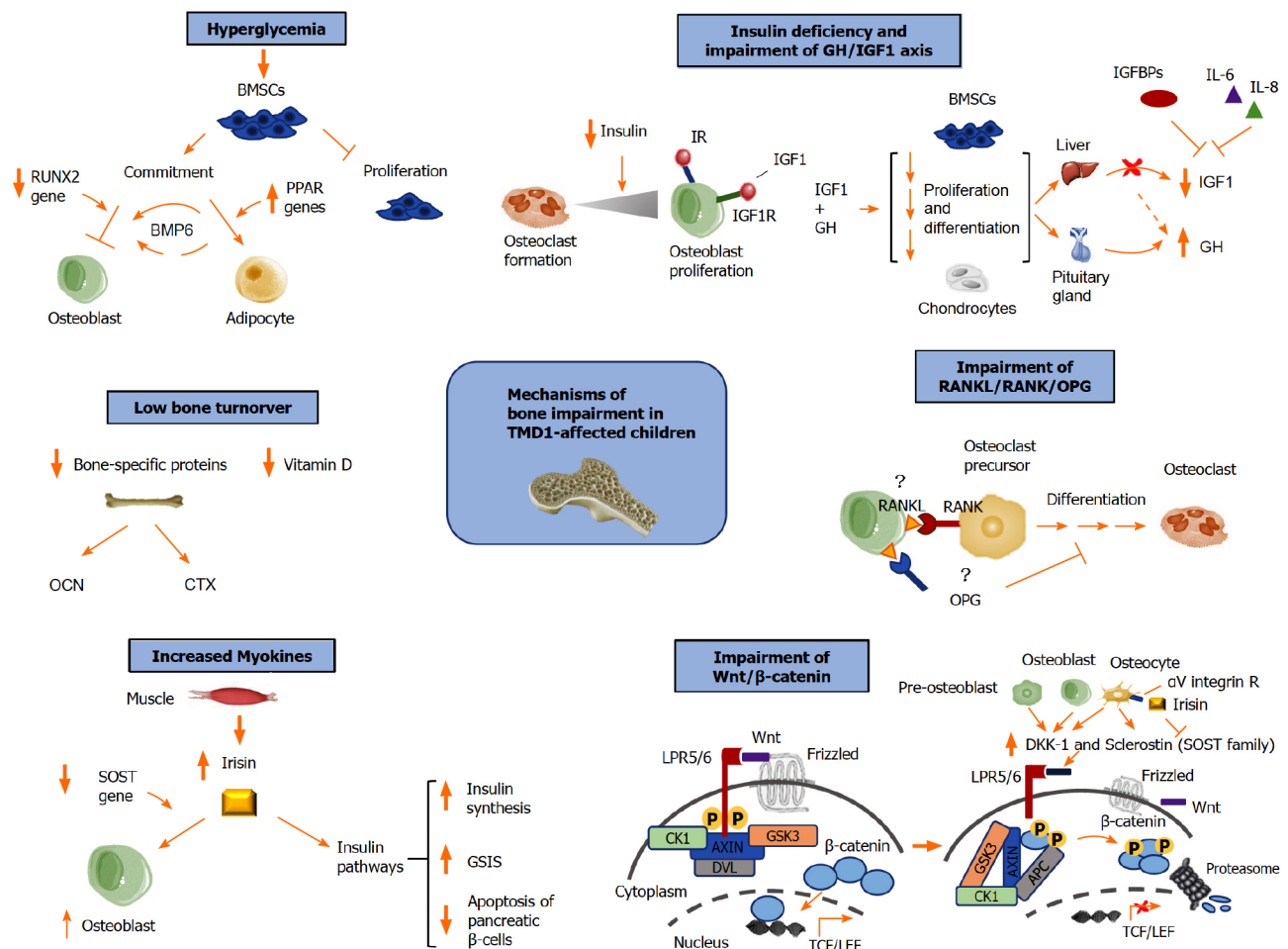


Figure 1 Mechanisms underlying altered bone remodeling in type-1-diabetes. APC: Adenomatous polyposis coli; BMP6: Bone morphogenetic protein-6; BMSCs: Bone marrow-derived mesenchymal stem cells; CK1: Casein kinase I; CTX: C-terminal cross-link of collagen; DKK-1: Dickkopf-1; DVL: Disheveled; GH: Growth hormone; GSIS: Glucose-stimulated insulin secretion; GSK3: Glycogen synthase kinase 3 beta; IR: Insulin receptor; IGF1: Insulin-like growth factor-1; IGF1R: Insulin-like growth factor-1 receptor; IGFBPs: IGF-1 binding proteins; IL-6: Interleukin-6; IL-8: Interleukin-8; LPR5/6: LDL receptor related protein 5; OCN: Osteocalcin; OPG: Osteoprotegerin; PPAR: Peroxisome proliferator-activated receptors; RANK: Receptor activator of nuclear factor-kappa B; RANKL: Receptor activator of nuclear factor-kappa B ligand; RUNX2: Related transcription factor 2; SOST: Sclerostin; TCF/LEF: T-cell factor/lymphoid enhancer factor.

RANKL/RANK/OPG pathway

Bone health depends on the balance between OCs, the bone-reabsorbing cells, and OBs, the bone-forming cells. In several pediatric diseases, bone impairment is due to an imbalance of OBs and OCs activity accomplishing the remodeling process[45]. OBs produce positive and negative regulators of osteoclastogenesis, such as the RANKL and the natural decoy receptor for RANKL, OPG, respectively[46]. Although OBs are a major source of RANKL, this cytokine is also expressed by osteocytes, fibroblasts, and immune system cells, including T cells and mature dendritic cells[47]. OCs differentiate under the control of RANKL, which binds to its receptor, RANK. OPG is the RANKL decoy receptor, thus acting as a negative regulator of osteoclastogenesis (Figure 1). OPG is produced not only by OBs but also by B lymphocytes and dendritic cells, as well as several cytokines[47,48]. In the last years, the impaired OB differentiation and function mechanisms in diabetic bone have been further elucidated, demonstrated by low serum levels of OB markers in T1DM subjects[49], and a decreased osteoblastic activity in streptozotocin-induced T1DM mice[50]. However, OC activity and bone resorption in T1DM are still debated. In diabetic animal models, an increase in OC numbers[51], as well as messenger RNA (mRNA) levels of tartrate resistant acid phosphatase (TRAP) and cathepsin K, bone resorption markers, has been demonstrated[52,53]. By contrast, bone resorption was unaffected or even decreased in T1DM rodents[54]. In a recent study by Yang *et al*[55] the OC activity of trabecular bone was increased in diabetic mice at the early stage, accompanied by an augmented protein expression of RANKL. Remarkably, the RANKL mRNA levels remained unchanged, suggesting that the increased bone resorption in early-stage diabetic mice is induced by RANKL derived from BMAT rather than from the bone tissue itself[55].

This finding indicates that BMAT could be a key factor in regulating bone homeostasis in pathological conditions such as diabetes.

Data about OPG and RANKL levels in T1DM children and adolescents are conflicting. Chrysis *et al*[56] found that serum OPG levels were significantly increased in patients with T1DM compared with controls, whereas RANKL levels did not change. The low RANKL levels in T1DM patients are probably due to blockade of the RANKL signal by an OPG increase on the OPG/RANKL/RANK axis[56]. Consistently, Galluzzi *et al*[57] observed significantly higher levels of OPG in children with long-lasting T1DM compared to the controls. In the study by Szymańska *et al*[58], OPG levels were higher in T1DM subjects at the onset as compared to the control group, and decreased thereafter, while on the contrary, RANKL levels were lower than in controls but increased during follow-up. The authors speculated that the decreased insulin secretion in patients at the onset of diabetes may result in decreased insulin binding to the OB receptor, leading to a transitory increase of OPG levels in the early stage of diabetes[58]. Loureiro *et al*[59] reported low OPG levels in T1DM children, which were correlated with the metabolic control level. In the recent study by Karalazou *et al*[60], T1DM patients showed higher RANKL levels and lower OPG levels than controls. Taking literature data into account, high OPG levels would seem to be positively associated with the progression of diabetes and the development of complications[61-63], while low OPG levels are not associated with microvascular alterations[64,65].

Wnt/ β -catenin pathway

The Wnt/ β -catenin pathway is a signal transduction cascade that controls numerous processes during development. Thus, aberrant Wnt signaling underlies a broad range of diseases in humans.

The pathway is regulated at several levels, also by secreted Frizzled-related proteins and Wnt inhibitory protein, both of which inhibit interactions between Wnt and Wnt receptors[66] (Figure 1). Other Wnt inhibitors belong to the Dickkopf-1 (DKK-1) and the WISE/SOST families, which antagonize signaling by binding low-density lipoprotein-related receptor-5/6[67]. DKK-1 is expressed by preosteoblasts, OBs, and osteocytes, and acts as an antagonist of the canonical Wnt signaling by binding to low-density lipoprotein-related receptor-5/6 (Figure 1). Sclerostin is a secreted protein encoded by the *SOST* gene and produced by mature osteocytes, which antagonizes Wnt/ β -catenin signaling by abrogating its bone anabolic actions[68,69] (Figure 1). DKK-1 and sclerostin are key regulators of bone mass, and high levels of these Wnt signaling inhibitors have been found in several bone diseases[70]. The important role of both molecules has also been demonstrated in a mouse model, showing that a bispecific antibody targeting sclerostin and DKK-1 supports bone mass accrual and fracture repair, exerting a greater effect compared to monotherapies[71]. In type 1 diabetic rats, an increased *SOST* mRNA and sclerostin expression has been observed [72]. Clinical studies and Homeostatic Model Assessment for Insulin Resistance have shown an inverse correlation between sclerostin and insulin levels, suggesting that sclerostin could modulate glucose homeostasis[73]. DKK-1 involvement has been demonstrated in a large cohort of T1DM children and adolescents affected by T1DM [74], in which DKK-1 levels were correlated with bone formation markers, the BMD-Z-score, sex, and pubertal stage[74]. Neumann *et al*[75] reported higher serum levels of sclerostin in T1DM subjects compared with controls but found no correlations between sclerostin levels and bone metabolism markers. On the contrary, Tsentidis *et al*[76] found comparable levels of sclerostin in T1DM children and controls. Recent data suggested that sclerostin levels are increased in pediatric T1DM patients and confirmed a relationship between sclerostin and the glucose metabolism[77]. In addition, in T1DM subjects' bone-derived OCN, as well as fat-derived leptin, appear to modulate sclerostin support in metabolic regulation[77]. Future studies are needed to clarify the role of sclerostin in bone impairment associated with T1DM.

Muscle-bone crosstalk

Bone and muscles are integrated organs that exert a mutual control and are in turn controlled by several factors, such as the GH-IGF-1 axis, sex steroids, adipokines (*e.g.*, leptin, adiponectin, visfatin, resistin), and vitamin D[78,79]. In addition to mediating the muscle-bone crosstalk, muscles release myokines that affect other organs and tissues, including the liver, intestine, and adipose tissue, which in turn release cytokines and hormones responsible for regulating bone homeostasis. Among the myokines, irisin is a small peptide derived from the proteolytic cleavage of fibronectin III domain-containing protein 5, produced during physical exercise[80]. This myokine has been associated with the browning response and thermogenesis of white adipose

tissue[80]. In addition, it has an essential role in the bone-muscle unit, and exerts anabolic effects on bone, both *in vitro* and *in vivo*[81]. Irisin acts through the activation of osteoblastic bone formation, the induction of the pro-osteoblastic genes, and the decrease of osteoblastogenesis inhibitors[81]. The direct effect of irisin on OBs is exerted by means of a downregulation of *SOST* expression, which negatively regulates bone formation[81] (Figure 1). In agreement with this finding, Zhang *et al*[82] demonstrated *in vitro* that treatment with recombinant irisin on OB precursors causes the accumulation of β -catenin in the nucleus, suggesting that irisin restores *SOST*-mediated inhibition of the Wnt/ β -catenin pathway by directly inhibiting *SOST*. In addition, irisin interacts with osteocytes by directly binding to α V integrin receptors, thus protecting them from apoptosis, and inducing the secretion of *SOST in vivo*[83]. Regarding its metabolic effects, recombinant irisin has been shown to stimulate insulin biosynthesis and glucose-stimulated insulin secretion in a protein kinase A-dependent manner. It also prevents saturated fatty acid-induced apoptosis in human and rat pancreatic β cells, as well as in human and murine pancreatic islets, *via* the AKT/B-cell lymphoma 2 signaling pathway[84] (Figure 1). Studies in humans have elucidated the role of irisin both in healthy subjects and in patients affected by diseases related to bone metabolism, such as hyperparathyroidism and T1DM. In a recent study, irisin was demonstrated to be one of the main determinants of bone mineral status during childhood[85]. In addition, high irisin levels have been found in adult patients with long-lasting T1DM that were correlated with positivity for anti-glutamic acid decarboxylase antibodies, suggesting that autoimmunity can have a role in regulating the levels of this myokine[86,87].

In T1DM children and adolescents, elevated irisin levels have been found to be closely related to better metabolic control and an improved bone mass[88]. These findings are in agreement with the recent data showing that irisin can promote insulin synthesis as well as glucose-stimulated insulin secretion[84]. In addition, irisin overexpression enhanced insulin sensitivity in mice while reducing hyperlipidemia and hyperglycemia[89], suggesting that irisin could have a key role in diabetes management.

BONE TURNOVER MARKERS IN T1DM CHILDREN

Bone is considered to be an endocrine “gland,” and its modulation of glucose tolerance by the secretion of bone-specific proteins, in particular OCN, has been clearly demonstrated[16]. OCN is the main non-collagen protein secreted by the OBs and stored in the bone extracellular matrix. The carboxylated form of OCN shows a high affinity to hydroxyapatite, the mineral present in bone. Instead, the uncarboxylated form is free in the circulation and regulates glucose metabolism and insulin resistance [90]. Several data have suggested that serum levels of uncarboxylated OCN are negatively correlated with insulin resistance, obesity, diabetes, and markers of the metabolic syndrome[91-93].

T1DM subjects show a low bone turnover, which is another mechanism underlying bone fragility in these subjects[94]. Previous studies demonstrated that both markers of bone resorption, such as the C-terminal cross-link of collagen (CTX), and markers of bone formation, such as OCN, were decreased in T1DM compared to healthy controls [94]. Furthermore, while levels of TRAP and procollagen type 1 amino terminal propeptide (P1NP) were comparable in patients with T1DM and healthy subjects, low vitamin D levels were found in T1DM patients[94]. Similarly, reduced OCN levels were observed in children and adolescents with T1DM, while P1NP levels would seem to be lower and CTX levels higher in T1DM than in healthy subjects[95]. Chen *et al*[96] showed low levels of bone alkaline phosphatase and CTX in T1DM children as compared to controls.

A recent report by Madsen *et al*[97] investigated bone turnover markers in relation to BMD and metabolic control in T1DM children and adolescents. The results of this study demonstrated that markers of bone formation and resorption were significantly decreased in both sexes, and HbA1c levels were negatively correlated to the resorption marker CTX but not to any of the bone formation markers[97]. Another important finding of this study was that the decreased levels of both markers of bone formation and bone resorption were independent of the T1DM duration and Tanner stage. Thus, the impairment of bone health in T1DM begins in early childhood, independently of age and pubertal stage.

A possible explanation for the low bone turnover in diabetic subjects may be an insulin deficiency, which contributes to a low bone formation, as demonstrated by low

bone turnover in a mouse model of insulinopenia and restoration following insulin treatment[98].

It is possible that the low bone turnover caused by insulin deficiency occurs over time and may not be detected in studies based on acute changes in insulin levels[99].

FUTURE PROSPECTS IN THE MANAGEMENT OF BONE IMPAIRMENT IN T1DM SUBJECTS

T1DM is the most frequent chronic disease in the pediatric population. It is associated with an increased bone fragility from childhood onward, and hence the risk of fractures later in life. Although a low BMD is documented in diabetic individuals, the precise mechanisms underlying bone loss are not yet fully understood. Hyperglycemia seems not to be the main cause of bone impairment in T1DM patients, but other factors, like insulin deficiency, the GH/IGF-1 axis, and low bone turnover, could contribute to the bone impairment observed in these subjects. The use of diabetes technologies, like the use of insulin pumps and continuous glucose monitors, to achieve glycemia control appears to be correlated with an improved bone health, although further studies are needed to confirm this finding. In addition, prospective studies should clarify the causal relationships among metabolic control, bone turnover markers, the RANKL/OPG ratio, Wnt-signaling inhibitors, myokine activity, and bone mineralization in T1DM subjects.

To date, no specific biomarkers are available to predict accurately fracture outcomes in T1DM patients. Additional large-scale prospective studies are needed to identify high-risk patients. In addition to dual x-ray absorptiometry, a fracture risk assessment tool and trabecular bone score could, in the future, offer additional technologies to evaluate better the bone quality of T1DM patients[100].

There is no clear evidence in support of early intervention to avoid the risk of osteoporosis or of the use of anti-osteoporotic drugs in diabetic subjects[101].

Preclinical studies indicated that denosumab, a human monoclonal antibody to RANKL approved for the treatment of osteoporosis or for patients at high fracture risk [102], may stimulate β -cell proliferation in humans[103] and improve liver insulin sensitivity[104].

No data are currently available on romosozumab, an anti-sclerostin antibody indicated to reduce the risk of clinical and vertebral fractures in postmenopausal women with osteoporosis[105]. In addition, there are still few data on the effects of vitamin D, calcium intake, and physical activity on bone health in T1DM subjects [106]. Recently, toll-like receptor-4 (TLR4) has been correlated with diabetic bone disorders *via* the nuclear factor- κ B pathway[107,108]. It has been demonstrated that TLR4 deletion improves streptozotocin-induced diabetic osteoporosis in mice, so TLR4 may be a possible therapeutic target for the treatment of diabetic osteoporosis[109].

CONCLUSION

T1DM has a strong impact on bone health, and skeletal fragility is now recognized among the complications of diabetes. The fracture risk is greater in patients with T1DM and increases linearly with the disease duration. T1DM subjects show a decreased BMD already in childhood, possibly due to an absolute insulin deficiency and the inability of exogenous insulin to reflect endogenous insulin secretion. However, the reduction in BMD does not entirely explain the increase in bone fragility observed in these subjects. It is unclear whether reducing hypoglycemic events by means of continuous glucose monitoring and a closed-loop insulin delivery system can improve bone health in subjects with T1DM. Randomized clinical trials to evaluate the efficacy of anti-fracture drugs in diabetes are lacking, while some observational data have indicated an analogous efficacy in those with or without diabetes, so such drugs should be used according to existing indications.

Further studies are warranted to clarify better the factors responsible for bone damage in diabetic subjects and to identify efficacious strategies to prevent osteopenia/osteoporosis and the risk of fractures in these subjects.

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Current cancer therapies and their influence on glucose control

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Abstract

This review focuses on the development of hyperglycemia arising from widely used cancer therapies spanning four drug classes. These groups of medications were selected due to their significant association with new onset hyperglycemia, or of potentially severe clinical consequences when present. These classes include glucocorticoids that are frequently used in addition to chemotherapy treatments, and the antimetabolite class of 5-fluorouracil-related drugs. Both of these classes have been in use in cancer therapy since the 1950s. Also considered are the phosphatidylinositol-3-kinase (PI3K)/AKT/mammalian target of rapamycin (mTOR)-inhibitors that provide cancer response advantages by disrupting cell growth, proliferation and survival signaling pathways, and have been in clinical use as early as 2007. The final class to be reviewed are the monoclonal antibodies selected to function as immune checkpoint inhibitors (ICIs). These were first used in 2011 for advanced melanoma and are rapidly becoming widely utilized in many solid tumors. For each drug class, the literature has been reviewed to answer relevant questions about these medications related specifically to the characteristics of the hyperglycemia that develops with use. The incidence of new glucose elevations in euglycemic individuals, as well as glycemic changes in those with established diabetes has been considered, as has the expected onset of hyperglycemia from their first use. This comparison emphasizes that some classes exhibit very immediate impacts on glucose levels, whereas other classes can have lengthy delays of up to 1 year. A comparison of the spectrum of severity of hyperglycemic consequences stresses that the appearance of diabetic ketoacidosis is rare for all classes except for the ICIs. There are distinct differences in the

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reversibility of glucose elevations after treatment is stopped, as the mTOR inhibitors and ICI classes have persistent hyperglycemia long term. These four highlighted drug categories differ in their underlying mechanisms driving hyperglycemia, with clinical presentations ranging from potent yet transient insulin resistant states [type 2 diabetes mellitus (T2DM) -like] to rare permanent insulin-deficient causes of hyperglycemia. Knowledge of the relative incidence of new onset hyperglycemia and the underlying causes are critical to appreciate how and when to best screen and treat patients taking any of these cancer drug therapies.

Key Words: Cancer therapy; Hyperglycemia; adverse drug effects; Immune checkpoint inhibitors; mTOR inhibitors; 5-fluorouracil analogs; Glucocorticoids; Diabetes mellitus

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Core Tip: Immune checkpoint inhibitors (ICI) rarely cause hyperglycemia, but glucose monitoring from their initiation is critical as rapid diabetic ketoacidosis can develop from underlying immune-mediated pancreatic beta-cell destruction. Therapy with mammalian target of rapamycin (mTOR) inhibitors, 5-fluorouracil (5-FU)-analogs and glucocorticoids have higher rates of hyperglycemia early in therapy that is not generally severe, but needs to be recognized and treated to optimize patient outcomes. The hyperglycemia occurring from the 5-FU and ICI classes is not reversible. The diabetes from ICIs arises from an absolute insulin deficiency vs the partial deficiency from the 5-FU class. Glucocorticoids and mTOR inhibitors predominantly cause insulin resistance.

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INTRODUCTION

Cancer therapies have had profound impacts on increased life expectancy over the past few decades, however, it is widely known to have a multitude of unintended effects. Quality of life concerns such as hair loss, intractable nausea or visible surgical scars are widespread in individuals initiating their treatment cycles. Physicians initiating chemotherapy are also concerned about treatment side effects and routinely monitor for signs or symptoms of serious complications that may require urgent hospitalization, a change in treatment management or a pause in therapy to avoid a life-threatening event. Hyperglycemia is a common and potentially significant adverse effect arising from the use of several widely applied cancer therapeutic classes including immune checkpoint inhibitors (ICIs), phosphatidyl inositol-3-kinase (PI3K)/AKT/mammalian target of rapamycin (mTOR) inhibitors, 5-fluorouracil (5-FU) analogs, and glucocorticoids[1-4]. The latest understanding of the characteristics of the hyperglycemia that is associated with the use of these drug classes is presented in order to raise awareness of the adverse effects these agents have on glucose control to enable its early recognition, trigger regular monitoring plus timely intervention, and to ultimately improve patient outcomes. Emphasized below is the current knowledge pertaining to these drug classes regarding the incidence, onset, reversibility and severity of hyperglycemia associated with their use in cancer therapy.

The significance of hyperglycemia on cancer therapy outcomes

Untreated hyperglycemia has been associated with a multitude of negative outcomes for cancer patients including longer hospital stays[5], worsened prognosis and decreased survival[6,7]. Glucose is a key substrate metabolized by cells to produce ATP and is a preferred energy supply; cancer cells are known to increase their glucose uptake, with the subsequent increase in energy reserves able to support further cellular proliferation[8]. Hyperglycemia has also been associated with a reduction in

cancer therapy effectiveness[9], an increased rate of infections and sepsis in those who may already have immunosuppression from their cancer treatments[10], and an increased length in hospital[11,12]. Hyperglycemia fosters a proinflammatory environment that enhances the production of cancer stimulating signals that promote cell proliferation, increase resistance to cell death and may also induce drug resistance to chemotherapy[11-16]. Clinically, hyperglycemia has been found to be an independent risk factor for earlier cancer recurrences, and higher mortality rates[17].

Glucose levels and clinical presentation define the severity of hyperglycemia

The research referenced below has graded both the severity of hyperglycemia and the degree of clinical symptoms as a means of comparing patient adverse events (AE) with drug use. Four grades of severity are defined that consider glucose levels, but also includes the severity of the clinical consequence such a diabetic ketoacidosis (DKA) or permanent diabetes. Grade 1 AE (G1) relates to asymptomatic or mild symptoms, no ketosis or evidence of type 1 diabetes (T1DM), fasting glucose (FG) above normal. Grade 2 AE (G2) involves moderate symptoms, FG > 8.9-14 mmol/L, or the presence of ketosis or T1DM at any glucose level. Grade 3-4 AE are severe symptoms, that are medically significant or life-threatening, differentiated from G2 and each other by the degree of glucose elevations with Grade 3 AE (G3) encompassing glucose levels between 13.9-27.8 mmol/L, and Grade 4 AE (G4) including glucose levels > 27.8 mmol/L[18].

IMMUNE CHECKPOINT INHIBITORS

Immune Checkpoint inhibitors target one of three T-cell ligands to promote antitumor activity

A relatively new class of chemotherapy agents that are recognized for their potential side effects on glucose control are the immunomodulators that target and inhibit immune checkpoints, resulting in an increase in T-cell mediated immune responses that benefit patient treatment responses[19]. These ICIs are monoclonal antibodies that bind and block (inhibit) immune cell-cell interactions that would normally suppress the immune response. The result is that there is an effective and durable increase in antitumour activity[20]. This class is very successful in the treatment of advanced melanoma including those with *BRAF* mutations[21], and have since been used successfully for treatment of additional advanced stage cancers including hepatocellular carcinoma[22,23], non-small-cell lung cancer[24], renal cell carcinoma[25] and metastatic clear cell renal cancer[26]. The ICIs in current use specifically block three T-cell checkpoints; the cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) receptor, the programmed cell death-1 (PD-1) receptor, and the third and most recent class of antibodies targeting the programmed cell death-Ligand 1 (PD-L1)[19,20].

ICIs trigger immune-related endocrinopathies, and the incidence of diabetes with ICI differs with the checkpoint being targeted

There is an association between the use of these ICIs and the frequent appearance of immune-related AE, including a wide-spectrum of endocrine dysfunctions. The onset of hyperglycemia in individuals taking ICIs is infrequent, and the incidence differs depending on the receptor being targeted, as well as whether receptor targeting combinations are used[27]. Not all ICIs appear to have the same potential. The highest probability appears to reside in those targeting either the PD-1 receptor (nivolumab, pembrolizumab) or PD-L1 (atezolizumab, durvalumab, avelumab), whereas the CTLA-4 targeting agent (ipilimumab) does not seem to have a significant risk when used alone, as only a handful of case reports were noted[28]. A recent 2020 meta-analysis estimated the incidence of serious (G3 and G4) and all-grade hyperglycemia (G1-G4) in every reported case of ICI-associated diabetes, noting that the PD-1/PD-L1 targeted therapies were associated with hyperglycemia in 0.2%-4.9%, with a 0.49% incidence of serious hyperglycemia in patients using these drugs[1]. A 2018 study reported an overall incidence of 0.9%[28]. The combination of PD-1/PD-L1 and CTLA-4 immune-targeted therapy showed the highest overall rates of diabetes, spanning 2.0%-3.4% in different cohorts studies, and a notably higher rate of serious hyperglycemia events at almost 2%[28]. This same study confirmed that the CTLA-4 inhibitors do not seem to have a risk of hyperglycemia when used without PD-1 therapies[28].

ICI therapy stimulates immune-mediated antitumor activities, but also stimulates autoimmune disorders

The inhibitory monoclonal antibodies used to interrupt immune response checkpoints results in a reinvigoration of the immune response. The ICI antibodies bind and block the specific inhibitory ligand on the T-cell surface, interrupting those activity-dampening signaling pathways[29,30]. The result is T-cell activation and stimulation of their immune surveillance and antitumor activity, to the benefit of the patient[31]. However, immune checkpoints are also central to maintaining immunological self-tolerance and preventing autoimmune disorders[32,33]. Immune-mediated self-damage causing endocrine dysfunctions are one of the most common side effects of the ICI class, including loss of thyroid, adrenal and pituitary activity, plus rare cases of pancreatic insulin deficiency[34]. Autoimmune recognition and destruction of pancreatic beta (β)-cells is the well-established mechanism resulting in classic T1DM [35,36], and the ICI drugs likely trigger this same destructive loss of function in cancer patients who developed hyperglycemia[37]. Human pancreatic islets lack CTLA-4 receptors, but do present PD-L1 to protect them against immune cells[38]. The ICI monoclonal antibodies that bind PD-1/PD-L1 should be capable of inhibiting this pathway in pancreatic β -cells, leaving them susceptible to (auto)immune destruction and diabetes, providing a rationale why PD-1/PD-L1 but not CTLA-4 inhibitors are associated with new onset diabetes.

The hyperglycemia associated with ICI use is due to autoimmune destruction of the pancreatic β -cells and loss of endogenous insulin release

With ICI use, the new onset of hyperglycemia found in those without diabetes, and the worsening glucose control in those with known diabetes, does appear to be directly due to immune-mediated pancreatic damage. Pancreatitis was found in 42% of individuals developing diabetes, and auto-antibodies classically associated with T1DM can be found elevated in these individuals, with 47% having glutamate decarboxylase autoantibodies[28]. The appearance of new hyperglycemia in those exposed to ICI therapy is not caused by an associated insulin resistance, as three large case series evaluating patients that developed diabetes after ICI exposure found low C-peptide (62%-93%), positive ketosis (59%-77%) and detectable autoantibodies (39%-56%)[28,37,39], with the antibodies in at least some cases not present prior to ICI treatment[28].

Loss of glucose regulation in type 2 patients taking ICIs may indicate a transformation into an insulin-deficient state

It is less well known how ICI use has impacted glucose levels in those with underlying T2DM as the stress of illness, pain, or other medical therapies may also contribute to loss of tight glucose control. It is well documented, however, that when blood glucose levels become acutely and significantly more difficult to control in known T2DM, that it is important to consider that the ICI therapy may have caused pancreatic β -cell dysfunction and insulin deficient diabetes[40].

The onset of Insulin-deficient diabetes after ICI therapy is unpredictable and is permanent

Of the cases of insulin-deficient diabetes (IDD) reported with ICI therapy, the onset is unpredictable and can appear as early as a few weeks after starting treatment, up to greater than one-year following therapy; over half occurred within 4 mo of treatment initiation, typically in their fourth cycle of therapy[28]. The presence of hyperglycemia with ICI therapy does not require cessation of the ICIs or provision of high dose steroid pulse therapy, as this does not appear to restore pancreatic function[41,42]. In fact, reversal of IDD after ICI use has rarely been reported. A single case of ICI-induced diabetes successfully used infliximab, an immunosuppressant, to reverse the hyperglycemia[43], yet in general, once present the hyperglycemia is persistent and does not appear to be mitigated by decreasing or stopping the ICI treatment[34,44].

ICI associated hyperglycemia has a high risk of serious and severe consequences, notably DKA and permanent diabetes

ICI therapy can lead to severe complications of hyperglycemia that can occur very rapidly. The severity is due to the damage to the pancreatic β -cells, leading to irreversible insulin deficiency. Because of this T1DM-like defect, there is a distinct risk of DKA, and this can be an acute and potentially life-threatening presentation. The association between ICI-dependent onset of hyperglycemia and ketosis/DKA was

remarkably high, at 77.8 % in newly diagnosed cases of diabetes[37]. There are many case reports of rapid DKA as the first presentation of hyperglycemia with ICI use, raising the possibility that this overlaps with Fulminant T1DM, a clinical presentation that is characterized by rapid development of markedly elevated glucose, near-normal glycosylated hemoglobin A1c (A1C), ketoacidosis, negative autoantibodies, severe insulin deficiency and elevated levels of pancreatic enzymes[45]. A careful review, however, revealed that there does appear to be distinct differences, including the presence of autoantibodies in ICI IDD, that are typically not found in Fulminant T1DM[37]. Due to the risk of DKA with this drug class, the practice guidelines developed to monitor for adverse effects of ICIs commonly recommend routine monitoring of glucose levels both at baseline, with each treatment cycle throughout induction and then every 3-6 wk thereafter for up to one year[18]. For safety, the use of insulin for diabetes developing from ICI therapy is recommended unless insulin deficiency can be ruled out[18].

PI3K/AKT/MTOR PATHWAY INHIBITORS

Inhibition of the PI3K/AKT/mTOR pathway interrupts multiple cancer promoting cell signals

The PI3K-AKT-mTOR signaling pathway plays a vital role in responding to nutrient abundance[46], making it an attractive target for blockade[47]. The proteins being inhibited are kinases that target downstream proteins for phosphorylation to change cellular responses including promoting normal cell growth and proliferation when nutrients are abundant[48]. They ultimately work within the same pathway as growth factors and insulin signaling, and can therefore also influence glucose and lipid metabolism[49].

mTOR, PI3K inhibitors and their derivatives are effective in many cancer types

mTOR inhibitors are derived from the original drug of this family, rapamycin, that was initially isolated as an antifungal agent[50], but was later determined to inhibit a kinase important in cancer growth[51]. This target was subsequently named “mechanistic target of rapamycin” or mTOR. mTOR inhibitors and their related analogs are used in many advanced stage solid tumors including renal cell, neuroendocrine tumors of the pancreas, and breast cancer[52]. There are presently three mTOR inhibitors approved by the United States Food and Drug Administration (FDA) that are derivatives of rapamycin; sirolimus, temsirolimus, and everolimus. Closely related medications are the PI3K inhibitors, of which there are four currently approved by the FDA; copanlisib, idelalisib, duvelisib, and alpelisib. These latter agents are approved for use in the treatment of breast cancer and hematological malignancies. AKT inhibitors and combination PI3K/mTOR inhibitors are still under development and some have entered Phase II clinical trials[53].

The hyperglycemia arising from the inhibition of mTOR is primarily due to insulin resistance

The usual activity of mTOR not only influences cell growth and development, but also affects glucose regulation[54]. mTOR inhibitors primarily promote hyperglycemia through increased insulin resistance *via* mTOR complex 1 (mTORC1) inhibition, as they impair the efficiency of the insulin signaling pathway at multiple points in its phosphorylation cascade[55,56]. In a diabetic rodent model, exposure to rapamycin resulted in a reduction in insulin signaling *via* proteins IRS1/2, a reduction in phosphorylation by AKT, and inhibition of PI3K activity[55]. Moreover, rapamycin increased the activation of Jun N-terminal kinase pathway, which is a pathway implicated in insulin resistance[55]. Together, the effect observed with these chemotherapy drugs is consistent with a predominant T2DM-like insulin resistant state, due to impaired insulin signaling[55]. Lastly, a component of insulin deficiency is also thought to play a role in the development of hyperglycemia as mTORC1 is a known positive regulator of pancreatic β -cell function, and molecular studies using pancreatic β -cells exposed to rapamycin detected a 33% reduction in glucose-induced insulin secretion[55].

There are two mTOR complexes that differ in their influence on glucose levels and sensitivity to inhibition

The mTOR complex is a serine/threonine protein kinase that exists in two different multi-protein complexes. The mTORC1 is sensitive to rapamycin, whereas complex 2 (mTORC2) is less responsive to rapamycin, although chronic exposure to rapamycin does ultimately result in reduced mTORC2 signaling[56]. The mTORC2 pathway is much less well characterized than the mTORC1 pathway. It was initially thought that the mTORC2 pathway was resistant to rapamycin treatment, but it was later discovered that long term exposure reduces mTORC2 signaling in some cell types by suppressing the assembly of the mTORC2 complex[57]. mTORC2 activates AKT, and the mTORC2-AKT pathway has been shown to promote pancreatic beta cell proliferation and survival, and to inhibit gluconeogenesis by blocking FoxO1 activity[57]. Normal mTORC2-AKT activity also induces glucose uptake in insulin-sensitive tissues and blocks protein catabolism. The loss of mTORC2 activity through inhibition, therefore, increases insulin resistance as well as promoting protein catabolism and reducing muscle mass. Inhibition of mTORC2 also leads to the loss of the mTORC2-AKT-dependent inhibition of gluconeogenesis as well as decreased insulin production, contributing further to hyperglycemia[56]. The effect of mTORC1 and mTORC2 inhibition on glycemia is complex, and related to the degree and chronicity of inhibition, but ultimately treatment with all mTOR inhibitors leads to hyperglycemia [56]. The three mTOR inhibitors approved by the FDA are derivatives of rapamycin; sirolimus, temsirolimus, and everolimus, and are primarily mTORC1 inhibitors, although dual mTORC1/C2 inhibitors are in development[57].

The PI3K/AKT/mTOR pathway inhibitors are potent drivers of hyperglycemia

The incidence of hyperglycemia associated with the use of PI3K/AKT/mTOR inhibitors is significant and ranges between 12%-50%[2]. A 2015 meta-analysis considered twenty-four trials of mTOR inhibitor use in solid organ cancer treatment and noted a 5.25-fold increased risk of significant hyperglycemia (blood sugars > 14 mmol/L)[58]. Pre-existing diabetes was an independent risk factor for glucose levels > 14 mmol/L[59]. It is worth noting that the PI3K inhibitors can also induce hyperglycemia[60], and AKT inhibitors have revealed significant hyperglycemia in preclinical studies[61].

Most cases of hyperglycemia occur during initial exposure, are mild and transient

A retrospective study of 341 patients treated with PI3K and mTOR inhibitors revealed that the mean FG increased from 5.3 mmol/L at baseline to 7.1 mmol/L during the first chemotherapy cycle, but returned to 5.4 mmol/L prior to the next cycle[59]. This supports the conclusion that the rise in blood glucose is transient. The majority of these patients experienced their highest glucose levels early on in therapy, during the first (87.9%) or second (14.4%) cycle of mTOR inhibitor treatment, and most cases of hyperglycemia in this study were mild (G1)[59]. However, more significant glucose elevations can occur, as 6.7% of patients receiving this therapy had glucose elevations > 14 mmol/L compared to controls not taking mTOR inhibitors[62]. Additionally, it was observed that the median time of elevated glucose levels (> 8.3 mmol/L) was 56 d in patients showing clinical benefit, and 113 d for those patients who progressed[62]. It remains to be determined if the timing of new hyperglycemia development after therapy initiation is predictive of treatment responses.

mTOR-induced hyperglycemia is typically managed with oral therapies

Insulin deficiency or DKA are not significant risks with using this class of drugs, as only a very small percentage of patients require insulin[59], and to our knowledge there have been no cases of hyperglycemic emergency or DKA in any clinical trials to date. A single case report was found that describes DKA and pancreatitis in a patient treated with everolimus for breast cancer, supporting that this is a very rare association with mTOR inhibitor drugs[63]. When uncontrolled hyperglycemia develops (defined as glucose > 14 mmol/L, A1C ≥ 9%), expert committee guidelines recommend stopping the chemotherapy medication and reintroducing it at a lower dose in the rare cases of uncontrolled hyperglycemia despite optimal diabetes management [2]. Both American and French guidelines for PI3K/AKT/mTOR use are available to direct surveillance and treatment best practices[2,64], and an A1C target of ≤ 8% is suggested for pre-existing patients with diabetes prior to mTOR inhibition[2].

5-FU AND DERIVATIVES

5-FU is an antimetabolite agent that has been used in the initial treatment of breast, gastric, colon and pancreatic cancers and has been in active use for over sixty years[65, 66]. It is a pyrimidine analogue that is structurally related to thymine, uracil and cytosine bases in DNA, RNA or both, respectively[67]. 5-FU acts as an antimetabolite to inhibit cell growth through its interference with DNA and RNA function upon its incorporation into newly synthesized DNA or RNA.

Derivatives of 5-FU have been created to increase their stability and to overcome their drug toxicities

Over the years, additional 5-FU oral prodrugs have been developed that reduce their toxicity and improve tumour selectivity, as well as increase their stability[68-70]. In the last 20 years, capecitabine has been developed and used predominantly for metastatic breast and gastrointestinal cancers[66,70]. It is activated into 5-FU through three sequential enzymes, with the final enzyme being found in high concentrations in tumour tissues[66]. As such, capecitabine activation is very targeted and is generally better tolerated[66,70]. There have been numerous reports of glucose disorders with 5-FU and its derivatives including case reports of hyperglycemia following the administration of the newest 5-FU prodrug, capecitabine[71].

5-FU prodrugs can contribute to new onset diabetes, and the majority have persistent hyperglycemia after therapy is stopped

There is a paucity of data on 5-FU therapies and their specific effects on glucose control. The majority of information comes from a 2013 study involving 362 patients with normal fasting plasma glucose prior to 5-FU-based therapies in which overt diabetes developed in 11.6% of individuals and impaired fasting glucose (IFG) in another 11.3%[3]. Of the 42 patients that developed diabetes, 32 occurred during therapy, with the remaining 10 being detected during follow-up after treatment was completed. Only 16% (7/42) of these patients had glucose levels spontaneously return to normal[3], indicating that the hyperglycemia related to 5-FU therapy is persistent in most cases. Those remaining were managed with a variety of interventions including diet (30%), insulin (10.8%) or oral medications[3]. Given that these patients did not have pre-existing risk factors for diabetes, it was thought that the development of diabetes was secondary to 5-FU chemotherapy[3].

Hyperglycemia typically develops early during 5-FU analog therapy, and is generally mild

The timing of new-onset hyperglycemia with 5-FU treatments varies, but most (77%) patients developed diabetes during their early chemotherapy cycles (median third cycle), and the remaining individuals present up to 1 year after completion of treatment[3]. It is unclear how 5-FU chemotherapy affects glucose control in those with established diabetes. In this study, the timing of the onset of IFG after 5-FU treatment was not reported[3]. While 5-FU-associated hyperglycemia was typically mild during active treatment (95% had glucose < 14 mmol/L), after therapy was complete it was noted that seven out of 42 patients developed significant hyperglycemia (>14 mmol/L), and one patient in the study died of ketoacidosis[3]. Aside from this study, there are two additional case reports of DKA associated with 5-FU based treatments [72,73].

5-FU therapies decrease pancreatic β -cell insulin storage and release

The underlying mechanism causing the hyperglycemia upon 5-FU exposure appears to be due to a decrease in insulin being released from the pancreatic β -cells[3,74]. Those patients who developed diabetes had a progressive decrease and delay in C-peptide secretion, seemingly due to a pancreatic deficiency in endogenous insulin processing and production[3]. A case control study also demonstrated that insulin levels failed to increase appropriately with the development of hyperglycemia[74]. Preclinical animal studies also suggest that hyperglycemia may result from impaired insulin production as there was a relative insulin deficiency in rats following 5-FU administration, as well as a decrease in the abundance of secretory granules in pancreatic islet cells[75]. Cellular studies designed to reveal how these drugs cause hyperglycemia have shown that 5-FU related therapy stimulates immune mediators in pancreatic β -cells, resulting in their destruction *via* cell-mediated T-cell infiltration[76]. Consistent with this, capecitabine has been linked to acute pancreatitis[77,78].

The rare cases of DKA reported with 5-FU therapies suggests that there is sufficient endogenous insulin production to offset severe hyperglycemia consequences in the majority of cases. Nonetheless, there is a real risk of significant glucose elevations, as 16.7% (7 of 42) of newly diabetic individuals had glucose levels > 14 mmol/L despite therapy[3]. Management of hyperglycemia following capecitabine therapy included successful treatment with dietary control and lifestyle changes[79,80], although some individuals did require insulin[3].

GLUCOCORTICIDS

Glucocorticoids are a class of medications that have been used to treat a plethora of medical conditions since the 1950's. Glucocorticoids are prescribed widely for a variety of medical conditions, with estimates of use approaching 1% of the general population [81]. Although their efficacy and adverse effect profile have been described extensively in the literature, their effect on the human body varies due to the heterogeneous nature of the underlying disease states they are treating and the individuals who are using them; hence there is variability in their use and dosage recommendations[82].

Steroids are useful as adjunct therapy to offset adverse side effect of cancer treatments

Glucocorticoids are often included as a part of cancer therapy to mitigate the adverse effects of the chemotherapies being used at the same time. They can be very useful in controlling nausea and improving appetite, and are frequently given as an antiemetic before and after chemotherapy[83]. The dosing and duration often depends on the emetogenic potential of the chemotherapy. Glucocorticoids are also given to prevent some of the other adverse effects of chemotherapy like generalized rash or thrombophlebitis when drugs are given through peripheral vein, or to offset hypersensitivity reactions[11,84,85]. Glucocorticoids may also be included as an inherent part of the cancer therapy, such as their use within the CHOP protocol in lymphoma. There are several other regimens used in multiple myeloma and prostate cancer that include glucocorticoids as a part of the treatment, and the dosing and formulation varies.

Glucocorticoid-induced hyperglycemia is a very common adverse effect of steroid use

Along with their known benefits, there are many recognized adverse effects of glucocorticoids, both acute and chronic. Supraphysiologic glucocorticoid use is known to raise glucose levels, particularly at the high doses that are required for therapeutic advantages. Glucocorticoid-induced hyperglycemia (GIH) is a well-known complication of their use in individuals with known diabetes (T1DM and T2DM) as well as those who were previously euglycemic[4,86]. Hyperglycemia is commonly reported in patients undergoing cancer therapy that includes glucocorticoids, however its true incidence is hard to define due to the variability in chemotherapy combinations, durations, and cycles. One study of hospitalized patients taking high dose glucocorticoids reported hyperglycemia in 52% of patients[87], with another two studies reporting 34%[88] and 37%[89] in patients during induction therapy for acute lymphocytic leukemia[88,89]. A more recent study found that 94% of women with gynecological cancer whose chemotherapy regimen included high dose dexamethasone experienced hyperglycemia[85]. These patients were undergoing continuous glucose monitoring (CGM) which the authors felt led to the remarkably high incidence rate, and postulated that glucose elevations may be significantly under-recognized in many previous clinical trials that did not utilize CGM[85].

GIH occurs acutely and is generally mild

GIH is a phenomenon that typically occurs acutely with initiation[85,87,90,91], and hyperglycemia was found to be significant by day 2 in those being treated systemically for hematologic malignancies[11]. The degree of glucose elevations range widely and are most frequently modest (< 14 mmol/L)[92], nonetheless severe hyperglycemia (> 28 mmol/L) and DKA have also been reported[11,93], with rare reports of hyperglycemic hyperosmolar syndrome as well[94]. Other AE associated with GIH range from mild to serious, such as increased infections and lengthened of hospital stays[11,16,86,95-98]. The acute hyperglycemia associated with glucocorticoids will typically resolve upon discontinuation[4,99,100].

The formulation and duration of steroid use influences the incidence of hyperglycemia

The most commonly used glucocorticoids in chemotherapeutic regimens are prednisone (oral) and dexamethasone (oral or intravenous). The dose and duration at which they are used varies with the chemotherapy and clinical situation, making general conclusions difficult[16]. To give an example of the variance that confounds these clinical assessments, a study by Ochola *et al*[95] considered patient outcomes with prednisone use; there was a range in total daily doses of 40-150mg; once to four times daily; and between 5-14 d duration.

It is commonly considered that higher glucocorticoid doses and longer durations of use confers a greater risk of developing GIH[11,16,101,102], yet there have been exceptions to this association[82,94,98]. Most hospitalized patients developed hyperglycemia after taking ≥ 40 mg/d of prednisone for two days[103]. There is some evidence that splitting the dose of prednisone, rather than administering it all at once in the morning, may help reduce GIH[104]. The type of glucocorticoid used may also correlate with the risk of hyperglycemia[92]. Healy *et al*[11] found that hyperglycemia was associated with higher doses and the longer-acting steroids in those without diabetes, yet it was not in those with previous diabetes.

Due to the differences in the pharmacokinetic profiles of shorter acting glucocorticoids (such as prednisone, prednisolone, and hydrocortisone) *vs* longer-acting glucocorticoids such as dexamethasone, one could anticipate a delayed effect with the latter[90]. Prednisone levels peak 4-8 h after ingestion and its duration of action is between 12 h to 16 h; these pharmacokinetics correlated with increases in postprandial glucose in the afternoon and evening when administered in the morning[11,87,92]. During induction therapy for acute lymphoblastic leukemia the use of long-lasting dexamethasone was linked with a significant increase in risk of GIH when compared to those prescribed the intermediate-acting prednisone[93]. In contrast, a comparison between dexamethasone 8-12mg IV and prednisone 40mg orally found extensive hyperglycemia in the majority of all patients, without differences between the two therapies[94].

Steroids induce a potent insulin resistance resulting in hyperglycemia

The effects of glucocorticoids on glucose levels are complex[4]; although GIH occurs most commonly in patients with pre-existing diabetes, it also presents in those without any prior history of hyperglycemia[82,105]. Glucocorticoids can cause an increase in both fasting and postprandial glucose levels, but it is generally recognized that the largest impact is on postprandial levels[16,87,92,95,96,105,106]. High dose glucocorticoid use impairs insulin signaling, leading to key increases in insulin resistance at the liver (promoting hepatic gluconeogenesis) and skeletal muscle (impairing glucose uptake)[4,92,106]. Glucocorticoids can also diminish normal insulin secretion by pancreatic β -cells[4,99]. Some of the predictors of risk for increased blood glucose with glucocorticoid use in the context of cancer therapy include older age and higher BMI [88,98,102] and while an elevated A1C was found to be a predictor, a discrete HbA1c cut-off was not determined[85].

SUMMARY AND DISCUSSION

For all of these classes of drugs, it would be prudent to initiate glucose monitoring upon the initiation of chemotherapy and to continue to do so throughout treatment. As summarized in Table 1, glucocorticoids and AKT/mTOR inhibitors can be expected to cause the majority of patients (up to 94%[85] and 50%[2] respectively) to develop hyperglycemia very early after drug initiation. In contrast, the diabetes that develops upon the initiation of ICIs and 5-FU therapies will affect fewer individuals (up to 5%[1] and 11%[3], respectively) and could be anticipated to present at slightly later timelines on average, with the 5-FU analogs typically in their third chemotherapy cycle[3] and ICIs in their fourth chemotherapy cycle (about 4 mo[28]). Despite searching the literature, it was not found that there are dosing ‘cut-offs’ for any drug class below which the risk of hyperglycemia is nil, nor are there specified doses above which there are significantly increased rates of hyperglycemia.

The insulin resistance arising from either glucocorticoids or AKT/mTOR inhibitors nearly always resolved once the treatments have stopped[4,59,99,100] and there have not been any reports of delayed reappearance, implying that ongoing daily glucose monitoring will not be necessary upon completion (Table 2). When mild hyperglycemia is present, standard management approaches used for T2DM have been

Table 1 Summary of reported characteristics of hyperglycemia incidence, onset and severity with the use of current chemotherapy agents

Characteristics by drug class	Glucocorticoids	5-FU and analogs	PI3K/mTor inhibitors	Immune checkpoint inhibitors
Incidence of new or worsening hyperglycemia	Significant, 34%-94%	Common, 11.6% DM, 11.3% IFG	Significant, 12%-50%	Rare, 0.2%-4.9%
Onset of hyperglycemia after first use	Acutely	Majority by 3 mo; 3/4 early (3 rd cycle); 1/4 up to 1 yr later	Majority after first use	Majority by 4 mo, can be after first use, can be up to 1 yr later
Severity of hyperglycemic events	Usually mild, Severe possible, Multiple reports of DKA and some HHS	Mild, Case reports of DKA	Mild, No DKA	Moderate to severe, 77.8% DKA

5-FU: 5-fluorouracil; CTLA-4: Cytotoxic T-lymphocyte-associated protein 4; PI3K: Phosphatidylinositol-3-kinase; mTOR: Mammalian target of rapamycin; DKA: Diabetic ketoacidosis; HHS: Hyperglycemic hyperosmolar syndrome; IFG: Impaired fasting glucose.

Table 2 Hyperglycemia can be a class or drug-specific effect and may not be reversible with discontinuation

Characteristics by drug class	Glucocorticoids	5-FU and analogs	PI3K/mTOR inhibitors	Immune checkpoint inhibitors
Class effect on hyperglycemia	Yes	Yes	Yes	Negligible risk with the CTLA-4 inhibitor, ipilimumab Does occur with all PD-1 and PD-L1 inhibitors, most significantly when combined
Reversibility of hyperglycemia	Yes	No	Yes	No

5-FU: 5-fluorouracil; CTLA-4: Cytotoxic T-lymphocyte-associated protein 4; PI3K: Phosphatidylinositol-3-kinase; mTOR: Mammalian target of rapamycin; PD-1: Programmed cell death-1; PD-L1: Programmed cell death-Ligand 1.

effective including diet adjustments, oral metformin or sulfonylureas[2,64] (Table 3). While there is little information specifically related to all of these drug classes, it would be anticipated that DPP-4 inhibitors, SGLT-2 inhibitors, or GLP-1 analog medications would also be effective at normalizing blood glucose levels. Increases to therapy intensiveness to manage more severe glucose elevations would follow usual best practices for T2DM management, and patients may ultimately require insulin for optimal control in the short term.

The ICIs and 5-FU analog classes cause hyperglycemia due to varying degrees of insulin deficiency at the level of the pancreatic β -cell, and once present the diabetes is generally permanent[3,34,44] (Table 2). As discussed above, it is very important to continue glucose monitoring even after therapy has been completed with these two classes, as diabetes can develop for up to at least one year. To date, there is little direction surrounding the specific monitoring and management of hyperglycemia in patients treated with 5-FU, in contrast to multiple current guidelines available for the numerous autoimmune adverse effects of ICI, including IDD[18] (Table 3).

The diabetes developing as a result of 5-FU analog therapies has rarely led to DKA, suggesting that the insulin deficiency is not absolute in the great majority of cases (Table 1). This raises the possibility that sulfonylureas may have a beneficial role in mild glucose elevations due to their ability to enhance pancreatic β -cell insulin secretion; this increased release of insulin may compensate for the underlying low insulin levels and thereby normalize blood glucose levels. This has neither been specifically investigated nor reported, but their use could be rationalized based on the underlying defect driving hyperglycemia with 5-FU therapy.

Independent of ICI therapy, the majority of T1DM occurs in children or young adults, and there is a global all-age incidence of 15 per 100000 persons[107]. The 0.2%-4.9% incidence of insulin-deficient hyperglycemia in adults after ICI therapy (median age > 60 years years[1]) is higher than global rates and presents in older than expected age groups, suggesting that its development may be more complex than merely unmasking those at inherent risk for developing T1DM. Without doubt there are complexities not yet appreciated, yet it is not known how to identify those at highest risk for the development of T1DM with ICI use. As these therapies become more

Table 3 The underlying mechanisms and treatment considerations of hyperglycemia differ between chemotherapy classes

	Etiology of hyperglycemia	Treatment considerations
Glucocorticoids	Major: Insulin resistance	Oral hypoglycemics possible for mild
	Minor: Decreased insulin release	Consider selecting insulins with duration of action to match that of the steroid being given
5-FU and analogs	Major: Decreased insulin release and production	Diet or oral hypoglycemics for mild
		Insulin for severe
PI3K/mTOR inhibitors	Major: Insulin resistance	Diet or metformin for mild
Immune checkpoint inhibitors	Major: Profound insulin deficiency	Immediate initiation of insulin in new onset hyperglycemia
		Switch to insulin in pre-existing T2DM

5-FU: 5-fluorouracil; PI3K: Phosphatidylinositol-3-kinase; mTOR: Mammalian target of rapamycin; T2DM: Type 2 diabetes mellitus.

widespread and cases rise, it may become more clear. At this time, it has been considered that the HLA-DR4 genotype and presence of other autoimmune diseases may correlate with increased risk[28].

For the ICI class, insulin therapy is essential in new onset diabetes given the extreme risk of IDD causing severe hyperglycemia and ketosis, reported to be as high as 77.8% [37]. Furthermore, insulin should be strongly considered in those with previous T2DM who fail to control their diabetes with ICI treatments, given the risk of a new underlying insulin deficiency. In patients with T2DM already taking non-insulin therapies, the initiation of a long acting basal insulin and rapid acting prandial insulin should be strongly considered, as simply adjusting their current medical therapy for T2DM may be ineffective as insulin-resistance may no longer be the main driving force for their hyperglycemia (Table 3). Insulin therapy would be necessary to reduce their risk of acute DKA in these cases[1].

CONCLUSION

Patient education regarding symptoms of hyperglycemia is an important safety component when initiating any of these medications, as are the more critical symptoms of hyperventilation and nausea or vomiting that may be associated with imminent DKA upon ICI therapy, in particular. The appearance of these symptoms should trigger an immediate evaluation for hyperglycemia, endogenous insulin levels (post-meal C-peptide and insulin), and acidosis/ketones to rule out developing DKA.

Given the consequences of uncontrolled blood sugars for these patients, it is important to recognize and manage hyperglycemia during cancer therapy, whether because of a worsening control of pre-existing diabetes or new onset hyperglycemia arising as a side effect of the chemotherapy itself. Current recommendations suggest tailoring glycemic control according to the underlying etiology of the hyperglycemia (insulin-resistance *vs* insulin-deficiency)[16] (Table 3) and to also consider that many cancer therapies are prescribed in cycles, which will require monitoring and perhaps intermittent treatment of the hyperglycemia[106].

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Immunometabolic bases of type 2 diabetes in the severity of COVID-19

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Abstract

The outbreak of coronavirus disease 2019 (COVID-19) is caused by the novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). COVID-19 and type 2 diabetes (T2D) have now merged into an ongoing global syndemic that is threatening the lives of millions of people around the globe. For this reason, there is a deep need to understand the immunometabolic bases of the main etiological factors of T2D that affect the severity of COVID-19. Here, we discuss how hyperglycemia contributes to the cytokine storm commonly associated with COVID-19 by stimulating monocytes and macrophages to produce interleukin IL-1 β , IL-6, and TNF- α in the airway epithelium. The main mechanisms through which hyperglycemia promotes reactive oxygen species release, inhibition of T cell activation, and neutrophil extracellular traps in the lungs of patients with severe SARS-CoV-2 infection are also studied. We further examine the molecular mechanisms by which proinflammatory cytokines induce insulin resistance, and their deleterious effects on pancreatic β -cell exhaustion in T2D patients critically ill with COVID-19. We address the effect of excess glucose on advanced glycation end product (AGE) formation and the role of AGEs in perpetuating pneumonia and acute respiratory distress syndrome. Finally, we discuss the contribution of preexisting endothelial dysfunction secondary to diabetes in the development of neutrophil trafficking, vascular leaking, and thrombotic events in patients with severe SARS-CoV-2 infection. As we outline here, T2D acts in synergy with SARS-CoV-2 infection to increase the progression, severity, and mortality of COVID-19. We think a better understanding of the T2D-related immunometabolic factors that contribute to exacerbate the severity of COVID-19 will improve our ability to identify patients with high mortality risk and prevent adverse outcomes.

Key Words: COVID-19; SARS-CoV-2; Type 2 diabetes; Inflammation; Hyperglycemia; Prothrombotic state

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Core Tip: Type 2 diabetes (T2D) acts in synergy with severe acute respiratory syndrome coronavirus-2 infection to increase the progression, severity, and mortality of coronavirus disease 2019 (COVID-19). Thus, the immunometabolic bases of the main etiological factors of T2D that contribute to the severity of COVID-19 should be studied. Here, we discuss the molecular mechanisms by which immune cells, hyperglycemia, hyperinsulinemia, loss of pancreatic β -cell mass, insulin resistance, advanced glycation end products, endothelial dysfunction, and prothrombotic state contribute to the severity of COVID-19. The syndemic between COVID-19 and T2D has challenged our ability to identify patients with high mortality risk based on scientific evidence.

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INTRODUCTION

The novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) was first identified in the city of Wuhan, China in December 2019[1]. Unlike the SARS-CoV and the middle east respiratory syndrome coronavirus, SARS-CoV-2 is highly transmissible to humans, with case fatality rates ranging from 3% to 11%[2]. A study conducted in 1099 patients from China showed that incubation of SARS-CoV-2 takes a median of 4 d on average[3], while in the United States, the Centers for Disease Control and Prevention has estimated that symptoms can appear within 2-14 d after exposure[4]. The main modes of SARS-CoV-2 transmission are respiratory droplets produced by infected individuals, aerosols, and direct contact with contaminated surfaces or objects[5]. Transmission of SARS-CoV-2 is more likely to occur in the early stage of infection; by day 10 after the onset of symptoms, 90% of patients with mild disease show a negative RNA test[6,7]. SARS-CoV-2 is the causal agent of the coronavirus disease 2019 (COVID-19), an ongoing global pandemic that is affecting the lives of millions of people worldwide[8].

Although more than 85% of patients with COVID-19 experience a self-limiting illness with symptoms such as fever, headache, myalgia, and diarrhea, some patients develop the most severe forms of the disease including pneumonia, acute respiratory distress syndrome (ARDS), sepsis, multiple organ failure, and death[9]. For this reason, there is a deep need to understand the variety of factors that increase the severity of COVID-19.

The most severe and fatal cases of COVID-19 have been reported to occur in patients with preexisting comorbidities such as cancer, hypertension, and diabetes mellitus[10,11]. In fact, diabetes mellitus is one of the most prevalent comorbidities in patients critically ill with COVID-19[12]. Diabetes mellitus is a complex disorder characterized by abnormally high blood glucose levels that affect blood vessels and nerves. Diabetes ultimately results in chronic damage to skin, feet, immune system, eyes, kidneys, brain, and heart[13]. People living with diabetes do not exhibit increased susceptibility to SARS-CoV-2 infection compared to non-diabetic individuals[12]. However, patients with diabetes and COVID-19 are at much higher risk for adverse outcomes including admission to intensive care units, invasive ventilatory support, hospital-acquired infections, and death[14,15]. Diabetic patients with COVID-19 have a mortality rate of 7.3% with respect to non-diabetic subjects, among whom a mortality of 2.3% has been reported[14].

Type 2 diabetes (T2D), formerly known as adult-onset diabetes, is the most common form of diabetes and is characterized by multiple disorders including hyperglycemia, insulin resistance, systemic inflammation, hyperinsulinemia, β -cell exhaustion, vascular damage, endothelial dysfunction, nerve degeneration, increased platelet reactivity and prothrombotic state, and dyslipidemia, among others[16,17]. These conditions affect the immune response to pathogens through different mechanisms that are not yet fully understood and might influence the severity of COVID-19, as will

be further reviewed[16,18-23].

HYPERGLYCEMIA

Hyperglycemia is the most common metabolic alteration associated with T2D and is characterized by persistently high blood sugar levels[24]. Hyperglycemia and the immune response are known to affect each other in ways that directly impact the severity of the SARS-CoV-2 infection. It is well known that high glucose levels can activate multiple immune cell types, leading to enhanced production of proinflammatory cytokines such as interleukin IL-1 beta, IL-6, and TNF- α , among others[25]. This phenomenon is especially relevant to SARS-CoV-2 infection, because patients with T2D and COVID-19 exhibit increased serum levels of proinflammatory cytokines including IL-1 β , IL-6, TNF- α , IL-8, and IFN- γ [26-30]. In patients with SARS-CoV-2 infection, this so-called “cytokine storm” is accompanied by other inflammation-related markers such as C-reactive protein, D-dimer, and ferritin, and linked to the severity of COVID-19[31]. Exacerbation of the inflammatory response causes a more severe acute infection that leads to ARDS and multiple organ failure[26]. Elevated levels of IL-6 have been found in both the airway epithelium and blood stream of patients with COVID-19 that develop severe ARDS[32].

Accumulating evidence confirms that hyperglycemia is a negative predictor in COVID-19 due to increased release of inflammatory mediators, endothelial dysfunction, thrombosis, and production of reactive oxygen species (ROS)[33-35]. Accordingly, T2D patients critically ill with COVID-19 that show acute hyperglycemic peaks at hospital admission have a worse prognosis than patients with glycated hemoglobin (HbA1c) levels near to 6.5%[36,37]. Therefore, a high blood glucose value at hospital admission is a risk factor for mortality in patients with severe SARS-CoV-2 infection[11,38].

Persistent hyperglycemia promotes mitochondrial oxidative stress and ROS production[39] that in turn leads to blood vessel damage, pancreatic beta cell dysfunction, and impaired insulin secretion[40,41]. Hyperglycemia-induced mitochondrial dysfunction triggers release of intracellular signaling molecules that can in turn inhibit the T cell response, a phenomenon that has been consistently reported in patients with severe COVID-19[42]. Moreover, SARS-CoV-2 can also directly induce mitochondrial ROS production by activating the HIF-1 α that in turn is able to promote the proinflammatory cytokine storm[42,43]. Therefore, it is feasible that hyperglycemia and ROS production from T2D act in synergy with SARS-CoV-2 infection to aggravate the cellular damage, organ failure, and progression of COVID-19.

In parallel, high blood sugar levels stimulate lactate dehydrogenase (LDH) activity and increase lactate production[44]. This phenomenon is of particular interest in COVID-19, where it has been reported that increased LDH levels are accurate predictors of mortality in patients with severe SARS-CoV-2 infection[45]. Notably, increased lactate levels in T2D patients might delay clearance of SARS-CoV-2 by inhibiting the retinoic acid-inducible RIG-1-like receptor *via* the mitochondrial antiviral-signaling protein, which results in blockage of interferon production and reduced anti-viral response[44].

Likewise, natural killer (NK) cells are innate lymphocytes that eliminate virally infected cells. In T2D patients, hyperglycemia appears to increase NK cells that express low levels of the NKG2D and the natural cytotoxicity receptor NKp46, resulting in decreased degranulation capacity and inefficient anti-viral activity[46-48]. In addition, hyperglycemia promotes viral replication in monocytes with concomitant inhibition of T cell activation[42]. Some studies have also found low numbers of dendritic cells (DCs) in T2D patients with poor glycemic control. In line with this finding, high glucose conditions in *in vitro* cultures appears to prevent monocyte differentiation into DCs[49,50]. Moreover, DCs from T2D patients poorly induce T cell proliferation *in vitro*[51]. Taken together, all of this evidence supports a decisive role for hyperglycemia in exacerbating COVID-19 progression, since T2D patients with severe SARS-CoV-2 infection exhibit low cell counts of NK cells, functional DCs, and CD4+ and CD8+ T cells[52].

Hyperglycemia in T2D patients has deleterious effects on numerous neutrophil functions including migration, phagocytosis, and bacterial killing[53]. Additionally, T2D patients have low numbers of IFN- γ -producing cells, which affects viral clearance in multiple infections such as those provoked by cytomegalovirus, Epstein-Barr virus, and influenza[54]. Moreover, hyperglycemia reduces antibody titers and the ability to kill bacteria able to invade the lungs and cause pneumonia such as *Staphylococcus*

pneumoniae and *Staphylococcus aureus*[55]. Considering the immune effects of hyperglycemia within the context of SARS-CoV-2 infection, the mechanisms discussed above might partially explain why T2D patients are at a higher risk of developing severe COVID-19 and adverse outcomes including increased viral load, sepsis, and death. For this reason, uncontrolled hyperglycemia should be considered as a crucial risk factor for COVID-19 progression in T2D patients.

HYPERINSULINEMIA AND PANCREATIC B-CELL EXHAUSTION

Pancreatic β -cells play a key role in the control of blood glucose levels by secreting insulin[56]. During the evolution of T2D, pancreatic β -cells are exposed to glucotoxicity, ROS, and endoplasmic reticulum stress, all of which increase β -cell apoptosis and dysfunction[56,57]. Additionally, chronic hyperglycemia increases M1-like macrophage infiltration in pancreatic islets, where these immune cells can secrete IL-1 β , IL-6, and TNF- α , promoting islet inflammation, β -cell malfunction, and apoptosis[58,59]. In response, pancreatic β -cells enhance insulin secretion in order to counteract persistently high glucose levels, leading to a state of hyperinsulinemia[60]. Nevertheless, β -cell mass is eventually exhausted, resulting in impaired insulin production. By the time diabetes is typically diagnosed, β -cells show less than fifty percent activity and are no longer able to secrete enough insulin to effectively maintain blood glucose levels[61,62].

In T2D patients, β -cell dysfunction can be aggravated during COVID-19 due to the ability of SARS-CoV-2 to enter the human pancreatic islets *via* angiotensin-converting enzyme 2 (ACE2)[62]. After SARS-CoV-2 invasion, inflammatory cells are recruited to pancreatic tissue, where they intensify local inflammation and injury resulting in increased peri- and intra islet fibrosis, β -cell mass loss, and hyperglycemia in both non-diabetic and diabetic patients[63]. Additionally, COVID-19 is characterized by persistent acute hypoxia that can affect numerous organs, including pancreatic islets, and provoke β -cell apoptosis directly[64]. In this way, SARS-CoV-2-induced pancreatic damage contributes to impaired insulin secretion that in turn may accelerate diabetes pathogenesis and/or aggravate preexisting diabetes[65]. Similarly, β -cell dysfunction that leads to chronic hyperglycemia is accompanied by ROS release, advanced glycation end product (AGE) formation, mitochondrial oxidative stress, and low antioxidant activity, worsening pancreatic β -cell damage during COVID-19[66-69].

A growing body of evidence suggests that SARS-CoV-2 infection not only affects the endocrine pancreas but also the exocrine pancreas[70]. In fact, SARS-CoV-2 appears to bind and enter the exocrine pancreatic ductal cells *via* ACE2[71]. Some studies estimate that the prevalence of the development of acute pancreatitis in patients with severe COVID-19 is as high as 17%[72].

The mechanisms discussed above highlight the importance of inflammation, hyperglycemia, and pancreatic dysfunction as potential contributors to the development of severe COVID-19 in patients with T2D[73].

INSULIN RESISTANCE

Insulin resistance is defined as the inability of insulin to exert its functions in insulin-dependent tissue such as liver, adipose tissue, and skeletal muscle[74]. Insulin resistance is the most important etiological factor contributing to the development of T2D[75]. There are multiple mechanisms whereby insulin resistance occurs in humans, however, systemic inflammation is one of the most recently studied. Obese subjects show a constant systemic proinflammatory state characterized by abnormally high circulating levels of TNF- α , IL-1 β , IL-6, IL-12, and MCP-1[76,77]. In adipose tissue, TNF- α induces insulin resistance by activating protein-tyrosine phosphatase 1B that in turn can dephosphorylate the insulin receptor substrate-2 (IRS-2) resulting in glucose transport arrest and hyperglycemia[78,79]. IL-6 and the NF- κ B pathway are also involved in insulin resistance and progressive loss of normal glucose tolerance[80,81]. In diabetic patients, NF- κ B upregulates PKC- θ , AP-1, and c-Jun kinase, which all act together to inhibit the insulin receptor *via* serine/threonine phosphorylation of the IRS[82].

SARS-CoV-2 infection in pancreatic β -cells not only reduces insulin secretion but also provokes a proinflammatory cytokine storm that exacerbates insulin resistance[15]. It is well known that even mild SARS-CoV-2 infection can trigger a proinflammatory cascade that mainly increases TNF- α , IL-6, MCP-1, and IL-1 β in the lungs and

blood stream[83]. Similarly, SARS-CoV-2 infection produces high levels of IFN- γ inducible protein-10 (IP-10) that can itself lower insulin sensitivity[84]. Thus, release of proinflammatory molecules in non-diabetic and diabetic patients with untreated insulin resistance might aggravate COVID-19 symptoms and increase its severity.

ACE2 is an important link between insulin resistance and severe COVID-19, since it acts as the main cellular entry point for SARS-CoV-2[85]. Under normal conditions, ACE2 converts angiotensin II into angiotensin 1-7 in order to prevent angiotensin II-related physiological disturbances such as vasoconstriction, inflammation, oxidative stress, and insulin resistance[86]. In mice fed a high-sucrose diet, ACE2 is upregulated to remove excess angiotensin II and mitigate its negative effects on insulin sensitivity and glucose transport *via* the glucose transporter protein family[87,88]. T2D patients demonstrate increased ACE2 receptor levels that in turn may help SARS-CoV-2 extend cellular binding, thus boosting viral load and severity of infection.

Likewise, IFN- γ increases in patients with severe SARS-CoV-2 infection and reduces insulin sensitivity *via* IP-10[89]. Also, IFN- γ produced in response to multiple viral infections can cause insulin resistance in skeletal muscle and adipose tissue by downregulating PI3K[90,91]. It is thus reasonable to speculate that increased IFN- γ production in patients with COVID-19 may aggravate pre-existing insulin resistance in both non-diabetic and diabetic patients.

Insulin resistance also seems to prevent the anti-inflammatory T-helper type 2 differentiation of CD4+ lymphocytes *via* the extracellular signal-regulated kinase[92]. In fact, CD4+ T cells appear to induce abnormal responses to insulin in conditions characterized by insulin resistance such as obesity and T2D[93]. Insulin resistance can also influence macrophages, an immune cell type thought to play a key role in preventing COVID-19-related organ damage[94]. Consistent with these findings, monocytes and macrophages that lack insulin signaling show impaired responses to a variety of pathogens[95]. In T2D patients, insulin resistance is also associated with high blood neutrophil count, which is of particular importance in severe COVID-19 that is characterized by neutrophilia and monocytopenia[18,96].

FORMATION OF ADVANCED GLYCATION END PRODUCTS

Pathogenesis of T2D is also characterized by the non-enzymatic covalent attachment of glucose to molecules such as proteins, lipids, and/or nucleic acids, a process that results in the formation of AGEs[97]. In addition to their negative effects on the insulin signaling pathway, AGEs have been shown to bind several surface receptors such as CD36, scavenger receptors type I and II, and galectin-3[98,99]. Upon receptor recognition, AGEs stimulate the release of pro-inflammatory cytokines in lymphocytes, monocytes, and macrophages and promote vascular inflammation and endothelial dysfunction[101]. AGEs can also directly bind to the receptor for advanced glycation end products (RAGE), a multi-ligand binding protein that promotes sustained inflammatory responses[100]. Notably, the lungs can express high RAGE levels, which may increase pulmonary inflammation in T2D patients in whom a wide variety of AGEs are produced[101]. RAGE is expressed in alveolar epithelial cells, vascular smooth muscle pulmonary cells, airway smooth muscle cells, and endothelial cells[102-105]. The AGE-RAGE interaction activates the NLRP3 inflammasome pathway. NLRP3 polarizes macrophages toward M1, inducing neutrophil extracellular trap formation and increasing the Th17 Lymphocyte population. Altogether, these inflammatory actions can perpetuate the cytokine storm, leading to pulmonary inflammation and fibrosis in patients with COVID-19[101,106]. This hypothesis is supported by the finding that RAGE-dependent inflammatory pathways play a detrimental role in pneumonia and ARDS[107].

AGEs produced in diabetic patients are also known to activate the classical complement pathway by recognizing C1q, which in turn inactivates CD59 and increases vascular injury in blood vessels of T2D patients[108]. In agreement with this concept, membrane attack complex deposits present in lung tissue from patients with severe COVID-19 has revealed complement-mediated damage which in turn induces vascular inflammation and results in extended lung damage[109].

It is well known that excess glucose can be non-enzymatically attached to hemoglobin to form HbA1c. This is particularly relevant to T2D and COVID-19 since SARS-CoV-2 is capable of altering the 1-beta chain of hemoglobin. This causes iron dissociation and porphyrin formation, thus affecting oxygen affinity and bioavailability in peripheral tissues[110]. It follows that excess glycation of hemoglobin in T2D patients may contribute to breathing difficulty that progresses to ARDS, a key

pathophysiological component of severe COVID-19. Indeed, a recent study reported that ACE2 can be glycosylated in hyperglycemic conditions[111]. Interestingly, ACE2 glycosylation appears to increase SARS-CoV-2 affinity and entry into pancreatic and lung tissue[112,113]. Good glycemic control has been shown to lower the amount of glycosylated ACE2 in lung tissue, ameliorating pneumonia and COVID-19 severity presumably by reducing the availability of viral entry points[113]. Conversely, uncontrolled hyperglycemia leads to aberrant formation of glycosylated ACE2 not only in lungs but also in nasal airways, tongue, and oropharynx, which may increase viral entry points and disease severity[113].

Last but not least, CD147 is a glycoprotein expressed in type II pneumocytes that binds the spike S1 protein, thus favoring SARS-CoV-2 entry into lung cells[114]. Evidence in T2D patients suggests that CD147 can be glycosylated in hyperglycemic conditions, which is linked to metalloproteinase upregulation and loss of tight junctions that may favor cell entry of SARS-CoV-2 and increase viral load[115]. As we have outlined, formation of AGEs appears to play a key role in the severity of COVID-19, which becomes more relevant in T2D patients with poor glycemic control, a condition that favors protein glycosylation.

ENDOTHELIAL DYSFUNCTION, VASCULAR DAMAGE, AND PROTHROMBOTIC STATE

The vascular endothelium maintains homeostasis by modulating blood flow, fibrinolysis, coagulation, platelet adherence, and immune cell trafficking in response to cell injury[116]. Impaired vascular endothelium function in patients with diabetes mellitus is considered a risk factor for cardiovascular disease[117]. Emerging evidence suggests that COVID-19 aggravates vascular pathology due to proliferation of SARS-CoV-2 in endothelial cells. This induces cellular damage, apoptosis, and disruption of the vascular barrier, which is especially relevant in T2D patients that show impaired angiogenesis[118-120]. Notably, endothelial dysfunction is a central feature in COVID-19 pathogenesis[121]. Patients with COVID-19 have nitric oxide (NO) deficiencies that lead to increased vascular contraction and reduced ROS neutralization[122,123]. Upon SARS-CoV-2 infection, the vascular endothelium undergoes vascular leakage and enhanced blood clotting. Subsequent recruitment of immune mediators results in inflammation that perpetuates tissue damage and vascular impairment[124]. As mentioned above, COVID-19 is accompanied by a high number of neutrophils, proinflammatory immune cells that also contribute to vascular damage in T2D. Diabetic patients have neutrophils with enhanced oxidative activity that produce high free radical levels and neutrophil extracellular traps (NETs) which can cause direct injury to blood vessels[125,126]. Neutrophils are also major producers of myeloperoxidase, a peroxidase enzyme that binds to the vascular endothelium and increases blood vessel damage in T2D patients[127]. These lines of evidence support a deleterious synergistic effect of T2D on COVID-19, wherein hyper-reactive neutrophils may directly injure the vascular endothelium and worsen the patient's outcome[96]. Interestingly, SARS-CoV-2 can increase NET release by infecting neutrophils. Increased formation of NETs can then directly injure the lung epithelium.

Proinflammatory cytokines play a decisive role in endothelial dysfunction. It is well known that IL-6 is upregulated in T2D and is associated with endothelial damage and atherosclerosis[128]. In patients with severe COVID-19, IL-6 induces chemokine expression, leukocyte trafficking, immune cell extravasation toward arterial walls, NO reduction, increased oxidative stress, and exacerbated inflammation of blood vessels[129]. TNF- α , another important proinflammatory cytokine involved in the COVID-19 cytokine storm, accelerates atherosclerosis *via* vascular cell adhesion molecule-1, E-selectin, and MCP1, which impairs vasodilatation and promotes endothelial cell apoptosis[81]. Post-mortem examination of lung tissue from patients severely infected with SARS-CoV-2 revealed massive mononuclear and polymorphonuclear cell infiltration, supporting the role of immune cell recruitment in COVID-19 progression[118]. These findings indicate that chemoattraction and recruitment of immune cells act together with endothelial dysfunction to induce vascular damage in patients with T2D, which may worsen the severity of COVID-19 by increasing vascular leaking and prothrombosis.

Disruption of vascular integrity promotes basement membrane exposure, coagulopathy, D-dimer release, and fibrinogen and platelet activation, all of which are important biomarkers for poor prognosis in COVID-19[130-133]. It is well known that the prothrombotic state common in patients with T2D may increase the occurrence of

severe coagulopathy in patients critically ill with COVID-19[134]. In fact, the severity of COVID-19 increases in parallel with pulmonary embolism, microcirculatory malfunction, and disseminated intravascular coagulation[135,136]. Microvascular and macrovascular thromboembolic events have been documented in the kidneys, lungs, spleen, and brains of SARS-CoV-2 infected patients[137-140]. Thrombotic incidence of about 30% has been reported in lungs[141] and incidence of deep venous thrombosis as occurs in the lower limbs of T2D patients has been reported at 46%[142].

The mechanisms underlying thromboembolic events in T2D patients with severe COVID-19 remain unclear, but persistent inflammation has now emerged as a potential contributor[143]. As described above, levels of several proinflammatory cytokines, including TNF- α , IL-6, and IL-8 are elevated in patients with COVID-19 who required hospitalization[144,145]. Interestingly, some of these cytokines have prothrombotic effects by themselves[146]. For instance, there is a positive association between elevated IL-6 and increased fibrinogen levels[146]. During sepsis, monocytes and macrophages release TNF- α as well as tissue factors that activate clotting pathways[147]. Besides inducing proinflammatory cytokine production, SARS-CoV2 has been shown to induce expression of procoagulant genes such as fibrinogen, tissue factor, factor II, and factor X[148,149] *in vitro* culture models. During numerous viral infections and sepsis, activation of the innate immune system leads to increased activation of the complement system, von Willebrand factor, tissue factor, and factor VIIa[148,150,151]. Likewise, complement activation during COVID-19-related sepsis intensifies the cytokine storm and perpetuates microvascular damage[152].

T2D increases mortality risk in COVID-19 due to the preexisting prothrombotic state secondary to diabetes, where hyperglycemia by itself appears to play a contributing role[151]. Human aortal endothelial cells cultured in high glucose *in vitro* were shown to trigger both inflammatory and prothrombotic pathways[153]. Similarly, hyperglycemia acts in synergy with neutrophils to release calprotectin, a protein that can bind RAGE on Kupffer cells and induce IL-6 synthesis. IL-6 increases thrombopoietin production, which enhances proliferation and expansion of thrombotic precursors and leads to thrombocytosis[154]. Similarly, P2Y₁₂, a receptor expressed on the surface of platelets that plays essential roles in platelet activation, may be elevated in T2D patients, and facilitate platelet adhesion to vascular endothelium[155,156]. Consistent with these findings, numerous reports have demonstrated that the prothrombotic state can be mitigated by lowering blood glucose concentration[154]. Thus, several factors associated with T2D including endothelial dysfunction, vascular damage, systemic inflammation, and hyperglycemia can directly aggravate the prothrombotic state and increase mortality risk in patients with severe COVID-19[138, 141,157].

CONCLUSION

COVID-19 is an ongoing global pandemic that has challenged the ability of healthcare providers to treat the most vulnerable patient populations, such as those living with preexisting T2D. Indeed, managing the syndemic between the two current pandemics of COVID-19 and T2D has become a major contemporary public health challenge. We have shown that T2D acts in synergy with SARS-CoV-2 infection to accelerate disease progression, increase severity, and heighten the mortality risk of COVID-19. We have discussed the mechanisms whereby hyperglycemia contributes to the “cytokine storm” characteristic of severe SARS-CoV-2 infection by stimulating monocytes and macrophages to produce IL-1 β , IL-6, and TNF- α in the airway epithelium. The main mechanisms whereby hyperglycemia promotes ROS release, inhibition of T cell activation, and NET formation in the lungs of patients with severe SARS-CoV-2 infection have also been examined. We have reviewed the molecular mechanisms by which proinflammatory cytokines induce insulin resistance and exert deleterious effects on pancreatic β -cell exhaustion in T2D patients critically ill with COVID-19. We have also studied the effect of excess glucose on AGE formation and the role of AGEs in perpetuating pneumonia and ARDS. Finally, we have discussed the contribution of preexisting endothelial dysfunction secondary to diabetes to the development of neutrophil trafficking, vascular leaking, and thrombotic events in patients with severe SARS-CoV-2 infection (Table 1). We have not, however, addressed the possible contribution of other components of T2D such as nerve injury, hyperglucagonemia, adiposity, dyslipidemia, endoplasmic reticulum stress, glomerular and myocardial damage, and hypovitaminosis D to the severity of COVID-19. Importantly, the efficacy of vaccines against SARS-CoV-2 should be rigorously scrutinized in patients with T2D,

Table 1 Immunometabolic mechanisms of the main etiological factors associated with type 2 diabetes and their implications in the development of severe acute respiratory syndrome coronavirus-2 infection

Etiological component of T2D	Effect on immune responses	Implications in COVID-19	Ref.
Hyperglycemia	Stimulation of monocytes and macrophages to release IL-1 β , IL-6, and TNF- α	Promotion of the cytokine storm and exacerbated inflammatory responses	Nielsen <i>et al</i> [23], Blair <i>et al</i> [24]
	Mitochondrial oxidative stress and production of reactive oxygen species	Activation of the proinflammatory cytokine storm	Robertson <i>et al</i> [39]
	Stimulation of lactate dehydrogenase activity	Upregulation of lactate pathway during severe COVID-19	Zhang <i>et al</i> [40]
	Increased NK cells with low levels of NKG2D and NKp46	Decreased degranulation and inefficient antiviral activity	Berrou <i>et al</i> [47]
	Low number of dendritic cells	Inefficient antigen presentation and decreased T cell activation	Zhong <i>et al</i> [52]
	Inhibition of T cell activation and proliferation	Increased viral load and COVID-19 progression	Macia <i>et al</i> [51]
	Decreased neutrophil migration and phagocytosis	Impaired viral clearance	Alba-Loureiro <i>et al</i> [53]
	Low number of IFN- γ -producing cells	Impaired antiviral response	Kalantar <i>et al</i> [54]
	Reduction of antibody titers	Inability to kill infected cells and increased viral load	Mathews <i>et al</i> [55]
Pancreatic β -cell exhaustion and hyperinsulinemia	β -cell apoptosis	Enhanced pancreatic damage through SARS-CoV-2 direct binding to ACE2 in β -cells	Weir[57]
	β -cell dysfunction through endoplasmic reticulum stress	Increased pancreatic inflammation	Butler <i>et al</i> [56]
	M1-like macrophage infiltration	Islet fibrosis and β -cell mass loss	Inoue <i>et al</i> [58], Westwell-Roper <i>et al</i> [59]
	Impaired insulin production	Increased hyperglycemia and promotion of proinflammatory cell activation	Zheng <i>et al</i> [64]
	Deterioration of exocrine pancreas	Increased pancreatic inflammation	Hayden <i>et al</i> [66]
Insulin resistance	Stimulation of proinflammatory cytokine release into circulation	Exacerbated systemic inflammation	Tabák <i>et al</i> [75], Akbari <i>et al</i> [80]
	Inactivation of the insulin signaling pathway <i>via</i> NF- κ B	Suppression of IP-10 production and reduced insulin sensitivity	Antuna-Puente <i>et al</i> [81]
	Increased ACE2 receptor levels	Increased viral load and COVID-19 progression	Kuba <i>et al</i> [85]
	Decreased Th2 cell differentiation	Reduction of lymphocytes with anti-inflammatory functions	Viardot <i>et al</i> [92]
	Impaired ability of macrophages to respond to pathogens	Monocytopenia, COVID-19 progression, increased mortality risk	Rizo-Téllez <i>et al</i> [96]
Advanced glycation end products	High blood neutrophil count	Neutrophilia, COVID-19 progression, increased mortality risk	DeFronzo <i>et al</i> [16]
	Activation of the RAGE and sustained inflammatory responses	Increased pulmonary inflammation and mortality risk	Oczypok <i>et al</i> [101]
	Increased Th17 lymphocytes	Perpetuation of the cytokine storm and pulmonary inflammation	Wang <i>et al</i> [30]
	Activation of the classical complement pathway	Complement-mediated damage and membrane attack complex formation in lung tissue	Lupu <i>et al</i> [150]
	Non-enzymatic attachment of glucose to hemoglobin	Alteration of the hemoglobin 1- β chain, less oxygen bioavailability in peripheral tissues and breathing difficulty	Means[110]
	Non-enzymatic attachment of glucose to ACE2	Increased SARS-CoV-2 affinity and infection in pancreatic and lung tissue	Zhao <i>et al</i> [112], Bao <i>et al</i> [114]
	Glycation of CD147 in type II	Promotion of SARS-CoV-2 cell entry and	De Francesco <i>et al</i> [115]

Endothelial dysfunction and prothrombotic state	pneumocytes	increased viral load in pneumocytes	
	Neutrophil trafficking impairment	Hyper-reactive neutrophils that injure the vascular endothelium	Kraakman <i>et al</i> [154]
	Increased prothrombotic state	Enhanced blood clotting and severe coagulopathy	McFadyen <i>et al</i> [134]
	Hyper-activation of neutrophils in blood vessels	Vascular damage, blood vessel leaking, and sepsis	Joshi <i>et al</i> [126]
	Impaired vasodilatation with release of IL-6 and TNF- α	Microcirculatory malfunction and increased fibrinogen levels	Chi <i>et al</i> [29], Mangalmurti <i>et al</i> [27]
	Recruitment of immune cells	Blood vessel leaking and thrombosis	Ranucci <i>et al</i> [146]
	IL-6 production	Increased thrombopoietin production	Kraakman <i>et al</i> [154]
	Increased P2Y12 platelet receptor	Enhanced platelet adhesion and thrombosis	Dorsam <i>et al</i> [155]

Summary of the main immunometabolic mechanisms by which immune cells and cytokines act in synergy with preexisting hyperglycemia, β -cell dysfunction, hyperinsulinemia, insulin resistance, advanced glycation end products, endothelial dysfunction, and prothrombotic state to increase the severity, progression, and mortality of coronavirus disease 2019 in patients with type 2 diabetes. COVID-19: Coronavirus disease 2019; SARS-CoV-2: Severe acute respiratory syndrome coronavirus-2; T2D: Type 2 diabetes; NK: Natural killer; ACE2: Angiotensin-converting enzyme 2; IP-10: IFN- γ inducible protein-10; RAGE: Receptor for advanced glycation end products.

with careful consideration for all of the factors discussed herein. A better understanding of the T2D-related immunometabolic agents that contribute to exacerbate the severity of COVID-19 will improve our ability to identify patients with high mortality risk and prevent adverse outcomes.

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Spatial epidemiology of diabetes: Methods and insights

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Abstract

Diabetes mellitus (DM) is a growing epidemic with global proportions. It is estimated that in 2019, 463 million adults aged 20-79 years were living with DM. The latest evidence shows that DM continues to be a significant global health challenge and is likely to continue to grow substantially in the next decades, which would have major implications for healthcare expenditures, particularly in developing countries. Hence, new conceptual and methodological approaches to tackle the epidemic are long overdue. Spatial epidemiology has been a successful approach to control infectious disease epidemics like malaria and human immunodeficiency virus. The implementation of this approach has been expanded to include the study of non-communicable diseases like cancer and cardiovascular diseases. In this review, we discussed the implementation and use of spatial epidemiology and Geographic Information Systems to the study of DM. We reviewed several spatial methods used to understand the spatial structure of the disease and identify the potential geographical drivers of the spatial distribution of DM. Finally, we discussed the use of spatial epidemiology on the design and implementation of geographically targeted prevention and treatment interventions against DM.

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Core Tip: With more than 400 million people having diabetes mellitus (DM), this disease emerges as one of the biggest public health challenges of our current times. However, one of the most significant public health advances in the study of DM is the demonstration that it can be prevented by the implementation of effective interventions targeting the factors that exacerbate the risk of the disease. Spatially informed tailored strategies that allocate resources in the high-risk areas where the most vulnerable populations reside would be an effective approach aimed to control and reduce the burden of the disease. Spatially explicit community-level policy interventions would offer great promise in effectively addressing the obesogenic and diabetogenic environment aimed to control the global DM epidemic.

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INTRODUCTION

Diabetes mellitus (DM) is an illness triggered by an incapacity of the insulin generated by the pancreas to effectively transfer glucose into cells *via* transporter recruitment, leading to uncontrolled hyperglycemia[1]. The common classifications of DM are the polygenic forms type I (T1DM) and type II (T2DM)[2]. T1DM is described by the absence of insulin production generated by the autoimmune destruction of pancreatic beta cells, whereas T2DM is an acquired disorder in which the pancreas either becomes insulin deficient or sufficient insulin is produced but the body cells cannot respond to the insulin, labeled insulin resistance[3,4]. In general, more than 90% of all DM diagnoses are T2DM. Other types of DM include gestational DM (any degree of glucose intolerance during pregnancy), monogenic DM syndromes, and drug (*e.g.*, steroid) or chemical induced DM, among others[4,5]. DM increases the risk of developing different comorbidities and other health complications including cerebrovascular accidents, hypertension, retinopathy and other ocular diseases, nephropathy, cardiovascular diseases, mental health conditions (*e.g.*, anxiety and depression), skin infections, and lower-limb compromise, among others[6].

Several genetic factors trigger the development of DM[7,8]. To date, more than 60 gene variants have been linked with the development of DM, but the actual effect size of each of these individual gene variants is largely unknown[9]. Behavioral, health-related, and environmental risk factors are also linked to increased risk of DM including obesity, physical inactivity, obesogenic environments, pollution, history of gestational DM, hypertension, and dyslipidemia, among others[10-13].

In 2019, 463 million adults aged 20-79 years (8.8% of the adult population) was estimated globally to be living with DM[14]. Among these people presenting the condition, 327 million were within the working age group (20-64 years), and 136 million people were aged 65-79 years. More than four million deaths were attributed to DM in 2019, ranking it as the ninth leading cause of death globally in that year. The latest evidence shows that DM continues to be a significant global health challenge and is likely to continue to grow substantially in the next coming decades. As a result, the global epidemic of DM has key implications for healthcare costs, with most countries allocating between 5% to 20% of their total healthcare resources to treat DM and its complications[15]. Likewise, an optimal DM treatment access at lower cost would increase the success of any intervention plan, particularly in developing countries.

The emergence of the global DM epidemic can be attributed to well-documented drivers like the increasing number of older people and increasing levels of physical inactivity and obesity. However, concerns have been increased in people under the age

of 60 since more than one-third of the DM-related deaths are occurring in this age group[16]. Increased consumption of unhealthy food and sedentary lifestyle boosting an obesogenic environment have been identified as potential drivers of these growing trends[17]. Likewise, an increased risk of DM has been linked to several other sociodemographic and economic factors including age, sex, ethnicity, education, health services, employment security, housing, and access to nutritious food. For example, it has been found that in regions with increased wealth, the rates of DM increase between two and four times in individuals with low socio-economic status, potentially linked with poor access to healthy food and adequate healthcare[18,19]. Poorer individuals are less likely to be diagnosed and to get treatment early enough, resulting in earlier adverse outcomes. These socio-economic determinants can also boost the development and progression of DM through the pathways of psychological, physiological, and behavioral responses like the development of mental health conditions and chronic stress[15].

Despite significant investments in research, public health interventions, and clinical care, the slackening of the growth rate of DM has been rather modest. This epidemic will involve an urgent and steady commitment aiming to implement assertive solutions at local and national levels with public health funding oriented towards public policies and economic boosting for local communities to start DM prevention programs. However, we first must understand the global burden of DM to plan for current needs, and to inform the design and implementation of cost-effective interventions. Geographic Information Systems (GIS) methods and spatial epidemiology concepts are important tools for recognizing the spatial and temporal dynamics of the epidemic. Understanding the critical geographical characteristics of the DM epidemic will provide valuable information to identify the potential environmental, demographic, and socio-economic drivers of the epidemic as well as the geographic areas where vulnerable populations are located, and where interventions should be implemented.

The main aim of this review is to summarize the main concepts and methods used in the spatial epidemiology of DM, and to discuss the advances in the study of the spatial structure of DM epidemics. The article starts with a brief summary of the general concepts and advances in the study of the spatial dynamics of diseases followed by a summary of the current knowledge of the spatial structure of DM. The article continues with a section discussing the interaction between DM and other communicable and non-communicable diseases. It finishes with the conclusions and the advances in the study of the spatial epidemiology of DM.

SPATIAL EPIDEMIOLOGY AND GIS

Epidemiology involves the study of the distribution and determinants of diseases in populations, particularly in human populations. Epidemiologic studies have focused on identifying the type and extent of illnesses affecting human populations, and recognizing the factors linked to disease outcomes[20]. Epidemiologists examine the interactions that emerge among the host, agent, and environment (the epidemiologic triangle) to identify the underlying causes of a disease and generate interventions for prevention and control[21]. Epidemiological studies aim to explain the amount and distribution of disease within a particular population by identifying the persons at risk, the time of disease onset, and the places where they are located[22].

Traditional epidemiology has historically focused on persons and time but less on place[23]. Only recently, the geographical place at which epidemics emerge and disperse started gaining relevance as an essential element for the understanding of epidemic dynamics, and for identifying the underlying factors boosting the epidemic. As a result, spatial epidemiology has emerged as a novel approach for the understanding and control of current epidemics. In spatial epidemiology, place is a very broad concept that refers to the 'lived space' in which individuals of a given community interact. The lived space includes the natural and built environment, and human social networks and interactions. It exists in different scales, from the global and regional spaces to the individual scale[24]. Place in spatial epidemiology involves exploring beyond individual characteristics to consider the social and environmental contexts experienced by individuals and how these interactions affect their health.

The capacity to study and understand the role of places in disease dynamics has substantially increased in the past several decades. This advance is mostly linked to advances in quantitative methods and geospatial technologies such as spatial analysis and GIS. Equally important, this development is linked to new concepts and

understandings about the social conformation of places, how people interact with these social and environmental elements, and ultimately, how these interactions affect an individual's health[25]. Alongside the rapid development of geographic tools, GIS methods, and spatial analysis, massive amounts of geocoded environmental and social data are now available[26,27]. These data and the methodological tools available for analyzing spatial data, provide a strong foundation for innovative spatially explicit approaches in epidemiological research by shedding light on the etiology of health outcomes, and providing a geographical foundation for health policy-making[28]. Spatial analysis methods can be used to understand mapped information by identifying patterns and drivers of disease distribution. These methodological tools also facilitate data exploration and pattern identification by detecting unusual geographical distributions of health events and following their evolution in space over time.

Spatial epidemiology has been mostly used for studying communicable diseases, but its application has currently expanded to the study of non-communicable diseases like DM[29-32]. The quantitative methods in spatial epidemiology for estimating the net contribution of geographical hotspots (areas experiencing a disproportionately large burden of the disease) and the disease burden determinants at the ecological and individual-level may facilitate the design and implementation of control measures. The identification of these areas can uncover the locations of high-risk populations as well as revealing the factors that facilitate the persistence and spread of epidemics. In this context, spatial epidemiology has become essential tool in the fight against devastating epidemics such as malaria and HIV[33-36], but it is also becoming a widely implemented approach for the study of non-communicable diseases like cancer [37] and cardiovascular diseases[38]. Geospatial analysis has significant potential for enhancing the effectiveness of both a single program at a given level of spending and the allocation of limited resources across several programs. In sum, one of the specific implementations of spatial analysis can be to investigate how prevention and treatment interventions can be combined in different geographical places and populations for maximizing cost-effectiveness under local or national funding constraints.

SPATIAL MAPPING OF DIABETES AND DISEASE DISTRIBUTION

Disease mapping is one of the first steps for understanding the spatial structure and dynamics of a disease. Spatial maps of diseases illustrate the distribution and intensity of a disease, facilitate the identification of the heterogeneous distribution of the disease in a specific region, and elucidate high burden areas in which the disease is concentrated in space. In this context, it has been shown that the burden of DM has considerable regional variation, with developing countries being the areas disproportionately affected by the current global DM epidemic, with approximately 75% of people with DM residing in low and middle-income countries[39,40]. Meanwhile, general distribution patterns of the global DM prevalence are consistent with socio-economic development (Figure 1). Developed regions, such as Western Europe, show substantially higher DM prevalence rates that continue to increase despite the implementation of several public health measures. In 2019 the age-adjusted DM prevalence was 4.7% in Africa, 6.3% in Europe, 11.4% in the Western Pacific and Southeast Asia, 8.5% in South and Central America, 12.2% in the Middle East and North Africa, and 11.1% in North America and the Caribbean[39].

All regions in the world are expected to have an upsurge in the numbers of people living with DM. Overall, the estimated number of adults with DM will increase by 51% by 2045. While the African region currently holds the lowest prevalence of adults living with DM, it is expected to have the largest proportional increase in the numbers of adults with DM by 2045, with an increase of about 140%[41]. Moreover, the majority of people with DM in high-income countries are over the age of 50, whilst in the middle- and low-income countries are under the age of 50. The demographic patterns observed are likely to change considerably over the next generations, with improvements in life expectancy and higher rates of urbanization in these low- and middle-income countries[42]. Of notice, current general patterns indicate that there are more people living with DM in urban areas (65%) than in rural areas (35%)[15].

There is also substantial spatial variation of the distribution of DM at the subnational and local levels. To illustrate these variations, we mapped the subnational prevalence of DM in nine countries using data from the Demographic and Health Survey conducted in these countries (Figure 2). The description of the methods used

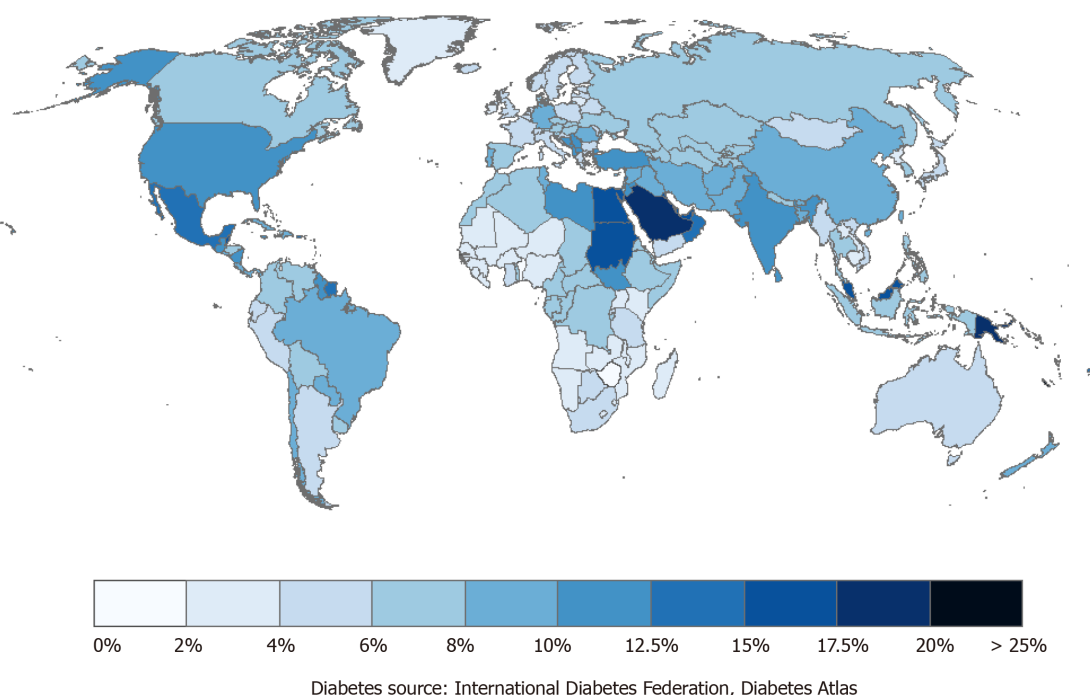


Figure 1 Global distribution of diabetes prevalence in 2017. Maps were created using ArcGIS® by ESRI version 10.5 (<http://www.esri.com>)[91].

for the generation of these maps can be found in Supplementary Material. The results of these maps illustrate the substantial local variation of DM prevalence within countries from different regions. The spatial structure of DM was characterized by local high DM prevalence areas where the burden of the disease was concentrated within a country (red areas in the map). These high burden areas identified locations in which the vulnerable population at high risk of the disease and the local drivers of the disease were concentrated. Such information would help to develop geographically targeted interventions tailored to the high-risk populations vulnerable to the disease at the subnational and local levels.

SPATIAL EPIDEMIOLOGY OF DIABETES

A spatial approach to disease analysis is relevant to any non-communicable disease linked to potential environmental and socio-economic drivers heterogeneously distributed in space. This approach is especially relevant to DM as recent research has identified potential associations between the spatial distribution of DM prevalence and geographical and environmental factors such as increased fast-food availability, green space, car-dominated transport, walkability and reduced spaces for exercise[43,44]. Many of these factors can be modified and included in health promotion programs, and spatial analysis can provide valuable evidence to inform resource allocation and public policy decisions targeting these potential geographical drivers of DM[45].

As mentioned previously, several demographic, clinical, and genetic factors are linked with an increased risk of developing DM[46]. In addition, there is now evidence of geographical and environmental factors associated with DM prevalence[47], and several of these factors are modifiable and candidates to be included in prevention programs, including lifestyle choices and associated cardiovascular risk, and other neighborhood factors amenable to health promotion programs. Therefore, the identification of areas where higher prevalence of environmental-related risk factors are concentrated would allow the design and implementation of geographically targeted health promotion programs oriented towards DM treatment and prevention. Moreover, spatial analysis designed to targeting health care needs at a local level can be essential in evaluating which areas are at higher risk of becoming unhealthy and thus need to be prioritized in the future by the identification of communities with a high-risk profile and the development of appropriate primary care interventions for DM prevention and treatment[48].

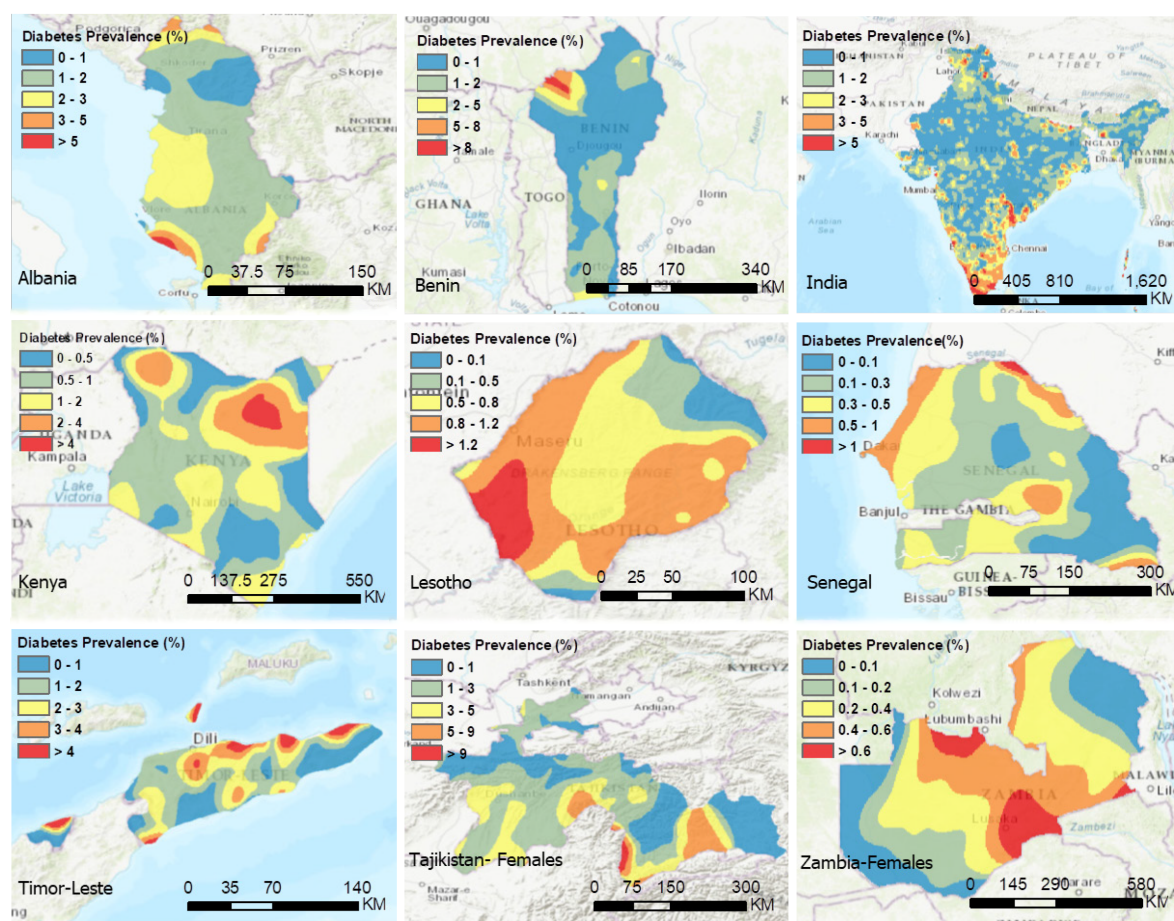


Figure 2 Spatial variations of diabetes prevalence in nine countries using a kernel smooth method. Maps were created using ArcGIS® by ESRI version 10.5 (<http://www.esri.com>)[91].

Several studies have identified geographical inequalities in the prevalence of risk factors and disease outcomes linked to complications of clinical DM. Disease clustering is observed not only among sociodemographic groups but also in urban geographies that boost obesity and physical inactivity[49-51]. Likewise, many built environment factors such as the rural-urban matrix[52,53], access to healthy foods[54], walkability [52], and crime levels[47] have been found to correlate with the heterogeneous distribution of DM prevalence. As the need for community-based interventions increases, it becomes essential to identify those communities at the highest risk of disease and DM complications in order to design suitable interventions based on their unique disease risk environment. Information on the relationship between DM prevalence and spatial factors such as the built environment could allow the design of better public health programs targeting populations at risk for DM. A short summary of several studies implementing different spatial methods to explore the spatial structure of DM is included in Table 1 and Supplementary Table 1.

Other recent important environmental factors have been linked with a higher risk of DM, particularly air pollution. Air pollution is an important global health problem, and $PM_{2.5}$, which is one of the most widely studied air pollutant, has been found to be associated with increased risk of several non-communicable diseases, including cardiovascular, pulmonary, kidney, and other diseases[55,56]. It has been estimated that this pollutant contributed to about 4.2 million premature deaths in 2015[57]. Growing evidence suggests a significant association between increased $PM_{2.5}$ exposure and the risk of DM, and it has been estimated that about 3.2 million cases of incident DM can be attributable to elevated concentrations of $PM_{2.5}$ in 2016[58]. Likewise, these studies have found substantial geographical variation in the burden of DM attributable to air pollution, and the link is stronger in less developed regions[58].

As countries develop economically and undertake an epidemiological transition, non-communicable diseases are likely to emerge even more prominent as major causes of disease and death, and the contribution of environmental factors including air pollution in the burden of non-communicable diseases in general, and specifically to DM, will probably become even more pronounced. The modifiable feature of these

Table 1 Methods for geospatial analysis with examples of applications and findings

Methods	Geospatial techniques	Ref.	Geographic unit and location	Key findings
Spatial clustering	Getis-Ord Gi	[92]	West Adelaide, Australia	Spatial distribution of dementia, depression, and type 2 diabetes varied across west Adelaide, respectively. Spatial convergence of the three diseases was identified in two large hot spot clusters
	Local Moran's I and the Getis-Ord Gi	[93]	Individual level in west Adelaide, Australia	Spatial heterogeneity in type 2 diabetes risk was present across communities, with significant clusters in the central part of the study area
	Moran's I	[31]	District level in India	The prevalence of diagnosed diabetes was substantially higher than that of self-reported diabetes in southern India (7.64% <i>vs</i> 2.38%) Diagnosed diabetes prevalence had positive moderate autocorrelation, and it varied from 10.52% in Goa to 4.89% in Telangana. The diagnosed diabetes prevalence was associated with higher proportion of people with secondary education and above, wealthy and Christian populations
	Moran's index and spatial regression	[94]	District level in Southern India	Spatial variations of high blood glucose (HBG) and very high blood glucose (VHBG) were observed across districts for women aged 15–49 years. District-level prevalence of HBG and VHBG were clustering across southern Indian districts. The HBG and VHBG prevalence were associated with district-level proportion of tobacco use, overweight, obese, and general caste
	Spatial statistic scan	[72]	Individual level in India	Substantial geographic variation in diabetes prevalence in India was found, with a concentrated burden at the southern coastline; Regional tuberculosis endemicity and diabetes spatial distributions showed that there is a lack of consistent geographical overlap between these 2 diseases
	Getis-Ord Gi	[95]	Individual and statistical area level 1 regions in western Adelaide, South Australia	The spatial heterogeneity of obesity, cardiovascular diseases (CVD), and type 2 diabetes was present across communities. Hot spots of these conditions clustered in three locations across western Adelaide. Area-level prevalence of CVD, obesity, and type 2 diabetes were negatively associated with socioeconomic status (SES)
	Global Moran's I, Local Moran's I and spatial regression	[32]	Individual and state level in Nigeria	Geographic clustering of diabetes mellitus (DM) and a DM pocket existed in the southeastern part of Nigeria. Obesity and education attainment were associated with the geographic variations of DM in the country
Spatial estimation models	Moran's I	[96]	Individual level in the city of Oslo, Norway	Diabetes prevalence clustered on the east side of Oslo. The diabetes prevalence was positively associated with neighborhoods with more fast foods and less healthy food shops and physical exercise facilities
	Spatial scan statistic and non-spatial linear regression	[47]	Administrative health area in the City of Winnipeg, Canada	Substantial clustering and small-area variations in DM prevalence existed in the city of Winnipeg. High rates of DM prevalence were associated with low SES, poor environmental quality and poor lifestyle
	Geographically weighted regression	[97]	Country-level of the continent United States	Significant spatial clustering of county-level diabetes prevalence was observed in the United State; the associations between diabetes prevalence and the percentage of poverty and percentage nonwhite population varied across regions in the United States.
	Geographically weighted regression	[98]	Country-level of the continent United States	The relationships between diabetes prevalence and poverty varied as a function of location
	Geographically weighted regression	[99]	Four-digit postal code level in Netherlands	Type 2 DM drug use is positively associated with population ageing, proportion of social welfare/benefits, proportion of low income, and proportion of pensioners. Spatial variabilities existed in these associations. Spatial analysis provided added value in predicting health care use at local level
	Tests of spatial autocorrelation and geographically weighted regression	[51]	Hospital referral regions in the United States	Lower-extremity amputation had spatial variations, with high rates clustered in southern states of the United States
	Spatial regression models	[100]	census-tract level in Chicago	Hypertension prevalence rates for patients were positively associated with areas with high rates of poverty, minority, and disability status. Neighboring tracts with high disease rates were the strongest predictor of cardiovascular-related chronic disease by several orders of magnitude. Diabetes had similar results
Multilevel models	Spatial autoregressive model	[101]	District-level in India	Spatial clustering was present in the burden of diabetes among women. The burden was relatively higher among women from the Southern and Eastern parts of the country. Diabetes was associated with obesity, hypertension, and living in urban areas
	Multilevel models	[102]	Individual level in Northern Netherlands	Individual risk factors at the neighborhood and municipality level explained 67.0% and 71.6% of the regional variations, respectively. Analysis on the smallest spatial scale best captured the regional variance. Individual and

				neighborhood body mass index (BMI) had significant interaction adjusting for the individual risk profile
	Multilevel negative binomial regression	[103]	Province level in China	Compared with the South, diabetes mortality was higher in the Northwest and Northeast. Diabetes mortality was higher in urbanized areas, with higher mean body mass index, and with higher average temperatures. Diabetes mortality was lower where consumption of alcohol was excessive
	Multilevel logistic regression	[104]	Province level in China	Diabetes prevalence and detection had widespread geographic variations across provinces in China. Adjusted regional diabetes prevalence was higher in the north (12.7%) than in the northeast (8.3%). Adjusted regional diabetes prevalence was higher in urban high socioeconomic circumstances (SEC) (13.1%) than in rural low-SEC counties/districts (8.7%). Adjusted diabetes detection was higher in the north (40.4%) and in urban high-SEC counties (40.8%) than in the southwest (15.6%) and the rural low-SEC counties (20.5%)
	Multilevel poisson regression	[105]	Canton-level in Southeastern France	Prevalence of treated diabetes was significantly higher in the more deprived and population-dense cantons
	Multilevel logistic regression	[106]	Census blocks in Paris, France	Prevalence of type 2 diabetes was higher in neighborhoods with the lowest levels of education attainment. Meanwhile, accounting for geographic variations in participation led to an 18% decrease in the log prevalence for low versus high neighborhood educations
Spatial analysis and GIS mapping	Choropleth mapping and logistic regression	[29]	County-level United States	Identifying a diabetes belt consisting of 644 counties in 15 mostly southern states in the United States. People in the diabetes belt were more likely being Non-Hispanic African American, leading a sedentary lifestyle, and being obese
	GIS methodology of spatial join	[107]	Census-tract level in greater Sacramento area United States	Neighborhood SES was a barrier to optimal glucose control, but not associated with low-density lipoprotein control. GIS analysis is useful for disease management programs
	Data aggregation to state-level and region-level	[108]	State-level United States	The spatial variations in the ratios of children with diabetes to pediatric endocrinologists were present: the ratios in Midwest (370: 1), South (335: 1), and West (367: 1) are twice as high as in the Northeast (144: 1). Across states, there is up to a 19-fold difference in the observed ratios of obese children to pediatric endocrinologists
	Data aggregation to district level and GIS mapping	[109]	Tower Hamlets, an inner city district of London, United Kingdom	Hot spots where up to 17.3% of all adults were at high risk of developing type 2 diabetes were identified. Small-area geospatial mapping is feasible for epidemiological and environmental data
	Data aggregation to electoral wards and Regression analysis	[110]	Electoral wards in England	The diabetes prevalence varied across different locations, ranging from 2.4% in Thames Valley to 4% in North East London. The methodology of prevalence estimates is applicable to developing small area prevalence estimates for a range of chronic diseases
	Data aggregation to electoral wards and GIS mapping	[111]	Electoral wards in Greater London	Environmental factors affected diabetes outcomes. The age-adjusted mortality rates in diabetic patients were higher in deprived areas than in prosperous areas
	Data aggregation to climato-geographic and administrative regions of the Ukraine	[112]	Administrative regions in Ukraine	Geographic variations in the insulin-dependent diabetes mellitus (IDDM) were present across various administrative regions of the Ukraine. The prevalence of IDDM varied from 1740 to 3813 patients per 1 million populations across Ukraine, with the west zone having lower prevalence than the average
Bayesian estimation approaches	Bayesian spatial analysis	[113]	Local administrative district level in Bangladesh	People of older age, higher education, better socio-economic condition, higher BMI were more likely to have hypertension and diabetes. Significant regional variations were observed with prevalence for hypertension ranges between 10% and 35% and for diabetes between 6% and 19% while their national prevalence were reported as 24% and 11%, respectively
	Bayesian hierarchical joint spatial analysis	[114]	Electoral wards in the Yorkshire, United Kingdom	Childhood lymphoblastic leukemia and type 1 diabetes varied across geographic locations, clustering in more rural areas
	Bayesian Small Area Estimates	[30]	County-level United States	Diabetes incidence was high in the southeastern United States, the Appalachian region, and in scattered counties throughout the western United States
	Bayesian estimation approach	[115]	Zip code census tract of United States	Significant spatial effects existed in the diabetes prevalence even after adjusting for age, education, ethnicity and known state predictors
Regression accounting for spatial variations	Regression-based β -convergence approach, accounting for spatial autocorrelation	[116]	County-level United States	County-level disparities in diagnosed diabetes prevalence in the United States broadened, while the disparities in diagnosed diabetes incidence narrowed. Demographic, socio-economic characteristics and risk factors of type 2 diabetes were associated with changes in disparities
	Sparse Poisson convolution; sparse Poisson missing-completely-at-random	[117]	County-level; Tract-level United States	The type 1 and type 2 DM incidences in young in United States varied across regions; the type 1 and type 2 DM incidences also differed across small areas within study region. The joint spatial correlation between type 1 DM and type 2 DM was present at the county level, but not at tract level

HBG: High blood glucose; VHBG: Very high blood glucose; SES: Socioeconomic status; DM: Diabetes mellitus; GIS: Geographic Information Systems; BMI: Body mass index; IDDM: Insulin-dependent diabetes mellitus.

attributes implies that changes in these factors can yield to positive reduction in risk and might generate substantial reductions in the burden of DM in high-risk areas.

DISEASE INTERACTIONS

Interactions between diseases are recently being recognized as a key factor that influences the natural history of the diseases[59-61]. Synergistic relationships between diseases coexisting in a population could influence epidemic dynamics, resulting in marked differences in health outcomes compared to the disease occurring isolated in the population[62,63]. Therefore, focusing on the dynamics of an isolated epidemic could prevent the identification of important processes that emerge from the syndemic relationship between diseases present in the affected population[61,63]. Understanding the mechanisms that shape within-population disease clustering could be essential for the design of disease control programs[61,63]. The spatial clustering of diseases and the identification of vulnerable populations to the disease must be recognized to integrate the key social and environmental risk factors that facilitate disease interactions among vulnerable populations. In this context, spatial epidemiology and disease mapping can help to provide effective information underlining the importance of the geographical clustering of several diseases within populations, the social and environmental contexts in which diseases cluster, the ways comorbidity affects the natural history of each other, the pathways of disease interaction, and how important these interactions can be to the health burden within affected populations.

The concept of disease interaction in the epidemiology of DM has been well documented at both population and individual levels. There is substantial evidence regarding the association between DM and other macro-and microvascular diseases such as hypertension, coronary arterial disease, and congestive heart failure. Other studies have also shown a significant association between DM and several cancer conditions such as colorectal cancer, pancreatic cancer, endometrial cancer, and prostate cancer. DM has also been associated with other non-communicable diseases such as acute pancreatitis, biliary disease, psoriasis, urinary tract calculi, and chronic obstructive pulmonary disease.

While the association between DM and other non-communicable disease are well investigated and repeatedly reported in the literature, the association between DM and communicable disease have been less investigated (and only within the last few decades) mainly due to the complex pathogenesis of the association. The comorbidity of DM and tuberculosis (TB) appears to be one of the syndemics between a non-communicable and communicable disease that have reached the interest of the public health practitioners[64-67]. The association between TB and DM has been documented first for over 1000 years ago by Avicenna (980-1027 AD). With the emergence of proper diagnostics and treatments (for both TB and DM) in the second half of the 20th century, the TB-DM association, along with its possible implications, had become neglected in policy and practice[68]. In recent decades, with the increasing DM (specifically T2DM) prevalence globally, particularly in low-income countries, the relationship has re-emerged as a significant public health problem—more so in developing countries where the prevalence of DM is rising, and TB is endemic[65]. DM increases susceptibility to TB by threefold and has an adverse effect on TB treatment outcomes[64,69-71]. The combination of TB and DM represents a global health threat, specifically in any setting where the overlap of populations at risk for both diseases is increasing. Regions like Western Pacific and Africa could be most affected by such interaction (*i.e.*, number of people with TB is high and DM is increasing substantially), while regions like Europe will not be substantially affected by such interaction. The spatial interaction between DM and TB has been explored and some evidence suggests that there is a spatial association between DM and TB. However, the evidence is inconsistent and more regional research is needed in this field[72].

Moreover, hepatitis C virus (HCV) infection and DM have been shown to coexist in an individual — DM modifies the course of HCV[73-75]. Based on the currently limited evidence, studies suggest that DM is associated with increased susceptibility to HCV infection[73,76-78]. This interaction could have an impact in countries such as

Egypt in which HCV prevalence is high and number of people living with DM is and will remain high. Malaria has also been documented to be more common in DM patients, in studies from Africa, but more evidence (and stronger) are needed in this regard as well[79]. Lastly, individuals with dengue fever and DM comorbidity seem to be at higher risk of developing complications and severe dengue compared to the general population[80,81]. However, a better understanding of the relevance of comorbidities in severe dengue are needed for regions with high prevalence of dengue infection (such as tropical and subtropical areas).

Some of the more recent evidence show that DM worsen the outcomes of other viral infections such as the severe acute respiratory syndrome coronavirus or the influenza A infection[82,83]. With the emergence of the novel RNA beta coronavirus, coronavirus disease 2019 (COVID-19) globally, DM has shown to affect the development and progression of COVID-19. Published evidence, though with limitations, has already reported that DM increases the risk of COVID-19 progression and severity of disease outcome[84]. A national-representative study that analyzed 61 million medical in-hospital records in the United Kingdom, reported that one-third of COVID-19 deaths occurred in people with T2DM[85]. Adjusted for previous hospital admissions with coronary heart disease, cerebrovascular disease, or heart failure, the study showed that odds of in-hospital deaths was 2.9 for T1DM and 1.8 for T2DM[85]. Data from the United States also highlighted that DM was reported as an underlying condition for approximately 4 in 10 COVID-19 patient and that about half of people younger than 65 who died from COVID-19 had DM. Hypotheses are still being explored to understand the biological mechanism(s) behind the collision of an old metabolic disease with a new infectious disease.

CONCLUSION

With nearly 400 million people around the world having prediabetes, DM emerges as one of the biggest public health challenges of our current times. However, one of the most significant public health advances in the study of DM is the demonstration that DM can be prevented by the implementation of effective interventions targeting the factors that exacerbate the risk of DM[86-89]. Early identification of vulnerable populations at higher risk of developing DM and the location of the areas where the risk is concentrated will help policymakers to tailor and target preventative interventions to communities with the greatest need. Likewise, more studies elucidating the direct role of spatial cofactors and the prevalence of diabetes are needed. Policymakers are interested in developing community-based interventions to manage DM, hence, it is of the greatest importance that we are able to identify communities at the highest risk so that appropriate intervention programs may be designed and implemented based on the community risk profile[90]. The value of spatial analysis could be fundamental in this task by identifying high burden areas or 'hotspots' of DM risk across high-risk communities. These spatial studies can highlight regions that can benefit from strategic geographically designed interventions aimed to manage and monitor the early emergence of DM epidemics, but also can identify potential areas with high burden of other diseases, where the interaction of these diseases and DM is high.

All countries, but particularly middle-and low-income countries with constrained resources, need to thoroughly maximize the benefits and reduce costs by efficiently allocate the scarce healthcare resources for targeted interventions for DM prevention and treatment. Spatially informed tailored strategies that allocate resources to prevent and treat DM would be an effective approach aimed to control and reduce the burden of the disease. Spatially explicit community-level policy interventions addressing key factors such as healthy food supply, a friendly built environment, tax policy, financial incentives and disincentives, and disease interactions would offer great promise in effectively addressing the obesogenic and diabetogenic environment aimed to control the global DM epidemic.

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Comprehensive overview of human serum albumin glycation in diabetes mellitus

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Abstract

The presence of excess glucose in blood is regarded as a sweet hurt for patients with diabetes. Human serum albumin (HSA) is the most abundant protein in human plasma, which undergoes severe non-enzymatic glycation with glucose in patients with diabetes; this modifies the structure and function of HSA. Furthermore, the advanced glycation end products produced by glycated HSA can cause pathological damage to the human body through various signaling pathways, eventually leading to complications of diabetes. Many potential glycation sites on HSA have different degrees of sensitivity to glucose concentration. This review provides a comprehensive assessment of the *in vivo* glycation sites of HSA; it also discusses the effects of glycation on the structure and function of HSA. Moreover, it addresses the relationship between HSA glycation and diabetes complications. Finally, it focuses on the value of non-enzymatic glycation of HSA in diabetes-related clinical applications.

Key Words: Diabetes mellitus; Human serum albumin; Non-enzymatic glycation; Advanced glycation end products; Glycation sites; Diabetic complications

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Core Tip: In the case of hyperglycemia state, the glycation level of albumin in plasma is significantly increased, which alters the structure and function of albumin. Herein we review the different glycation sites and functional changes of glycated albumin, and discuss the relationship between albumin glycation and diabetes complications. The

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potential application value of glycosylated albumin in clinical is also discussed.

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INTRODUCTION

Diabetes is a metabolic disease caused by an absolute or relative deficiency of insulin in the human body related to various pathogenic etiologies; it leads to metabolic disorders involving sugars, lipids, and proteins, with severe hyperglycemia as the main clinical manifestation[1,2]. Abnormally high glucose concentrations in patients with diabetes can cause proteins in the body to undergo non-enzymatic glycation (*i.e.*, without the involvement of glycosyltransferase), which is the initiating factor of diabetes-related complications[3,4]. Human serum albumin (HSA) is a high-abundance protein in plasma that is mainly responsible for binding and transporting various endogenous or exogenous substances (*e.g.*, fatty acids, cholesterol, and many drugs); thus, it has a profound impact on the pharmacokinetic properties and efficacy of many drugs[5,6]. In patients with diabetes, HSA has a higher probability of glycation than other proteins, so it is regarded as an indicator of glycemic control[7]. Elevated glycation levels can lead to changes in the structure and function of HSA, thus influencing the normal physiological activities of the body[8]. The distinct distributions of multiple glycation sites on the three-dimensional structure of HSA cause different degrees of glycation under a range of glucose concentrations. A non-enzymatic glycation modification at the main drug-binding site substantially affects the ability of this region to bind drugs, thereby influencing the pharmacokinetic properties and efficacies of therapeutic drugs[9]. In this paper, seven aspects of HSA and its non-enzymatic glycation are reviewed.

EXPLANATION OF NON-ENZYMATIC GLYCATION AND ITS REACTION MECHANISM

Non-enzymatic glycation (sometimes described simply as glycation) is an important post-translational modification that does not involve the catalytic activity of glycosyltransferase[10]. The reaction mainly begins with a nucleophilic addition reaction between the carbonyl group of reducing sugar and the amino group of lysine, arginine, or the N-terminus of protein[11]. Fructose and lactose are important reducing sugars in food, while glucose is the main source of energy in the human body[12]. Therefore, glucose is the primary raw material for non-enzymatic glycation in the human body. The non-enzymatic glycation process is mainly divided into three steps: (1) The carbonyl group of a reducing sugar undergoes a condensation reaction with the amino group of the protein to form a thermodynamically unstable Schiff base; (2) The unstable Schiff base is converted into a relatively stable Amadori product[13,14]; and (3) Amadori product undergoes a series of spontaneous reactions (*e.g.*, dehydration, oxidation, rearrangement, and isomerization) that can generate various carbonyl compounds, such as methylglyoxal, glyoxal, 3-deoxyglucosone, and dehydroascorbic acid[15]. These carbonyl compounds usually react more strongly than the original reducing sugars and can quickly react with proteins to form various irreversible heterostructures, which are regarded as advanced glycation end products (AGEs)[16].

GENERAL STRUCTURE AND FUNCTION OF HSA

HSA is a highly abundant protein in plasma; its concentration of approximately 35-50 g/L comprises approximately 60% of the total plasma protein content[17]. It is mainly

responsible for the regulation of plasma osmotic pressure[18] and pH, and binding various endogenous or exogenous substances (*e.g.*, fatty acids, cholesterol, and many drugs)[19]. Additionally, HSA serves as an antioxidant, mediates lipid metabolism, and sequesters toxins[17]. It is composed of 585 amino acids and 17 intramolecular disulfide bonds, with a molecular weight of 66437 kDa[8]. Crystal structure analysis has shown that HSA possesses a spherical "heart-shaped" structure comprising approximately 67% of α -helices, 23% of extended chains, and 10% of β -sheets. HSA contains three homology domains: I (amino acids 1-195), II (amino acids 196-383), and III (amino acids 384-585); each of these domains contains two subdomains (A and B). The A subdomains of both domains II and III constitute the major drug-binding regions of HSA; these are regarded as sites I (amino acids 196-292) and II (amino acids 384-489)[20].

OVERVIEW OF HSA GLYCATION

Due to the high abundance of HSA, its non-enzymatic glycation represents approximately 80% of all glycation involving circulating proteins[21]. Amadori products are the main form of glycated HSA present in the body; their amounts increase as the blood glucose concentration increases in the blood of patients with diabetes[22]. The proportion of glycated HSA in healthy people is approximately 1%-10% and can increase by 2-3-fold in patients with diabetes[8,17]. Basic amino acids on HSA, specifically, 59 lysines and 24 arginines, are regarded as potential sites of glycation.

Glucose-induced modifications strongly influence HSA functional properties and have important implications for protein activity, folding, degradation, and cell function[23,24]. Although initially harmless, these modifications can become destructive and pathogenic when they become sufficiently widespread. **Figure 1** shows the mechanism of the different effects of HSA glycation on the body. First, HSA glycation change the intrinsic conformations and binding efficiencies of its major binding regions, thereby changing the drug efficacy[25]. Second, the interactions of AGEs with their receptors [receptor for AGEs (RAGE)] or other macromolecules will activate various signaling pathways such as nuclear factor κ B, as well as tissue damage and metabolic complications[26]. Third, glycated HSA can also stimulate platelet activation and aggregation, thereby enhancing thrombosis and inhibiting cellular uptake of glucose[27-31]. As the main drug-binding protein in plasma, HSA strongly influences drug absorption, distribution, excretion, and efficacy characteristics[32]. Changes in HSA function caused by the pathological environment can lead to unexpected types of toxicity. Drug molecules either combine with proteins and lipids in plasma or exist in a free (*i.e.*, unbound) state in the aqueous blood environment[33]. Only free drug molecules interact with their intended targets to produce therapeutic effects[33]. In some instances, the excessive modification of HSA by non-enzymatic glycation can increase the free drug concentration, which can produce severe drug toxicity[34,35].

METHODS FOR ASSESSMENT OF GLYCATED HSA

Glycated HSA has been used as a complementary indicator to standard assays involving glycated hemoglobin (HbA1c) or real-time glucose monitoring to assess glycemic control in patients with diabetes[10]. Notably, real-time glucose monitoring only provides a single data point concerning the glycemic status of patients with diabetes, while HbA1c provides an assessment of glycemic control over 2-3 mo and may be influenced by chronic kidney disease in some patients[36,37]. In contrast, glycated HSA provides an assessment of glycemic control over 21 d and can be used as an indicator with intermediate duration (*i.e.*, between real-time glucose monitoring and assessment of HbA1c)[38]. Many methods have been developed to detect and quantify glycated HSA with the aim of predicting or preventing potential complications; these methods mainly involve the determination of total glycated HSA, as well as the qualitative and quantitative assessment of HSA glycation sites.

Methods for assessment of total glycated HSA

Immunoassays such as enzyme-linked immunosorbent assays and radio-immunoassays are often used to detect total glycated HSA[39,40]. In addition, other traditional methods for evaluation of glycated HSA include boronate affinity

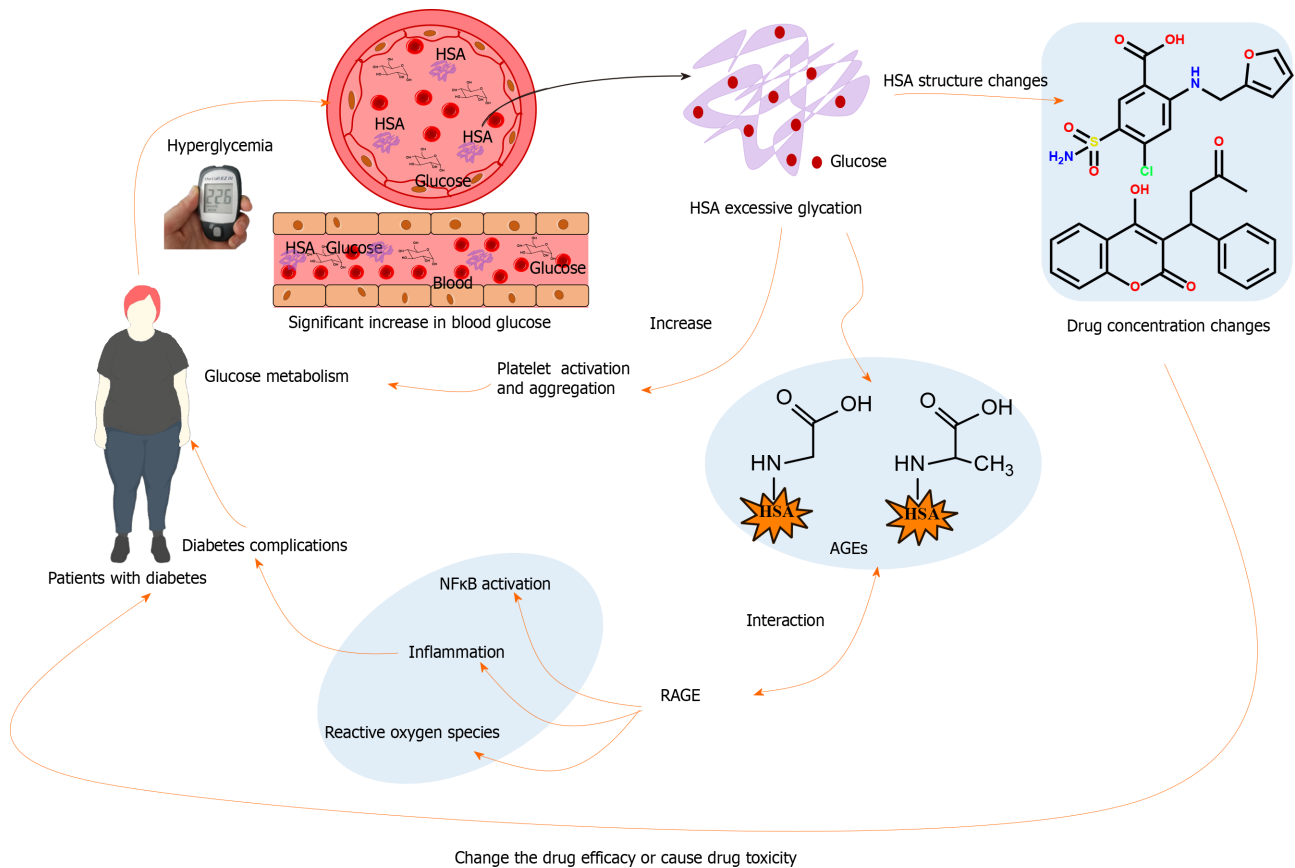


Figure 1 Mechanism of different effects of human serum albumin glycation on the human body. AGEs: Advanced glycation end products; RAGE: Receptor for advanced glycation end products; HSA: Human serum albumin.

technology; thiobarbituric acid analysis; nitro-blue tetrazolium colorimetric analysis; phenylhydrazine formation reaction; fructosamine assays; ketoamine oxidase analysis; high-performance liquid chromatography (HPLC) analysis of furosine hydrolysis by strong acid; phenylborate-containing acrylamide gel electrophoresis; and the analysis of reductive activity following alkaline solution treatment, using redox indicators[41-48]. However, the above traditional analysis methods have their own characteristics or drawbacks. For example, colorimetric analysis methods such as nitro-blue tetrazolium and thiobarbituric acid have high unspecificity[49]; fructosamine assays provide higher specificity and reliability[50]; HPLC method has a high sensitivity[41]; phenylborate-containing acrylamide gel electrophoresis method is time-consuming and not suitable for clinical measurement[51]. In recent years, electrochemical quantitative analysis methods with high sensitivity and specificity have also been developed[52]. Intact protein analyses by high resolution mass spectrometry (MS) can also be used to determine the total glycation degree of HSA[53].

Methods for qualitative and quantitative analysis of glycation sites on HSA

HSA is rich in basic amino acids that can undergo glycation; thus, the analysis of glycation sites on HSA mainly involves the application of high-resolution MS[54]. A "Top-Down" approach combined with tandem MS is considered a standard method to accurately assess glycation sites[55-57]. In the "Top-Down" approach, HSA is first enriched and then digested with trypsin or Lys-C[7,10]. Because of glucose steric hindrance, peptides will have missed cleavage to form peptides containing glucose modifications[58]. Thus, glycation peptides exhibit a mass shift of 162 kDa in primary MS analysis, as well as a neutral loss in tandem MS analysis, and these findings can be used to locate the accurate glycation site[12]. Many types of MS with ionization modes of matrix assisted laser desorption/ionization (MALDI) or electrospray ionization (*e.g.*, IT-TOF, LTQ-Orbitrap, Q-TOF, hybrid linear ion trap-Orbitrap, and MALDI-TOF MS) have been used to identify glycation sites[10,12,55,59,60]. For the quantitative analysis of glycation peptides, many approaches have been developed thus far[12,53,55,61]. Frolov *et al*[55] used the integral peak area to compare amounts of glycation peptides. In another study, isotopic labeling with ^{13}C was performed to label native proteins,

which were then digested with trypsin; the coupled ^{12}C and ^{13}C isotope peaks provided different types of quantitative information concerning the same glycated peptides[12]. Furthermore, ^{18}O - and ^{16}O -labeled H_2O has been used to hydrolyze normal and glycated HSA, respectively. The $^{16}\text{O}/^{18}\text{O}$ ratios in each digested peptide were measured to compare glycation levels[61]. Furthermore, Qiu *et al*[53] have developed an isobaric tags for relative or absolute quantitation (iTRAQ) labeling technology combined with three-stage MS (MS^3) method to compare glycation levels between healthy individuals and patients with diabetes. The iTRAQ- MS^3 method makes good use of the neutral loss of glycated peptides under collision-induced dissociation in MS/MS, and high-energy collisional dissociation in MS^3 fragmentation of the neutral loss ions were performed to precise quantification of the glycated peptides[53]. Table 1 shows the glycation sites that have been identified through qualitative and quantitative analyses. Notably, specific basic residues in HSA are involved in glycation *in vivo*[62]. Sites K525, K199, and K351 were reportedly the predominant glycation sites on HSA[62,63]. Figure 2 shows the number of reports for each potential glycation sites. Sites K12, K64, K137, K199, K233, K262, K274, K317, K378, K414, K525, K545, and K574 have been more easily identified than other sites (reported ≥ 8 times), which suggests that they are more sensitive to changes in serum glucose concentrations[7]. The underlying mechanism may be that these sites are both distributed on the HSA surface and spatially located near basic amino acids[53]. Although K199 is not completely distributed on the HSA surface, its low pKa value and spatial proximity to basic amino acids make it suitable for glycation reactions[62]. In Figure 2, we can find that some sites (*e.g.*, K20, K41, R145, R197, R209, K212, R222, R337, and K524) had never been identified in analyses of glycation modifications, indicating that they are insensitive to changes in glucose concentrations, and further explorations of the underlying mechanism are needed to determine their roles[64-71].

EFFECTS OF GLYCATION ON THE STRUCTURE AND FUNCTION OF HSA

Many functions of HSA can be attributed to its structural characteristics. The relative structural stability of HSA is mainly dependent on 17 intramolecular disulfide bonds [50]. This structural flexibility enables HSA to bind to many molecules with distinct structures[72]. The affinities of various metabolites and drugs depend on the multistage structures of binding sites, which are distributed throughout the whole HSA molecule. The major drug-binding sites of HSA are known as sites I and II[20,35,73]. Glycation contributes to various changes in HSA structure and function[74]. First, it enhances the molecular weight of HSA by attaching one or several glucose units to the basic amino acid residues of the protein. Second, glycation will change the original conformation of HSA. The intrinsic fluorescence of HSA is mainly derived from tryptophan-214 located in site I; its fluorescence is extremely sensitive to changes in the HSA environment[24,35,73]. Glycated sites located in or near Site I, such as K199, will alter the HSA structural microenvironment, thereby altering the intrinsic fluorescent characteristics of the protein. The relative fluorescence intensity of glycated HSA is reportedly reduced by 51% compared with normal HSA[75]. In addition to fluorescence chromatography, circular dichroism has also been used to study the effects of glycation on the structure of HSA[76]. Nakajou *et al*[75] used circular dichroism to compare different HSA molecules, which revealed that the secondary structure of HSA was altered after glycation with 50 mmol/L glucose. Third, the glycation of HSA will act as an oxidant and a pro-inflammatory mediator through different mechanisms[77].

Glycation-related changes in the structure of HSA can have varying effects on its abilities to bind a range of ligands. The main mechanisms that affect binding may involve steric hindrance of covalently bound glucose, the blockage of charged residues, or a combination of these two mechanisms[75]. Techniques used to study the binding affinity of glycated HSA include fluorescence spectroscopy, circular dichroism, HPLC with ultraviolet detection, and nuclear magnetic resonance[78-80]. Changes in the binding affinities of glycated HSA to various ligands are influenced by drug concentration and the degree of protein glycation[35,53,75] (see Table 2 [81-85]). Warfarin, tryptophan, and dansylsarcosine have often been used as probe compounds for HSA sites I and II in binding studies[75,76]. *In vitro* analysis has shown that HSA glycation with a range of glucose concentrations (2.5 mmol/L, 12.5 mmol/L, and 50 mmol/L) enhanced the binding of warfarin, but weakened the binding of dansylsarcosine[75]. Another study showed that both *ex vivo* (purified from the plasma of patients with diabetes) and *in vitro* glycated HSA exhibited weakened binding

Table 1 Review of the *in vivo* glycation sites of human serum albumin

Ref.	Glycation sites reported so far	Analysis tools
Iberg <i>et al</i> [63]	HSA from a diabetic patient: Lys-12, Lys-199, Lys-233, Lys-281, Lys-317, Lys-351, Lys-439, Lys-525, Lys-534	Amino acid analysis after hydrolysis in HCl
Garlick <i>et al</i> [64]	Freshly purified human serum albumin: Lys-525	Cation exchange chromatography
Frolov <i>et al</i> [55]	HSA from five T2DM patients: Lys-12, Lys-51, Lys-64, Lys-162, Lys-174, Lys-181, Lys-233, Lys-262, Lys-276, Lys-351, Lys-359, Lys-378, Lys-414, Lys-475, Lys-525, Lys-545	Q-TOF-MS
Kisugi <i>et al</i> [56]	HSA from a female diabetic patients: Lys-64/Lys-73, Lys-199, Lys-136/ Lys-137, Lys-233, Lys-274/Lys-276, Lys-317, Lys-389, Lys-439, Lys-534, Lys-525	QSTAR Pulsar-i mass spectrometer
Frolov <i>et al</i> [57]	HSA from 5 T2DM patients and 4 healthy subjects: Lys-12, Lys-51 ¹ , Lys-64 ¹ , Lys-73, Lys-93, Lys-137, Lys-162, Lys-174 ¹ , Lys-181 ¹ , Lys-205, Lys-233 ¹ , Lys-262 ¹ , Lys-274, Lys-351, Lys-359 ¹ , Lys-378 ¹ , Lys-414, Lys-475, Lys-525, Lys-545 ¹ , Lys-557 ¹ (detected only in diabetic samples), Lys-574	Nano-ESI-LTQ Orbitrap XL MS with ETD
Bai <i>et al</i> [10]	HSA from a healthy subject and a diabetic patient: Lys-64, Lys-93, Lys-190, Lys-199, Lys-205, Lys-225, Lys-233, Lys-240, Lys-262, Lys-274, Lys-281, Lys-317, Lys-323, Lys-351, Lys-372, Lys-378, Lys-413, Lys-432, Lys-475, Lys-525, Lys-545, Lys-557, Lys-557/ Lys-560/ Lys-564, Lys-564, Lys-573/ Lys-574	IT-TOF-MS/MS
Zhang <i>et al</i> [7]	HSA from clinical T2DM, IGT, NGT and 389 volunteers: Lys-12/ Lys-20 ¹ , Arg-144, Arg-186/ Lys-190 ¹ , Arg-222/ Lys-225, Lys-240, Arg-336, Lys-372, Lys-414/ Arg-428 ¹ . (8 glucose sensitive sites)	Agilent MSD trap
Anguizola <i>et al</i> [59]	HSA from individual clinical plasma samples: Arg-10, Lys-12, Arg-10/Lys-12 ¹ , Arg-98 ¹ , Arg-160, Lys-162, Lys-190, Lys-199, Lys-276, Lys-281, Lys-276/Lys-281 ¹ , Lys-286 ¹ , Lys-313, Lys-317, Lys-372, Lys-428, Lys-432, Arg-484, Arg-485, Arg-484/ Arg-485 ¹ , Lys-545, Lys-557, Lys-560, Lys-564 ¹ , Lys-573/ Lys-574 ¹	MALDI-TOF-MS
Priego-Capote <i>et al</i> [12]	HSA from human Plasma: Lys-64, Lys-73, Lys-93, Lys-106, Lys-136, Lys-137, Lys-159, Lys-174, Lys-181, Lys-195, Arg-218, Lys-233, Lys-240, Lys-262, Lys-274, Lys-323, Lys-359, Lys-372, Lys-378, Lys-389, Lys-402, Lys-413, Lys-432, Lys-436, Lys-439, Lys-444, Lys-466, Arg-472, Lys-475, Lys-500, Lys-519, Lys-525, Lys-573	Hybrid linear ion trap-Orbitrap MS
Korwar <i>et al</i> [65]	HSA from clinical plasma samples: Lys-12, Lys-64 ¹ , Lys-136, Lys-137, Lys-159 ¹ , Lys-402 ¹ , Lys-414 ¹ , Lys-466 ¹ , Lys-525 ¹	Hybrid quadruple Q-Exactive Orbitrap MS
Zhang <i>et al</i> [60]	HSA from 12 NGT, 11 IGT and 8 T2DM: Lys-4 ¹ , Lys-12, Lys-51, Lys-64 ¹ , Lys-73, Lys-136, Lys-137, Lys-159, Lys-162, Lys-181 ¹ , Lys-190 ¹ , Lys-195, Lys-199 ¹ , Lys-205, Lys-225, Lys-233 ¹ , Lys-262, Lys-274, Lys-276, Lys-317 ¹ , Lys-351, Lys-378, Lys-414, Lys-432 ¹ , Lys-436 ¹ , Lys-475, Lys-525, Lys-538, Lys-545, Lys-562 ¹ , Lys-573, Lys-574	Ion Trap LC-MS
Miyamoto <i>et al</i> [66]	HSA from 8 diabetic patients: Lys-51, Lys-64/ Lys-73, Lys-136/ Lys-137, Lys-159/ Lys-162, Lys-190/ Lys-195/ Lys-199/ Lys-205, Lys-233, Lys-262, Lys-274/ Lys-276, Lys-313/ Lys-317, Lys-351, Lys-378/ Lys-389, Lys-432/ Lys-436/ Lys-439, Lys-525, Lys-534/ Lys-536/ Lys-538/ Lys-541, Lys-545, Lys-573/ Lys-574	QSTAR Pulsar-i MS
Brede <i>et al</i> [67]	HSA from plasma: Lys-12, Lys-137, Lys-414, Lys-525 ¹	Q-TOF MS
Spiller <i>et al</i> [68]	HSA from 48 T2DM patients and 48 non-diabetic: Lys-64, Lys-73, Lys-93, Lys-174, Lys-181, Lys-233, Lys-262, Lys-359, Lys-378, Lys-414, Lys-525, Lys-545, Lys-574	QTRAP 4000
Spiller <i>et al</i> [69]	HSA from 5 T2DM patients and 5 non-diabetic individuals: Lys-64 ¹ , Lys-73 ¹ , Lys-181 ¹ , Lys-262 ¹ , Lys-378 ¹ , Lys-574 ¹	ESI-QqLIT-MS (4000
Takátsy <i>et al</i> [70]	HSA from diabetic patients and healthy individuals: Arg-81, Lys-93, Arg-98, Lys-106, Arg-114, Lys-190, Lys-199, Arg-218, Arg-257, Lys-276, Lys-317, Arg-348, Lys-372, Lys-378, Lys-389, Lys-413, Lys-436, Lys-439, Lys-444, Lys-466, Arg-484, Arg-485, Lys-500, Lys-519, Arg-521, Lys-564, Lys-536, Lys-538, Arg-445, Lys-541, Lys-560, Lys-573	MALDI TOF MS
Greifenhagen <i>et al</i> [71]	HSA from 5 diabetic patients: Lys-12, Lys-64, Lys-137, Lys-190, Lys-199, Lys-274, Lys-276, Lys-525	ESI-Orbitrap-MS
Qiu <i>et al</i> [53]	HSA from 4 diabetic patients and 4 healthy subjects: Lys-4, Lys-12, Lys-51 ¹ , Lys-64 ¹ , Lys-73, Arg-81, Lys-93 ¹ , Arg-98, Arg-117, Lys-136, Lys-137, Lys-162 ¹ , Lys-174, Lys-181, Arg-186, Lys-199 ¹ , Lys-205, Lys-233 ¹ , Lys-240, Arg-257, Lys-262 ¹ , Lys-274, Lys-276, Lys-281, Lys-286, Lys-313 ¹ , Lys-317, Lys-323 ¹ , Lys-351, Lys-359, Lys-372, Lys-378 ¹ , Lys-389, Lys-402 ¹ , Lys-410, Lys-414 ¹ , Lys-436, Lys-439, Lys-466 ¹ , Lys-475 ¹ , Lys-519, Lys-525 ¹ , Lys-538, Lys-541, Lys-545 ¹ , Lys-557 ¹ , Lys-564 ¹ , Lys-573, Lys-574 ¹	LTQ Orbitrap Velos Pro MS

¹Represents glycation sites detected at higher quantities in diabetic patients than in healthy individuals. HSA: Human serum albumin; ESI: Electrospray ionization; NGT: Normal glucose tolerance; T2DM: Type 2 diabetes mellitus; MS: Mass spectrometry.

interactions with warfarin[35]. Joseph *et al*[76] proved that the binding of L-tryptophan was enhanced by 4.7-5.8 fold under glycation conditions similar to those in patients with diabetes, although the binding of warfarin remained unchanged. Notably, the above contradictory results concerning warfarin were obtained under relatively nonphysiological conditions *in vitro*. Qiu *et al*[53] found that the affinity of warfarin for HSA was greater in plasma from patients with diabetes. The level of free warfarin was also reduced in subsequent pharmacokinetic experiments[53]. Furthermore, a retrospective clinical study revealed that the anticoagulant effect of warfarin was

Table 2 Effects of glycation on the binding of human serum albumin to various ligands

Ref.	Ligands	<i>In vivo/ vitro/ex vivo</i>	Glycation level of HSA	Binding affinity
Nakajou <i>et al</i> [75]	Warfarin	<i>In vitro</i>	HSA glycated with 2.5 mmol/L, 12.5 mmol/L, and 50 mmol/L glucose	↑
Baraka-Vidot <i>et al</i> [35]	Warfarin	<i>In vitro</i> and <i>Ex vivo</i>	HSA purified from blood and HSA glycated with 25 mmol/L or 100 mmol/L glucose	↓
Joseph <i>et al</i> [76]	Warfarin	<i>In vitro</i>	HSA glycated with 0.5 mol/L glucose	→
Qiu <i>et al</i> [53]	Warfarin	<i>In vivo</i>	HSA from diabetic patients	↑
Joseph <i>et al</i> [76]	Tryptophan	<i>In vitro</i>	HSA glycated with 0.5 mol/L glucose	↑4.7-5.8-fold
Nakajou <i>et al</i> [75]	Dansylsarcosine	<i>In vitro</i>	HSA glycated with 2.5 mmol/L, 12.5 mmol/L, and 50 mmol/L glucose	↓
Qiu <i>et al</i> [53]	Heparin	<i>In vitro</i> and <i>in vivo</i>	HSA from diabetic patients	→
Guerin-Dubourg <i>et al</i> [81]	Copper	<i>In vivo</i>	HSA purified from diabetic patients and control individuals	↓16%
Koizumi <i>et al</i> [82]	Furosemide	<i>In vitro</i>	Prepared from HSA, and commercial HSA	↓
Okabe <i>et al</i> [83]	Phenylbutazone	<i>In vitro</i>	Each mole of HSA contains 1.94 moles of glucose	↓
Yamazaki <i>et al</i> [84]	Fatty acids	<i>In vitro</i>	HSA glycated with 100 mmol/L glucose	↓
Karp <i>et al</i> [85]	Diazepam	<i>In vitro</i>	HSA glycated with 140 mmol/L glucose	→
Karp <i>et al</i> [85]	Bilirubin	<i>In vitro</i>	HSA glycated with 140 mmol/L glucose	↓30%
Okabe <i>et al</i> [83]	Ibuprofen	<i>In vitro</i>	Each mole of HSA contains 1.94 moles of glucose	↓20
Okabe <i>et al</i> [83]	Dansylproline	<i>In vitro</i>	Each mole of HSA contains 1.94 moles of glucose	↓25%
Okabe <i>et al</i> [83]	Flufenamic acid	<i>In vitro</i>	Each mole of HSA contains 1.94 moles of glucose	↓
Koizumi <i>et al</i> [82]	Naproxen	<i>In vitro</i>	Prepared from HSA, and commercial HSA	→

“→”: No change; “↑”: Increase; “↓”: Decrease; HSA: Human serum albumin.

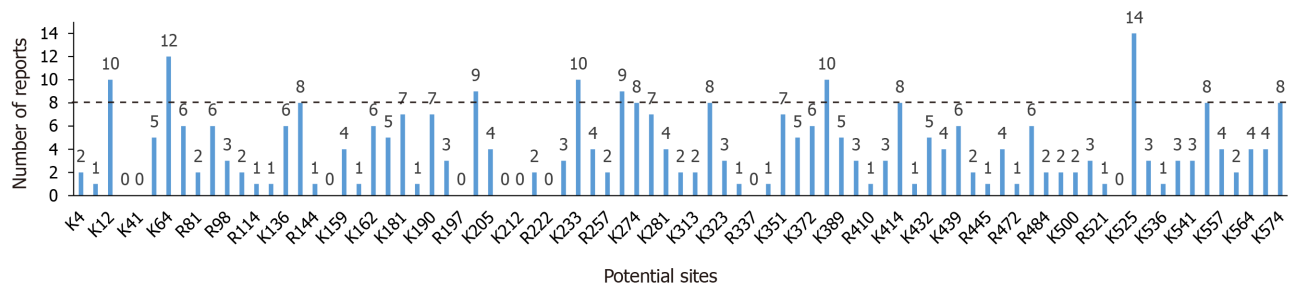


Figure 2 Number of reports for each potential glycation site. Dotted line represents that the number of reports reaches 8 times.

reduced in patients with diabetes[53]. These *in vivo* findings may provide better reference data with respect to warfarin binding.

HSA GLYCATION AND COMPLICATIONS

Chronic hyperglycemia is the primary condition associated with complications of diabetes. Hyperglycemia leads to excessive irreversible accumulation of AGEs on long-lived proteins, such as HSA and HbA1c. The degrees and durations of protein exposure to abnormally high levels of glucose are closely related to the degrees and rates of progression of nephropathy, stroke, neuropathy, retinopathy, and cardiovascular disease[86]. There remain questions concerning how the accumulation of AGEs promotes the development of these lesions. There are three main consequences of the formation of AGEs: (1) Cross-linking of various extracellular proteins[87]; (2) Changes in cell-matrix interactions[88,89]; and (3) Changes in DNA

structure and function[90]. HSA is the main protein in blood circulation; patients with diabetes exhibit significantly greater levels of the HSA-related AGEs[91]. Interactions between AGEs and RAGEs alter cellular signals and gene expression, thereby enhancing the secretion of pro-inflammatory molecules and leading to oxidative stress reactions in patients with diabetes[92].

HSA GLYCATION AND CLINICAL APPLICATIONS

Glycation is a continuous process in the human body. Elevated levels of glycated proteins are associated with elevated levels of blood glucose in patients with diabetes. Thus, there is considerable interest in measuring the glycation levels in patients with diabetes; these data can be used for diagnosis, treatment, and prognosis[93,94]. For many years, HbA1c has been used for the clinical monitoring of long-term blood glucose control[95]. However, HbA1c monitoring has some limitations. Because the lifespan of HbA1c is approximately 3 mo, rapid changes in serum glucose status (*e.g.*, treatment response) are not clearly reflected in HbA1c measurements[96,97]. In some individuals, an abnormally elevated HbA1c value may be recorded, such as patients with hemoglobin variants[96,98], patients with rapid changes in glucose control, patients with iron-deficiency anemia, patients with HIV, or pregnant patients[99-102]. In patients with reduced erythrocyte lifespan, such as those with liver cirrhosis[103], hemolytic anemia[104], chronic kidney disease, and/or hemorrhage, the recorded values of HbA1c will decrease[105,106]. HSA glycation has been suggested as an alternative clinical indicator to circumvent many limitations of HbA1c assessment. The level of HSA glycation is not affected by hemoglobin genetic variations or changes in erythrocyte lifespan[107]. Compared with HbA1c, glycated HSA has a much shorter half-life and is therefore more sensitive to changes in glycemic status. The levels of glycated HSA reflect the average plasma glucose level over a 2-wk interval[94,108]. Therefore, glycated HSA is a more dynamic indicator of glycemic control, which can be used to evaluate the drug treatment efficacy and short-term changes in glucose control. In patients with pre-diabetes, the total degree of HSA glycation does not provide all possible information regarding short-term fluctuations in plasma glucose concentrations because of the high number of possible glycation sites. Therefore, the comparison of the glycation degree of specific HSA sites sensitive to glucose (*e.g.*, K525 and K199) can be used as clinical biomarkers for the occurrence and early diagnosis of diabetes[53,65]. However, it is noteworthy that glycated HSA levels are also influenced by hypoalbuminemic conditions such as malnutrition, nephrotic syndrome, liver cirrhosis, or other liver and renal disease[109]. Further verification is needed to determine whether and how glycated albumin can be used as an indicator of hyperglycemia under these conditions.

CONCLUSION

Hyperglycemia leads to enhanced HSA glycation in patients with diabetes; this highly non-enzymatic glycation at multiple sites can impact the function of HSA as a drug carrier. In this review, we have presented a detailed summary of non-enzymatic glycation sites identified thus far *in vivo*; we have also discussed the impacts of non-enzymatic glycation on the three-dimensional structure and biological functions of HSA. It would be useful to determine how modifications in HSA glycation affect drug treatments for a range of diseases. Glycated HSA may serve as a new clinical indicator for assessment of glycemic control, potentially as an alternative for the long-term indicator HbA1c. Additional *in vivo* studies are needed to determine the effects of glycated HSA on combinations and efficacies of various drugs, thereby providing reference data to aid in the guidance of clinical treatment for patients with diabetes.

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Multi-omics: Opportunities for research on mechanism of type 2 diabetes mellitus

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Abstract

Type 2 diabetes mellitus (T2DM) is a burdensome global disease. In-depth understanding of its mechanism will help to optimize diagnosis and treatment, which reduces the burden. Multi-omics research has unparalleled advantages in contributing to the overall understanding of the mechanism of this chronic metabolic disease. In the past two decades, the study of multi-omics on T2DM-related intestinal flora perturbation and plasma dyslipidemia has shown tremendous potential and is expected to achieve major breakthroughs. The regulation of intestinal flora in diabetic patients has been confirmed by multiple studies. The use of metagenomics, 16S RNA sequencing, and metabolomics has comprehensively identified the overall changes in the intestinal flora and the metabolic disturbances that could directly or indirectly participate in the intestinal flora-host interactions. Lipidomics combined with other “omics” has characterized lipid metabolism disorders in T2DM. The combined application and cross-validation of multi-omics can screen for dysregulation in T2DM, which will provide immense opportunities to understand the mechanisms behind T2DM.

Key Words: Type 2 diabetes mellitus; Gastrointestinal microbiome; Intestinal flora; Lipid metabolism disorders; Dyslipidemias; Metabolomics

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Core Tip: The prospects of multi-omics in the study of the mechanisms of type 2 diabetes mellitus (T2DM)-related intestinal flora perturbation and plasma dyslipidemia are tremendous. The use of multi-omics has identified variations in T2DM intestinal

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flora composition and human-microbiota interactions. However, further sequencing is required, and the clinical application needs to be clarified and simplified. Multi-omics is also identifying T2DM lipid profiles, which will provide immense opportunities to understand the mechanisms of T2DM-related dyslipidemia.

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INTRODUCTION

According to the World Health Organization, about 422 million people worldwide have diabetes and 1.6 million deaths are directly attributed to diabetes each year. Diabetes is a chronic, metabolic disease characterized by elevated blood glucose (or blood sugar) levels, which increases morbidity and mortality. When the body does not produce enough insulin or does not use it efficiently, diabetes manifests. The number of patients with diabetes is increasing, which expands the magnitude of the disease burden[1]. The most common type of diabetes is type 2 diabetes mellitus (T2DM)[2]. When genetics, age, and family history are fixed, reducing exposure to other known risk factors for T2DM using a variety of interventions and improving access to and quality of care decrease the incidence of T2DM and benefit patients with T2DM[3]. The effectiveness of these interventions depends largely on the understanding of the mechanism of T2DM. Due to the complexity of the mechanisms and causes of T2DM, traditional bench science has limitations. Multi-omics, including genomics, transcriptomics, proteomics, glycomics, metabolomics, epigenomics, ncRNomics, lipidomics, and interactomics, offers a fresh and exciting conceptual lens that will aid scientists to comprehensively and systematically understand the physiological processes and regulatory mechanisms of T2DM[4].

ADVANTAGES OF MULTI-OMICS ON STUDY OF MECHANISM OF T2DM

Since the concept of genomes and genomics was introduced, "omics" research has profoundly affected systems biology discoveries. Multi-omics research enables researchers to identify the differences in genes, proteins, and metabolites that lead to understanding overall functional disturbances in diseases, including T2DM.

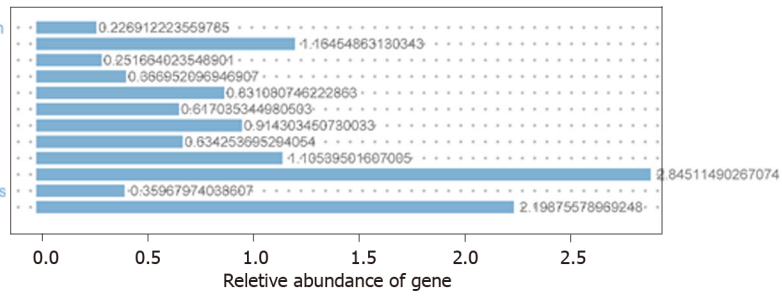
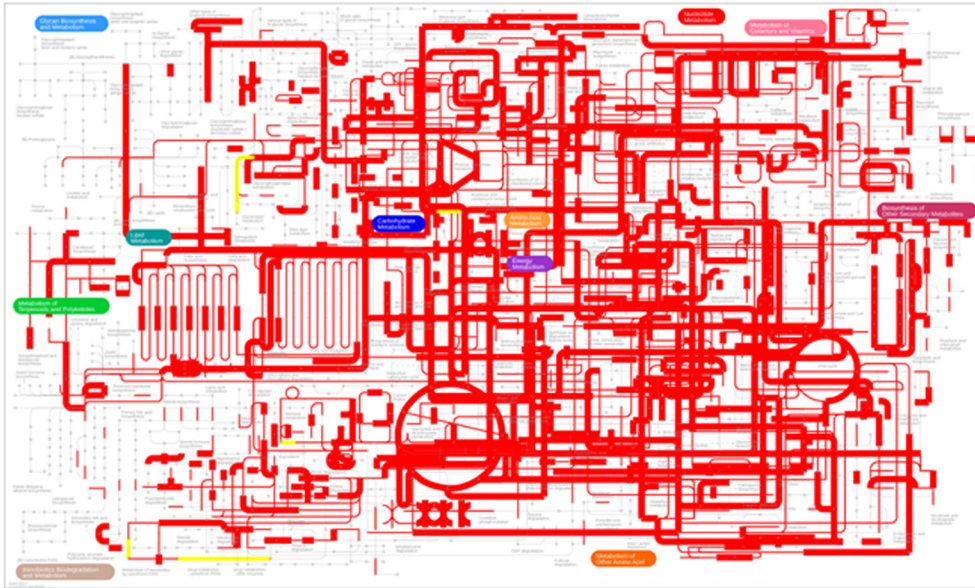
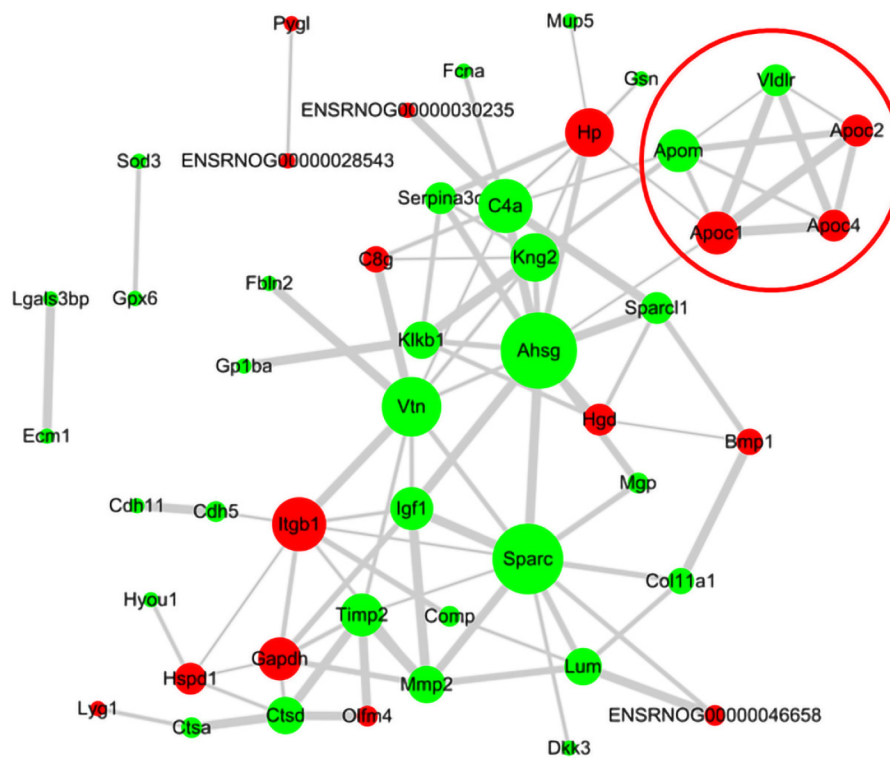
Using multi-omics, our previous research[5,6] described the intestinal flora alterations and the plasma protein metabolic profile perturbations in the Zucker diabetic fatty rat, which is a spontaneous T2DM animal model commonly used to develop drugs for treating diabetes[7-10]. The altered intestinal microbiota and differentially expressed proteins and metabolites clearly distinguished the treatment group [T: Zucker leptin receptor gene-deficient rats (fa/fa) treated by Purina #5008] from the control group [C: basic diet-fed litter mate wild-type controls (fa/+)]. This provided an important reference for screening and verifying T2DM by utilizing intestinal flora and plasma biomarkers. Using "omics" techniques, the increased levels of glycated hemoglobin, ceruloplasmin, triacylglycerols, diacylglycerols, phosphatidylethanolamines, *etc.* in plasma/urine have been verified in the human population. They are gradually being introduced in the early diagnosis of diabetes and the prediction of serious adverse complications[11-13].

Further functional analysis of the differential molecules using multi-omics revealed the pathophysiological mechanism of T2DM (Figure 1). The intestinal flora and the host exhibit similar features that focus on oxidative stress, insulin resistance, and metabolic disorders. This data confirmed previous T2DM mechanism research[14-16] and provided insight into the overall levels of molecules.



E**Metabolism**

Xenobiotics biodegradation and metabolism
 Nucleotide metabolism
 Metabolism of terpenoids and polyketides
 Metabolism of other amino acids
 Metabolism of cofactors and vitamins
 Lipid metabolism
 Glycan biosynthesis and metabolism
 Enzyme families
 Energy metabolism
 Carbohydrate metabolism
 Biosynthesis of other secondary metabolites
 Amino acid metabolism

KEGG pathway annotation**F****G**

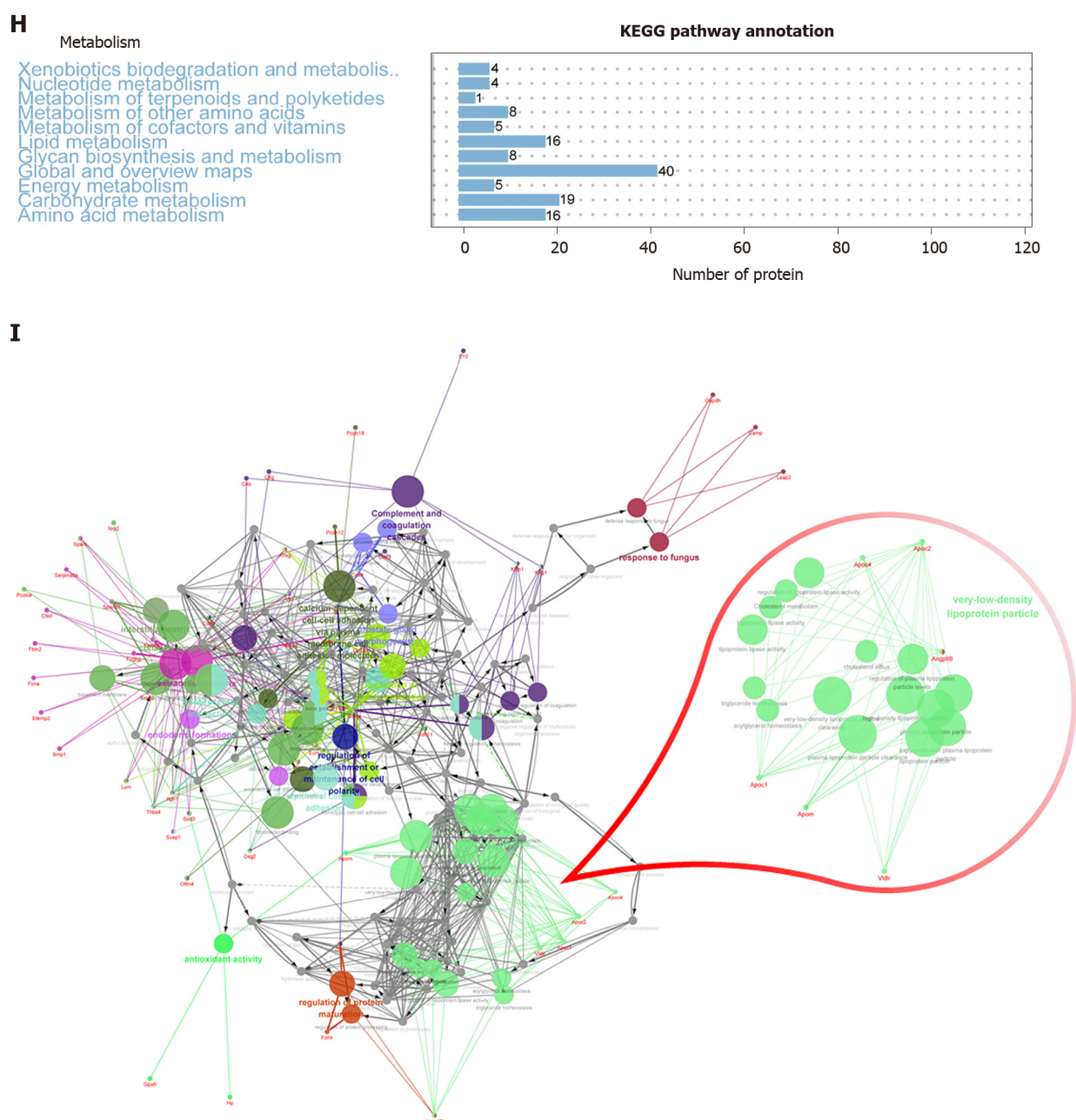


Figure 1 Multi-omics verification of the mechanism of type 2 diabetes mellitus. A: Schematic diagram of multi-omics verification; B: Conceptual diagram of the Zucker diabetic fatty rat modeling process; C: Body weight (left) and blood sugar (right) before and after basic diet feeding in B; D: Fecal 16S rRNA sequencing biomarkers; E: Genomic functions of the disturbed intestinal flora; F: Overview of the complete metabolism in the two biological system; G: Protein-protein interaction network of plasma differentially expressed proteins (DEPs); H: Functional enrichment of DEPs; I: Visualization of G and H. The cross-validation of intestinal flora and the plasma proteome further emphasizes that oxidative stress, insulin resistance, energy intake and consumption imbalances, and lipid metabolism disorders play an important part in the occurrence of type 2 diabetes mellitus (T2DM). Dyslipidemia may be a major hub for the *in vivo* and *in vitro* changes in T2DM (unpublished data). The data used in the figure are our published and public data in open access journals, which are displayed after further analysis. C and G: Citation: Wang S, Lu Z, Wang Y, Zhang T, He X. Metalloproteins and apolipoprotein C: candidate plasma biomarkers of T2DM screened by comparative proteomics and lipidomics in ZDF rats. *Nutr Metab (Lond)* 2020; 17: 66. Copyright ©The Author(s) 2020. Published by Springer Nature[6]. T: Zucker leptin receptor gene-deficient rats (fa/fa) treated by Purina #5008 for 3 wk; C: Basic diet-fed litter mate wild-type controls (fa/+); DEPs: Differentially expressed proteins; T2DM: Type 2 diabetes mellitus.

MULTI-OMICS AND T2DM-RELATED INTESTINAL FLORA DISTURBANCE

Multi-omics aided the dramatic discovery that diabetes was associated with the intestinal flora. The altered microbiota observed in genetically obese mice[17] or people[18–20] is sufficient to promote increased adiposity in lean mice that receive a microbiota transplant. Germ-free mice, which lack a microbiota, have reduced adiposity and improved tolerance to glucose and insulin when compared to their counterparts[21]. They are also free from diet-induced obesity when fed a Western-

style diet[22-24]. Taken together, the correlation between intestinal flora, obesity, and diabetes demonstrates that the microbiota contributes to the regulation of adiposity and T2DM[25]. However, the precise mechanism is still not clear.

Increased metagenomics data (usually 16S RNA sequencing) suggest that the extent of biodiversity within an ecosystem can be an important mechanism and serve as a measure of stability and robustness. In other words, a reduction in gut microbiome diversity and richness is linked to susceptibility to T2DM[26,27]. The complex composition of the intestinal flora can quickly change in response to a diverse diet, while simpler flora composition can only interact with specific diets and increase the vulnerability of the intestinal tract[28]. In T2DM rats and patients, the proportion of *Firmicutes* decreased and that of *Bacteroidetes* increased[29]. This ratio can be used as a simple indicator of intestinal flora diversity in T2DM. Although metagenomics has an irreplaceable advantage in T2DM-related intestinal flora studies, sequencing depth and defects in methods still need to be paid more attention. 16S RNA sequencing enables taxonomic identification to at least the family level but is rarely able to make a distinction between different strains of the same species or related species[30]. *Salmonella*, *Escherichia coli*, and *Shigella* would be identified by the same sequence, yet their significance in T2DM may vary.

Although the intestinal flora ratios may be important, the metabolic function of the intestinal flora on nutrients and food likely plays a more significant role[31,32]. Metabolites of the intestinal flora are involved in numerous functions. They can affect the absorption of nutrients (bile acid metabolism is closely related to lipid absorption [33,34]), and they can be absorbed to provide nutrients for the host (carbohydrates are fermented to form short-chain fatty acids to provide energy for the host[35-37]). Metabolites can be signaling molecules to regulate inflammation and immunity inter- or intra-intestinally. Bacterial L-tryptophan metabolites enhance the secretion of glucagon-like peptide-1[38-40]. Endotoxins (lipopolysaccharides) induce inflammation [41] and limit the autoimmune response[42,43]. Many metabolites produced due to the interaction of numerous species, the allocation of resources, and the dynamic response to perturbation within the gut may serve as potential T2DM biomarkers[44]. Table 1 briefly summarizes related gut microbiota metabolites and their interactions with the host in diabetes. The complementation of intestinal metabolomics and metagenomics will enhance the research on T2DM-related intestinal flora disturbance[45].

Discovering the interactions of the intestinal microbiota under complex conditions, such as diet[46], drugs[47], genetic background of the host[48] and colonizing flora [49], modification of the intestinal flora through antibiotics[50-54], probiotics, prebiotics[55-57], and fecal microbiota transplantation, and causal relationships in people and precision treatment[58] will become more accessible using multi-omics. The potential of understanding the mechanisms of diabetes using multi-omics is tremendous. However, the systematic examination of T2DM-related colonic flora studies in therapeutic and clinical application must still be completed.

An interesting example of fully understanding the mechanism of intestinal bacteria is *Akkermansia muciniphila* (*A. muciniphila*). *A. muciniphila* is a mucosal-dwelling anaerobe and the only known member of its genus. Animal and human data have indicated an inverse correlation between the intestinal abundance of *A. muciniphila* and obesity, dyslipidemia, and T2DM[59-61]. *A. muciniphila* supplementation restores epithelial mucosal integrity, reduces weight gain and fat accumulation, improves glucose tolerance, and reduces inflammation and metabolic endotoxemia in animal models. It may be a potential treatment for T2DM. However, *A. muciniphila* levels are increased in patients with Parkinson's disease, multiple sclerosis, or Alzheimer's disease[62-64], suggesting that this bacterium may have unforeseen harmful effects on the nervous system. Pure culture, sterilization, and component extraction can reduce this risk[65], which is consistent with the recently proposed concept of culturomics [66]. In short, through multi-omics it is likely that major breakthroughs in the study of the mechanism of T2DM-related intestinal flora perturbation will be made and that these breakthroughs will be gradually applied in the clinic.

MULTI-OMICS AND T2DM-RELATED DYSLIPIDEMIA

While intestinal flora disorder is a diet-related *in vitro* regulatory mechanism of T2DM, glucose and lipid metabolism disorders and insulin resistance are *in vivo* mechanisms [67]. In addition to glycomics[68,69], we want to emphasize the role of lipidomics in T2DM-related dyslipidemia. Dyslipidemia in T2DM, characterized by a high concentration of triglycerides, low concentration of high-density lipoprotein cholesterol, and

Table 1 Intestinal flora-related metabolites and their host interaction mechanism

Metabolites	Potential interaction mechanism between intestinal flora-related metabolites and the host
Bile acids	Promotes fat absorption; serves as signaling molecule [acts with G-protein-coupled bile acid receptor 1 (Gpbar1, TGR5) and the bile acid receptor FXR]; limits the autoimmune response
SCFA	
Acetate and butyrate	Acts as histone deacetylase inhibitors; ameliorates inflammation
Propionate	Participates in carbohydrate esterification
Valeric	Provides calories; affects inflammation; enteroendocrine regulation through G-protein-coupled receptors (<i>e.g.</i> , GPR41, GPR43)
Indole	Promotes the function of the intestinal cell epithelial barrier; enhances the secretion of glucagon-like peptide-1 (GLP-1)
Endotoxins (LPS)	Induces inflammation; limits the autoimmune response
H ₂ S	Destroys the intestinal barrier function
TMA	Interferes with metabolism

Gpbar1 (TGR5): G-protein-coupled bile acid receptor 1; FXR: Farnesoid X receptor; SCFA: Short-chain fatty acid; GPR: G-protein-coupled receptors; GLP-1: Glucagon-like peptide-1; LPS: Lipopolysaccharide; H₂S: Hydrogen sulfide; TMA: Trimethylamine.

increased concentration of small, dense low-density lipoprotein cholesterol particles, is associated with insulin resistance. It is also one of the major risk factors for cardiovascular disease in patients with diabetes[70]. Although active control of triglycerides and low-density lipoprotein cholesterol can delay the progression of T2DM and reduce the risk of adverse cardiovascular outcomes in patients, interventions to increase high-density lipoprotein cholesterol have had little success. Niacin was thought to raise high-density lipoprotein cholesterol and was used to control diabetic dyslipidemia previously. However, it was proven to be ineffective and removed from the treatment guidelines[71-75]. Lipidomics, the systematic analysis of lipid composition and expression changes, can intensify the understanding of lipid metabolism alterations in T2DM. Recent population lipidomics data revealed that the T2DM-related lipid profile included decreased lysophospholipids, phosphatidylcholines, sphingomyelins, and cholesterol esters and increased triacylglycerols, diacylglycerols, and phosphatidylethanolamines[76-78]. Although these indicators can be used as potential biomarkers to predict the risk of T2DM, its prediction for a particular disease has not yet been verified. Balgoma *et al*[79] compared the lipid profiles from patients with non-alcoholic fatty liver disease, cardiovascular incidents, hepatocellular carcinoma, and T2DM. They noted that the upregulation of triacylglycerols, palmitic acid, palmitoleic acid, stearic acid and oleic acid is a fingerprint of liver X receptor-mediated lipogenesis in the liver. To thoroughly understand the mechanisms of T2DM-related lipid metabolism disorders, the utilization of lipidomics, and the integration of databases will undoubtedly achieve this goal.

CONCLUSION

Multi-omic studies have provided new breakthroughs and directions to guide traditional molecular biology research. The expansion of “omics” data and the continuous advancement of bioinformatics analysis technology will surely continue the advancement of our knowledge on the mechanisms of T2DM, especially on intestinal flora perturbation and dyslipidemia.

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Role and function of granin proteins in diabetes mellitus

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Abstract

The granin glycoprotein family consists of nine acidic proteins; chromogranin A (CgA), chromogranin B (CgB), and secretogranin II-VIII. They are produced by a wide range of neuronal, neuroendocrine, and endocrine cells throughout the human body. Their major intracellular function is to sort peptides and proteins into secretory granules, but their cleavage products also take part in the extracellular regulation of diverse biological processes. The contribution of granins to carbohydrate metabolism and diabetes mellitus is a recent research area. CgA is associated with glucose homeostasis and the progression of type 1 diabetes. WE-14, CgA₁₀₋₁₉ and CgA₄₃₋₅₂ are peptide derivatives of CgA, and act as CD4⁺ or CD8⁺ autoantigens in type 1 diabetes, whereas pancreastatin (PST) and catestatin have regulatory effects in carbohydrate metabolism. Furthermore, PST is related to gestational and type 2 diabetes. CgB has a crucial role in physiological insulin secretion. Secretogranins II and III have angiogenic activity in diabetic retinopathy (DR), and are novel targets in recent DR studies. Ongoing studies are beginning to investigate the potential use of granin derivatives as drugs to treat diabetes based on the divergent relationships between granins and different types of diabetes.

Key Words: Granin; Chromogranin A; Chromogranin B; Diabetes Mellitus; Mice; Inbred nonobese diabetic; Secretogranin III

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Core Tip: Granin glycoproteins are secretory proteins that are widely produced by neuronal, neuroendocrine, and endocrine cells throughout the human body. Recent data have shown that the granin proteins chromogranin A and B, and secretogranin II and III play a role in carbohydrate metabolism and in the pathophysiology of diabetes mellitus. In this review, the current state of knowledge concerning the relationship between granin proteins, diabetes and glucose homeostasis is discussed in detail, including several ongoing studies investigating granin-based drug therapies of future promise in diabetes care.

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INTRODUCTION

Neuronal, neuroendocrine, and endocrine cells are involved in the production of many peptides and proteins with diverse functions. During the secretion of these biologically active molecules, secretory proteins play an important role in the protein sorting that takes place in the secretory vesicles of the Golgi apparatus. The members belonging to the granin glycoprotein family, chromogranin A (CgA), chromogranin B (CgB), and secretogranin (Sg) II-VIII (Table 1), participate in protein sorting[1]. Granin proteins all have an acidic pH, calcium-binding ability, and are produced throughout the body by several types of neuronal-, neuroendocrine-, and endocrine cells[1-4]. In addition to protein sorting, secondary functions that are related mainly to the cleavage products of the granin proteins (Table 2) have emerged during evolution. Some of these biologically active products have been described as participating in pathogen control, psychiatric disorders, and metabolic disorders such as diabetes mellitus[1,3,5-7]. The function of many other granin protein products is still unclear. The available literature on granin proteins and their cleavage products is discussed in this review, focusing on their relationships to diabetes mellitus and carbohydrate metabolism. The in-depth presentation of the biochemistry, genetics, distribution, and function of the various granin proteins is not the aim of the current review, but publications on those subjects are available[1,8-14].

THE ROLE OF GRANINS IN THE SECRETION OF INSULIN

The presence of CgA[15], CgB[16-18], SgII[15] and SgVII (VGF, non-acronymic)[19,20] as secretory proteins has been described in animal and cellular models of pancreatic islets. Pancreatic beta cells of chromogranin A gene (*CHGA*) knockout (KO) mice were reported to have compensatory overexpression of CgB and SgII, with simultaneous insulin overproduction and fewer immature secretory granules. The CgA cleavage products betagranin (CgA₁₋₁₂₆)[21], vasostatin-I (CgA₁₋₇₆) and catestatin (CST, CgA₃₅₂₋₃₇₂) are found in beta cells; pancreastatin (PST, CgA₂₅₀₋₃₀₁) is found in alpha cells[15,22], indicating different protein cleavage products mediated by different endoproteases [14].

Betagranin was reported to have a negative effect on glucose-stimulated insulin secretion (GSIS). Betagranin treatment of murine insulinoma cell lines was found to inhibit insulin secretion in a dose-dependent manner that was associated with dysfunction of the calcium response[21]. Normal cell function was restored when betagranin was removed. Antibodies against CgA or PST have no effect on insulin secretion, while the partial absence of CgB results in increased proinsulin synthesis [23]. Colocalization of insulin and CgB was confirmed in the *trans*-Golgi network of human and murine islet cells from healthy and insulinoma tissue[17]. Glucose-stimulated insulin, glucagon, and somatostatin secretion were decreased in chromogranin B gene (*CHGB*) KO mice in parallel with a decrease in the amount of circulating insulin and a slight decrease in renal glucose clearance. The insulin sensitivity of *CHGB* KO mice did not differ from that of wild-type mice[18]. Proinsulin processing was slowed in the absence of CgB. The density of proinsulin-containing secretory

Table 1 Names, loci, and molecular masses of granin proteins[1,2]

Name	Synonym	Locus	Number of amino acids and calculated molecular mass (kDa)
Chromogranin A	Parathyroid secretory protein 1	14q32.12	439 (49 kDa)
Chromogranin B	Secretogranin I	20pter-p12	657 (77 kDa)
Secretogranin II	Chromogranin C	2q35-q36	587 (68 kDa)
Secretogranin III	-	15q21	449 (51 kDa)
HISL-19 ¹	Secretogranin IV	-	-
7B2	Secretogranin V	15q13-q14	186 (21 kDa)
NESP55	Secretogranin VI	20q13.2	201 (23 kDa)
VGF	Secretogranin VII	7q22.1	593 (65 kDa)
proSAAS	Secretogranin VIII	Xp11.23	227 (24 kDa)

¹HISL-19 has only been confirmed with monoclonal antibodies; *in vivo* isolation has not been successful to date[2,87]. NESP55: Neuroendocrine secretory protein with an apparent molecular weight of 55,000 Daltons.

granules was altered, causing significantly slower detachment of these granules from the *trans*-Golgi network, which ultimately delayed the translocation of the granules to the plasma membrane. Although the function of cell surface receptors was not different from that of wild-type mice, the initial, rapid phase of GSIS was virtually absent in *CHGB* KO mice. The loss of rapid GSIS was compensated by increased basal insulin production, and the beta cells of *CHGB* KO mice stored and secreted twice as much proinsulin than the beta cells of wild-type mice[16,18]. These observations, seen in KO mice, are similar to the characteristics of type 2 diabetes mellitus (T2DM) in humans[18]. Stimulus-coupled insulin secretion was decreased in *VGF* (the gene that encodes SgVII protein) KO mice. An impairment of the second phase of insulin secretion was described, and secretory granules detached significantly more slowly from the *trans*-Golgi network, and was accompanied by an increase in the proinsulin level[20], similar to the effect observed in the case of *CgB*.

GRANIN PEPTIDES IN GLUCOSE HOMEOSTASIS

Pancreastatin

PST negatively regulates insulin sensitivity and glucose homeostasis. PST-mediated inhibition of insulin secretion promotes a high blood glucose level (hyperglycemia). Moreover, PST can: (1) Reduce the hepatic glucose uptake through inhibiting the insulin-stimulated glycogenesis in primary hepatocytes; (2) Decrease the insulin-stimulated synthesis of lipids; and (3) Regulate the expression and secretion of leptin in adipocytes, which also increases blood glucose levels[24-27]. G-protein-activated phospholipase C β 3 isoforms[5,28-30] or activation of nitric oxide pathways[31-33] in hepatocytes inhibit insulin but only the former pathway has been described in adipocytes[5,30]. *CHGA* KO mice are obese, have hypertension, diminished baroreflex sensitivity, increased plasma catecholamine and adipokine levels, and lower interleukin-6 and lipid levels compared with wild-type animals[32,34]. A normal blood glucose level (euglycemia) is maintained by increased liver insulin sensitivity in *CHGA* KO mice, which is supported by the abundance of hepatic phosphoenolpyruvate carboxykinase (PEPC) and glucose-6-phosphatase (G6Pase) mRNAs. *CHGA* KO mice treated with PST are euglycemic, even in the absence of PEPC and G6Pase mRNAs[32].

The PST inhibitor peptide-8 (PSTi8)[35-39] reduces the effects of PST-induced insulin resistance. PSTi8 increases translocation of glucose transporter type 4 to the cell surface in hepatocytes and adipocytes, thereby promoting glucose uptake. It also reduces hepatic glucose release, lipid deposition, dexamethasone-induced oxidative stress; stimulates hepatocellular energy levels, and enhances the activity of glucose response protein 78[37,40]. PSTi8 treatment reduces lipogenesis, enhances fatty acid oxidation, improves glucose homeostasis *via* increased glycogenesis and glycolysis, and decreases gluconeogenesis in streptozotocin-induced diabetic mice[35,38]. The

Table 2 Cleavage products of granin proteins[1,3,88-90]

Granin protein	Cleavage product
CgA ¹	Vasostatin-I (CgA ₁₋₇₆) and -II (CgA ₁₋₁₁₅) Betagranin (CgA ₁₋₁₂₈) CgA ₁₀₋₁₉ and CgA ₄₃₋₅₂ ¹ Chromofungin (CgA ₄₇₋₆₆) Vasoconstriction-inhibiting factor (CgA ₇₉₋₁₁₃) Chromostatin (CgA ₁₂₄₋₁₄₃) Chromacin (CgA ₁₇₃₋₁₉₄) Pancreastatin (CgA ₂₅₀₋₃₀₁) ¹ WE-14 (CgA ₃₂₄₋₃₃₇) ¹ Catesliten (CgA ₃₄₄₋₃₅₈) Catestatin (CgA ₃₅₂₋₃₇₂) ¹ Parastatin (CgA ₃₅₇₋₄₂₈) GE-25 (CgA ₃₆₇₋₃₉₁) Serpinin (CgA ₄₁₇₋₄₄₂)
CgB ¹	CgB ₁₋₄₁ GAWK (CgB ₄₂₀₋₄₉₃) BAM-1745 (CgB ₅₇₉₋₅₉₃) PE-11 (CgB ₅₅₅₋₅₆₅) Secretolytin (CgB ₆₄₇₋₆₅₇) 43kDa large CgB fragment
SgII ¹	Secretoneurin (conjugate of SgII ₁₃₃₋₁₅₁ and SgII ₁₅₄₋₁₈₆) EM66 (66 amino acid long) Manserin (SgII ₄₉₇₋₅₃₆)
SgIII ¹	— ²
HISL-19	— ²
7B2	— ²
NESP55	LSAL (NESP55 ₁₅₉₋₁₆₂) GAIPRRH (NESP55 ₂₃₄₋₂₄₁)
VGF	Neuroendocrine regulatory peptide-1 (VGF ₂₈₁₋₃₀₆) Neuroendocrine regulatory peptide-2 (VGF ₃₁₀₋₃₄₇) NAPP129 or VGF20 (VGF ₄₁₇₋₆₁₇) TPGH (VGF ₄₂₂₋₄₃₀) TLQP-21 (VGF ₅₅₆₋₅₇₆) TLQP-62 or VGF10 (VGF ₅₅₆₋₆₁₇) HHPD-41 (VGF ₅₇₆₋₆₁₇) AQEE-11 (VGF ₅₈₈₋₅₉₉) AQEE-30 (VGF ₅₈₈₋₆₁₇) LQEQ-19 (VGF ₅₉₉₋₆₁₇)
proSAAS	KEP (proSAAS ₁₋₇) Big SAAS (proSAAS ₁₋₂₆) Little SAAS (proSAAS ₉₋₂₆)

GAV
 PEN (proSAAS₁₈₈₋₂₀₉)
 PEN-LEN (proSAAS₁₈₈₋₂₂₇)
 Little LEN (proSAAS₂₁₂₋₂₂₁)
 Big LEN (proSAAS₂₁₂₋₂₂₇)

¹Granins and their cleavage products involved in carbohydrate metabolism.

²No cleavage product described to date. CgA: Chromogranin A; CgB: Chromogranin B; NESP55: Neuroendocrine secretory protein with an apparent molecular weight of 55000 Daltons; SgII: Secretogranin II.

insulin-sensitizing effect of PSTi8 is equivalent to that of metformin, one of the most commonly used oral antidiabetic agents. Therefore, its potential role as a new antidiabetic agent is an ongoing area of research[39].

Catestatin

CST is indirectly associated with diabetes and carbohydrate metabolism by its effects on hypertension, obesity, and metabolic syndrome, and its possible use as a future antihypertensive or antiobesity agent has been considered[41]. External administration of CST reduces the bodyweight of obese *CHGA* KO mice[42] and can normalize catecholamine levels and baroreceptor function[34] to a state similar to that of wild-type mice. The obesity-reducing effects of CST result from enhancement of leptin receptor signaling and inhibition of α_2 -adrenergic receptor signaling[43]. *CHGA* KO mice fed a high-fat diet have elevated insulin levels. Treatment with external CST normalizes the glucose metabolism of hepatocytes and improves the insulin sensitivity of the animals[44]. Obese children and adolescents have a significantly lower serum CST levels than those in healthy controls. In a cohort of obese children, those with any symptoms of metabolic syndrome or increased cardiovascular risk had the lowest serum CST levels[45].

ROLES OF GRANINS IN DIABETES MELLITUS

Diabetes mellitus is one of the most prevalent diseases in our time. Recent estimates of the prevalence range from 4% to 10%, and there are more than 460 million diabetes patients worldwide. Approximately 10% of diabetes patients have type 1 diabetes mellitus (T1DM); most of the remaining patients have T2DM[46]. The former has an autoimmune pathomechanism; the latter is a consequence of insulin resistance. Furthermore, T1DM develops mostly in younger people, while T2DM develops at later ages[47,48]. Although our knowledge on the pathomechanism of diabetes is very extensive, new relationships between diabetes and molecules involved in the development or subsequent progression of the disease is still a recent and popular area of research[49]. Examples of these recently described molecules include CgA, CgB, SgII, and secretogranin III (SgIII), the CgA cleavage peptide derivatives PST, WE-14, and small N-terminal fragments CgA₁₀₋₁₉ and CgA₄₃₋₅₂.

Chromogranin A

CgA in T1DM

The role of CgA in the development of T1DM has been demonstrated by the absence of T1DM in *CHGA* KO nonobese diabetic (NOD) mice, in contrast to wild-type NOD mice (a T1DM animal model system)[50]. Furthermore, insulinitis, the inflammation of the pancreatic islets, occurred in only one-fifth of *CHGA* KO NOD mice, but did occur in all wild-type NOD mice. Insulinitis was accompanied by significantly decreased numbers of infiltrating CD4⁺ and CD8⁺ T cells in *CHGA* KO NOD mice. It should be noted that it was not possible to investigate more accurately whether the absence of the entire CgA molecule or any of its cleavage products prevented the development of T1DM in the *CHGA* KO NOD mouse model.

CgA has been reported to be elevated in approximately 20% of patients with T1DM when examined many years after the onset of the disease[51]. An even greater

prevalence of high CgA levels was found in another study[52]. A positive correlation has been found between serum CgA and glycated hemoglobin (HbA_{1c}) levels, with a slight but steady elevation of CgA with the increased duration of T1DM, indicating that CgA does not only contribute to T1DM pathogenesis, but also to disease progression[51].

Blood CgA level is elevated in enterochromaffin-like (ECL) cell hyperplasia, autoimmune gastritis, and in gastrointestinal neuroendocrine tumors[53,54], which are more frequent in T1DM patients than in the healthy population[53,55]. A significant proportion of patients with a high CgA level have ECL cell hyperplasia[51,55]; hence early detection of these conditions is possible with regular serum CgA level measurements[51,56]. There is a possible connection between ECL cell hyperplasia and high HbA_{1c} in T1DM patients with high CgA. It is known from animal experiments that 70%-90% of the circulating PST is produced by gastric ECL cells[57], and PST is actively involved in the regulation of glucose homeostasis[5]. The worsened metabolic status and high CgA levels may result from the hyperplasia of ECL cells, which can be further impaired by the appearance of more advanced clinical symptoms and comorbidities.

CgA cleavage products in T1DM

The CgA cleavage products WE-14 (CgA₃₂₄₋₃₃₇)[7], CgA₁₀₋₁₉, and CgA₄₃₋₅₂[58] are newly discovered autoantigens involved in the pathogenesis of T1DM. Embryonic medullary thymic epithelial cells do not contain CgA mRNA, which may serve as a cause for the insufficient deletion of CgA-reactive T cells[7,59] and autoimmunity against CgA-producing pancreatic beta cells. Among the aforementioned peptide products, CgA₁₀₋₁₉ and CgA₄₃₋₅₂ induced CD8⁺ T cell proliferation and displayed increased cytotoxic activity in both human T1DM patients and NOD mice[58]. In contrast, WE-14 has been shown to have CD4⁺ T cell autoreactivity[7] that does not occur in other gastro-entero-pancreatic tissues, except for pancreatic beta cells[60]. WE-14 presumably interacts with the major histocompatibility complex (MHC) class II antigens outside of the normal peptide binding grooves of MHC molecules, as WE-14 lacks the N-terminal amino acids that easily bind to the MHC class II antigen-binding sites[7]. The above observation that the antigenicity of WE-14 occurs only in pancreatic islets is presumably depends on a difference in the proteolytic processing of CgA in beta cells [7].

The modification of WE-14 by enzyme tissue transglutaminase (TGase)[61,62] or *in vitro* N-terminal arginine-leucine-glycine-leucine amino acid addition[63] dramatically increases its antigenic activity. Covalent cross-linking[14] between the side chains of glutamine and lysine caused by TGase[64] treatment increases the antigenicity of WE-14[65]. Similar to animal models, newly diagnosed T1DM patients have also been shown to exhibit elevated WE-14 antigenicity[62]. Antigenicity can be further increased if the patient's blood has been treated with TGase *in vitro*[62].

Hybrid insulin peptides (HIPs) are formed by the coupling of proinsulin and other peptides, are stored within the same secretory granules[66], and include a peptide called 2.5HIP, which is formed by a fusion of a C-peptide fragment and WE-14[67]. CD4⁺ T cell autoimmunity against 2.5HIP was demonstrated in NOD mice[66,67]. Peripheral NOD mouse-specific CgA-reactive T cells (BDC2.5) can bind 2.5HIP with up to 100 times higher affinity than WE-14 or CgA₂₉₋₄₂ alone[68], and the number of these HIP-reactive T cells increases with disease progression[66,67]. Human HIP-reactive CD4⁺ T cells have also been identified[66]. The development of T1DM can be prevented for more than 2 mo by transferring preactivated BDC2.5 T cells and 2.5HIP nanoparticles into NOD mice, whereas the disease manifested in untreated mice within 10 d[69].

Treating young NOD mice with liposomes containing a CgA mimotope (amino acid chain: AHHPIWARMDA) and the immunomodulator calcitriol (1 α ,25-dihydroxyvitamin D3) can postpone the development of T1DM[70]. Furthermore, the adoptive transfer of CD4⁺ T cells from liposome-treated animals into NOD severe-combined-immunodeficiency mice also suppressed the development of the disease[70].

CgA and its cleavage product PST in other forms of diabetes

The few published data on the relationship between CgA and T2DM are somewhat controversial. Kogawa *et al*[71,72] reported that salivary and serum CgA were significantly higher in T2DM patients than in healthy controls and patients with higher CgA values had worse glycemic control (HbA_{1c} \geq 7.0%)[71]. Impaired salivary flow was correlated with increased serum and salivary CgA levels and was associated with two genetic variants of *CHGA* (rs9658635 and rs9658655)[72]. In contrast to those findings, another study found that an almost negligible portion of T2DM patients had

serum CgA levels above the normal upper limit (> 98.1 ng/mL)[73], and no differences were found in the laboratory results and anamnestic data between the groups with normal or high serum CgA levels[73].

Postprandial serum PST levels are significantly higher in patients with prediabetes [74] or T2DM[75] compared with healthy controls, and are associated with consequent hyperglycemia[75], possibly because of the effect of PST on GSIS[75,76]. Fasting PST levels of the patients and controls did not differ[75]. Another study found that obese T2DM patients had significantly higher PST levels than obese and healthy nonobese control subjects, and that weight loss did not affect the differences in PST levels[77]. Serum PST is increased in patients with gestational diabetes, and positive correlations of PST, epinephrine, and norepinephrine levels have also been observed[78].

CHROMOGRANIN B AND SECRETOGRANINS

Even though a few hundred publications on CgB are available, very little is known about its relationship to diabetes. CgB has been reported to play a role in physiological insulin secretion[16-18] and its posttranslational changes[79], altered processing[80], and decreased serum values[81] that have been observed in human diabetes. The expression of *CHGB* in the pancreatic islets was lower in human T2DM patients compared with healthy subjects[79]. T2DM patients treated with intensive conservative insulin treatment had a significantly (approximately 20%) lower CgB level than T2DM patients treated with other regimens of antidiabetic drugs, or healthy controls. The serum CgB levels in T1DM were approximately 80% of the levels in control subjects, suggesting that pancreatic beta cells may produce a significant amount of circulating CgB. Furthermore, an assumption has been made that diabetes heavily affects CgB production. The autoimmune destruction of pancreatic beta cells in T1DM, and the more advanced state of the disease in T2DM, which is usually also associated with beta cell impairment, could cause the lower CgB levels. However, further studies are needed to test that hypothesis[81].

Diabetic retinopathy (DR), in which choroidal and retinal microvascular changes occur as complications of diabetes mellitus[82], can be characterized by an altered processing of granins in the vitreous[80]. Small peptide fragments of CgA, CgB, and SgII, which have been proposed to have anti-inflammatory properties, are rare in the vitreous of DR patients, but large fragments are rare in healthy subjects. Some authors have raised the possibility that the absence of small granin fragments may play a role in the pathogenesis of DR: Posttranslational processing of granins may be damaged because of some diabetes-specific reasons that ultimately lead to the impairment of the intraocular angiogenic balance, thus contributing to the neovascularization[80].

SgIII is a recently discovered DR-associated ligand with pro-angiogenic activity and selective binding. Based on cellular and animal-model studies, the effects of SgIII are restricted to the pathological condition, suggesting that the antibody against SgIII might be useful as a selective, anti-angiogenic drug in DR[83]. The angiogenic effect of SgIII could have been blocked *via* inhibition of the mitogen-activated protein kinase and extracellular signal-regulated kinase signaling pathways[84]. Consistent with the findings of animal studies, SgIII has been found only in the vitreous in humans[85]. Increased SgIII levels has been found in DR patients compared with retinopathy originating in patients without diabetes. Moreover, high lipid levels and a high body mass index, which are characteristic of T2DM[48] have been described as risk factors of DR[86], and have been associated with even higher SgIII levels[85].

CONCLUSION

Granin proteins are produced by various neuronal, neuroendocrine, and endocrine cell types of different organs throughout the body. They contribute intracellularly to the selective secretion of various peptides. A variety of extracellular functions of biologically active cleavage products have also emerged during their evolution. Recent studies have reported that CgA, CgB, SgII, SgIII, SgVII and some of the CgA cleavage products influence glucose homeostasis and different forms of diabetes mellitus. CgA and its peptide derivatives take part in the development and subsequent progression of T1DM, and also regulate glucose homeostasis. CgB and SgVII are prominent in physiological insulin secretion, and SgII and SgIII mainly contribute to DR. More data on the activity of granins is available for T1DM than for T2DM. The potential application of PSTi8, CST, and antibodies against SgIII as future medications further

increases the importance of granins in diabetes. Although our understanding of granin proteins in relation to glucose homeostasis and diabetes mellitus continuously extends, the most recent studies pose new challenges and raise more questions than they answer. To properly answer these questions, further clinical and experimental studies are needed.

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Diabetes remission after bariatric surgery

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Abstract

Over the last decade, obesity rates have continued to rise in the United States as well as worldwide and are showing no signs of slowing down. This rise is in parallel with the increasing rates of type 2 diabetes mellitus (T2DM). Given the association between obesity and T2DM and their strong correlation with increased morbidity and mortality in addition to healthcare expenditure, it is important to recognize the most effective ways to combat them. Thus, we performed a review of literature that focused on assessing the outcomes of T2DM following bariatric surgery. Available evidence suggests that bariatric surgery provides better T2DM resolution in obese patients when compared to best medical management alone. Additionally, Biliopancreatic diversion with duodenal switch as well as Roux-en-Y gastric bypass have demonstrated higher rates of T2DM resolution when compared with other bariatric procedures.

Key Words: Bariatric surgery; Diabetes; Remission; Gastric Bypass; Obesity

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Core Tip: Bariatric surgery is a safe and effective way to achieve diabetes remission in those with obesity via a variety of mechanisms, the majority of which are independent of weight loss. Available evidence suggests that bariatric surgery provides better type 2 diabetes mellitus resolution in obese patients when compared to best medical management alone.

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INTRODUCTION

Obesity rates continue to rise in the United States as well as worldwide. In fact, obesity prevalence doubled from 15% to 33% between 1980s and 2004 and was estimated to be 37.7% from 2013 to 2014[1,2]. Interestingly, some of the recent reports project that nearly 1 in 2 United States adults will have obesity [defined as body mass index (BMI) ≥ 30 kg/m²] by 2030 and nearly 1 in 4 adults will have severe obesity (defined as BMI ≥ 35 kg/m²) by then[3]. These numbers are alarming as obesity has been linked to developing type 2 diabetes mellitus (T2DM), coronary artery disease, non-alcoholic fatty liver disease, malignancy, amongst others, as well as lower life expectancy. Obesity was also attributable to 365000 deaths in 2000, second to only tobacco smoking [4]. Insulin resistance has been described as the main culprit for the development of T2DM in obese patients[5]. In fact, there is a > 6-fold increase in risk of developing T2DM in those with morbid obesity or BMI ≥ 40 kg/m²[6]. Diabetes remains one of the most prevalent chronic diseases in the United States affecting about 9% of the population in 2011, with rates continuing to grow in parallel with obesity[6].

This association between obesity and diabetes has detrimental effects on morbidity and mortality and creates a significant economic burden as a result. The cost of diabetes in 2012 was reported to be 45 billion dollars, with 69 billion dollars attributed to reduced productivity and 176 billion dollars attributed to direct medical costs[7]. Additionally, the cost of diabetes is projected to reach nearly 500 billion dollars by 2030[8]. This has led to an increased interest in finding ways to successfully treat diabetes and maintain remission.

While lifestyle modifications such as diet and exercise along with pharmacotherapy can be successful in treating both obesity and T2DM, few achieve sustained weight loss and only 10% of those with T2DM achieve favorable disease control in order to minimize and prevent long-term complications[9]. This article will thus focus on reviewing the most current data on diabetes remission following bariatric surgery.

ASSOCIATION OF T2DM AND OBESITY

Obesity has been linked to the development of T2DM *via* insulin resistance. Several mechanisms have been described. One of such proposed mechanisms involves increased release of a variety of factors including non-esterified fatty acids (NEFAs), glycerol, leptin, adiponectin, proinflammatory cytokines among others from adipose tissue which in turn leads to insulin resistance[10]. This occurs *via* reduced phosphorylation of phosphatidylinositol-3-OH kinase in muscle and increased gluconeogenic enzyme expression in the liver[9]. While this leads to insulin resistance, not all obese patients will go on to develop T2DM as they are able to overcome this by increased insulin release from pancreatic β cells to correct for decreased insulin sensitivity[9]. Thus, those with β cell dysfunction are at the highest risk of developing T2DM *via* increased release of NEFAs as they not only reduce insulin sensitivity but also decrease pancreatic β cell function[9].

Standard treatment of T2DM focuses on achieving good glycemic control in order to minimize cardiovascular and other risks and is mainly achieved *via* medical management. However, this treatment modality can become challenging in patients with obesity as a variety of pharmacotherapy agents can in fact cause weight gain and thus further worsen insulin resistance[11]. This is when bariatric surgery comes into play. Though initially described as surgical treatment for weight loss, bariatric surgery has demonstrated significant effects on reducing rates of T2DM in addition to improving cardiovascular health and thus reducing morbidity and mortality[12]. These beneficial effects are achieved *via* a multitude of mechanisms beyond weight loss.

MECHANISMS OF T2DM REMISSION FOLLOWING BARIATRIC SURGERY

Weight loss

While the exact mechanism for T2DM remission following bariatric surgery is not fully understood, several have been proposed. One such mechanism involves reduced caloric intake which in turn leads to significant weight loss and subsequently improved glucose sensitivity. This was thought to be achieved *via* restrictive and/or malabsorptive properties of bariatric surgery. However, this does not explain some of

the drastic effects seen on glucose control immediately following surgery, and thus the majority of glucose-lowering is achieved prior to weight loss[13]. Additionally, scintigraphy studies demonstrate that nutrient delivery through gastric pouch is actually increased rather than restricted following Roux-en-Y gastric bypass (RYGB)[14].

Insulin sensitivity

One of the most important factors contributing to improved glucose tolerance is a significant decrease in insulin resistance fairly early following bariatric surgery. In fact, insulin resistance decreases about 50% in 1 wk following surgery and into the normal range seen in glucose tolerant patients when measured homeostatic model assessment of insulin resistance[15-17]. In addition to improved liver insulin sensitivity, insulin clearance also increases and is thought to be due to decreased caloric intake which in turn leads to decreased liver fat content. This has been demonstrated using post-operative magnetic resonance imaging of the liver following RYGB[14]. These combined effects in turn lead to decreased basal glucose concentration and are thought to improve pancreatic β cell function by decreasing the toxic effect of glucose[18].

Foregut/hindgut hypothesis

According to the foregut-hindgut hypothesis, there is an increased amount of incompletely digested food delivered to the distal intestine due to bypassed foregut. This in turn stimulates specialized L cells which facilitate the release of glucagon-like-peptide-1 (GLP-1) and peptide YY, both of which have been implicated in achieving weight loss. Additionally, both provide a favorable effect on pancreatic β cells leading to increased insulin sensitivity[18,19]. Interestingly, GLP-1 Levels rise dramatically within days of bariatric surgery stimulating pancreatic β cells. This effect of β cell stimulation is further amplified by a temporary early increase in plasma glucose levels eventually leading to increased insulin release[17]. While this hypothesis may explain the benefits seen following RYGB and biliopancreatic diversion with duodenal switch (BPD-DS), it does not explain the beneficial effects on glucose metabolism seen following sleeve gastrectomy (SG) as the intestinal tract remains in continuity[16].

Bile acids

Circulating bile acids (BA) levels also increase following bariatric surgery and are correlated with improved glucose sensitivity. This is thought to occur following reduced mixture of partially digested nutrients with BAs following surgery thus leading to higher concentration of free circulating BAs. This, in turn, leads to reduction in hepatic glucose production as well as glucogenesis within gut segments that are devoid of BAs[20].

METHODS

A comprehensive search of the published literature in PubMed, PubMed Central (PMC), EMBASE, Medline, and the Cochrane Register of Controlled Trials databases was conducted until January 2021. We used the guidelines of 2015 Preferred reporting items for systematic review and meta-analysis protocols (PRISMA-P). Randomised controlled trials with at least 12 mo of follow-up and prediction models of diabetes remission after bariatric surgery were included. Keywords containing "obesity", "metabolic [or] bariatric surgery", "type 2 diabetes", "diabetes remission", "predict", "prediction models" and "score" were constructed for inclusion. Only studies in english language were included.

TRIALS COMPARING T2DM REMISSION FOLLOWING BARIATRIC SURGERY

Mingrone *et al*[12] designed a randomized clinical trial (RCT) looking at 60 patients who were randomly assigned to one of the 3 groups: Conventional medical therapy, RYGB or BPD-DS. Their primary endpoint included diabetes remission which was defined as fasting glucose level < 100 mg/dL and glycosylated hemoglobin (HbA1c) < 6.5mmol/L without the use of pharmacotherapy. Fifty-six patients completed their 2 year follow up and at that time no patients in the medical group achieved remission while 75% in the RYGB and 95% in the BPD-DS were able to achieve remission ($P < 0.05$). Additionally, while the HbA1c levels did decrease significantly in all 3 groups

from average baseline of $8.65\% \pm 1.45\%$, the 2 surgical groups had greater degree of lowering with average numbers at 2-year follow up being the following: $7.69\% \pm 0.57\%$ for the medical group, $6.35\% \pm 1.42\%$ in the RYGB group and $4.95\% \pm 0.49\%$ in the BPD-DS group. The authors of this study concluded that bariatric surgery was able to achieve higher rates of remission in patients with severe obesity ($\text{BMI} \geq 35 \text{ kg/m}^2$), and $\text{HbA1c} < 6.5 \text{ mmol/L}$ without the use of pharmacotherapy[12].

Calorie reduction or surgery: Seeking to Reduce Obesity and Diabetes Study was an RCT that assigned patients with obesity ($\text{BMI} \geq 30 \text{ kg/m}^2$) and T2DM to either RYGB ($n = 23$) or intensive lifestyle and medical management ($n = 20$). Patients were followed for 1 year with primary outcome measured being T2DM resolution (defined as $\text{HbA1c} < 6\%$ and being off medications). During this follow up, 60% of patients following RYGB achieved remission while nearly 6% of the medical group were able to do so ($P < 0.05$). This study reported no life-threatening complications in the surgical group. The authors concluded that RYGB yielded higher rates of T2DM remission at 1 year when compared to medical therapy alone[21].

Surgical Treatment and Medications Potentially Eradicate Diabetes Efficiently (STAMPEDE) RCT published by Schauer *et al*[22] in 2017 provides some of the longer-term data shedding light on the effectiveness of bariatric surgery on T2DM resolution. The study randomized 150 patients with obesity and T2DM to intensive medical therapy alone *vs* medical therapy and either RYGB or SG. One hundred and thirty-four patients completed 5 year follow up with primary endpoint being achievement of HbA1c level of $\leq 6\%$. Of those who underwent intense medical therapy alone, 5% were able to achieve this endpoint *vs* 29% of those who also underwent RYGB (adjusted $P < 0.05$) and 23% of those who underwent SG (adjusted $P = 0.07$). In the surgical group, this endpoint was achieved without the need for hypoglycemic medications in the majority of patients, whereas none of the patients in the medical group were able to achieve that endpoint without pharmacotherapy. Additionally, 89% of patients in the surgical group were off insulin during a 5 year follow up compared to 61% of patients in the medical group[22].

Hofsø *et al*[23] designed a triple blind RCT that was conducted in Norway comparing 109 patients with morbid obesity and presence of T2DM who were randomly assigned to SG (55/109) or RYGB (54/109). The primary outcome measured during their 1 year follow up was diabetes remission defined as having $\text{HbA1c} \leq 6\%$ while being off pharmacotherapy. 107/109 patients completed 1 year follow up demonstrating that 47% of SG patients had diabetes remission and 74% of RYGB patients had diabetes remission ($P < 0.05$). This study also reported 57 adverse reactions during a follow up period with 1 patient returning back to the operating room following an intra-abdominal bleed following SG, 1 patient needing blood transfusions 10 days following RYGB. No deaths were observed in this study. Thus, the authors concluded that even though pancreatic β cell function improved after both types of surgery, RYGB was found to have greater effect on T2DM resolution when compared to SG at 1 year[23].

Another recent 3-arm RCT assigned 61 patients with obesity and T2DM to one of the 3 groups: RYGB, adjustable gastric banding (AGB) or intense medical therapy and were followed for 1 year initially. After 1 year follow up, the patients were assessed for additional 4 years following introduction of lower-level lifestyle interventions. Primary endpoint of this study was T2DM remission rates (partial: Fasting plasma glucose (FPG) $\leq 125 \text{ mg/dL}$, $\text{HbA1c} < 6.5\%$ and off medications and complete: FPG $\leq 100 \text{ mg/dL}$, $\text{HbA1c} < 5.7\%$ and off medications). At 5 years, partial or complete T2DM remission was achieved in 30% of RYGB group, 19% of AGB group and 0% of medical management group ($P < 0.05$). Additionally, 56% of RYGB patients were off medications at 5 years as compared to 45% of AGB group and 0% of medical management group ($P < 0.05$). Thus, the authors concluded that their surgical management was more effective in T2DM resolution than best medical management alone[11].

More recently, a study by Mingrone *et al*[24] published their 10 year follow up results comparing metabolic surgery and medical management for T2DM at a single center in Italy. This RCT included 3 treatment arms: BPD-DS, RYGB and medical management. They had 20 patients in each arm group with 60 patients total, 57 of which completed follow up. Remission was defined as FPG $\leq 100 \text{ mg/dL}$, $\text{HbA1c} \leq 6.5\%$ and being off medications. Ten-year remission rates in the intention-to-treat analysis demonstrated that 5.5% [95% confidence interval (CI) 1.0-25.7] of medical group achieved remission when compared to 50% in BPD-DS [95%CI 29.9-70.1] group and 25% in RYGB [95%CI 11.2-49.9] group ($P < 0.05$)[24] (Table 1).

Table 1 Bariatric surgery vs medical management for type 2 diabetes mellitus remission

Ref.	Pts w/ follow up/enrolled pts	Study duration, years	Medical management T2DM resolution %	RYGB T2DM resolution %	SG T2DM resolution %	BPD-DS T2DM resolution %	AGB T2DM resolution %	T2DM resolution definition	P value
Mingrone <i>et al</i> [12], 2012	56/60	2	0	75	N/A	95	N/A	FPG < 100 mg/dL + HbA1c < 6.5 mmol/L + no pharmacotherapy	< 0.05
Cummings <i>et al</i> [21], 2016	43/43	1	6	60	N/A	N/A	N/A	HbA1c < 6% + no pharmacotherapy	< 0.05
Schauer <i>et al</i> [22], 2017	134/150	5	5	29	23	N/A	N/A		< 0.05
Hofsø <i>et al</i> [23], 2019	107/109	1	N/A	74	47	N/A	N/A		< 0.05
Courcoulas <i>et al</i> [11], 2020	50/61	5	0	30	N/A	N/A	19		< 0.05
Mingrone <i>et al</i> [24], 2021	57/60	10	5	25	N/A	50	N/A		< 0.05

T2DM: Type 2 diabetes mellitus; RYGB: Roux-en-Y gastric bypass; SG: Sleeve gastrectomy; BPD-DS: Biliopancreatic diversion with duodenal switch; AGB: Adjustable gastric banding; FPG: Fasting plasma glucose; HbA1c: Glycylated hemoglobin.

PREDICTORS OF DIABETES REMISSION AFTER BARIATRIC SURGERY

Several prediction models have been developed in order to assess diabetes remission following bariatric surgery. The models used are either scoring systems, in which each variable is given a specific score and the addition of scores gives the probability of diabetes remission; or a logistic regression model in which higher odds means a higher probability of diabetes remission[25]. Relevant scoring systems include the DiaRem, age, bmi, c-peptide level and duration of diabetes score (ABCD), and individualized metabolic surgery scores (IMSS).

DiaRem and DiaRem2

This model described by Still *et al*[26] in 2014 is based on a retrospective study of 690 diabetic obese patients who underwent RYGB. The preoperative factors which demonstrated to be independent predictive factors of diabetes remission were: Age, insulin use, HbA1c measurement, and type of antidiabetic medications. Preoperative insulin use was associated with the higher severity of diabetes and lower percentage of remission and was given the highest score of 10 points. The score range goes from 0 to 22, and the patients fall into one of five groups. The higher the score, the lowest the probability of diabetes remission.

Additionally, in 2019, the DiaRem2 score incorporated the duration of diabetes to the already validated DiaRem[27]. The association between “early remission” (defined as remission within the first 2 mo after surgery) and duration of diabetes, as well as early remission and score was analyzed. Patients were allocated into one of three remission groups according to their score: High (0-5), Intermediate (6-12) or Low (13-25). A highest score was associated with a decreased percentage of early remission.

ABCD

In this score proposed by Lee *et al*[28] in 2013, a first cohort of 63 patients who underwent either RYGB or mini-gastric bypass in Asia was analyzed. The four preoperative factors identified as independent risk factors for remission were: Age, baseline BMI, C-peptide level, and duration of diabetes. Patients with higher scores had higher remission rates. A modified scoring system was then tested in 510 patients, including SG patients. It showed lower remission levels after SG than those correlated to RYGB. One of the limitations of this score was that insulin and other antidiabetic medications used were not taken into account.

IMSS

IMSS was designed by Aminian *et al*[29] with the objective to guide procedure selection based on long-term diabetes remission. A sample of 659 patients who underwent RYGB or SG was analyzed. Duration of diabetes, number of diabetes medications, insulin use, and HbA1c were the four independent predictors used to develop this score. Patients were allocated into one of three stages of diabetes severity. This study included recommendations on what type of surgery to perform: RYGB for mild disease and moderate disease, and SG for severe disease. In severe diabetes, the rate of remission is lower, so the least demanding technique is preferred. Unfortunately, biliopancreatic diversion with duodenal switch was not included in this score even though this procedure has been associated with higher remissions of associated comorbidities.

Improved DiaRem model

The general limitations of the scoring systems commented is that they were based on one or two procedure types, with RYGB as the leading procedure, and they are usually limited to a population with a defined race/ethnicity. That is why Duke Group developed a logistic regression model including a diverse racial/ethnicity and a large BPD/DS sample[30]. This model was based on a retrospective review of 602 patients who underwent RYGB, SG, LAGB or BPD/DS. The objective was to analyze the relation of remission to procedure type. DiaRem score was used to assess the performance of this model in their cohort. The results showed BPD/DS patients have an approximately 229% increase in odds of having remission at 1 year compared with RYGB patients (adjusted OR 3.29; 95%CI: 1.27, 8.5).

Independent of the predictive model used, the procedure type is an independent risk factor for diabetes remission. Our results indicate BPD/DS as the procedure with a higher percentage of diabetes remission (Table 2). We believe that this procedure should be taken into account in future tools that include a recommendation of the procedure of choice.

CONCLUSION

Bariatric surgery is a safe and effective way to treat T2DM in those struggling with obesity. The effects can be seen fairly early prior to any substantial weight loss, thus highlighting the interplay of hormonal factors that leads to increased insulin sensitivity *via* activation of pancreatic β cells.

Several efforts have been made to prove the effectiveness of bariatric surgery in diabetes remission, including randomized clinical trials with 1, 3, 5 and even 10 years of follow-up. A variety of bariatric surgical procedures have demonstrated to be more effective than medical management for T2DM control, and BPD-DS and RYGB have shown some of the highest remission rates.

The literature available up to date still encounters certain limitations. For instance, in the STAMPEDE trial, patients had a relatively low BMI (mean 37 ± 3.5 kg/m²) with 37% of them having a BMI value < 35 kg/m². This leaves aside the morbid and super obese population, but opens the discussion to lower the current indication guidelines to serve patients with T2DM and lower BMI.

In addition, remission was achieved in 23%-29% of patients submitted to surgery, but nothing is said about the remaining 70% who did not benefit from RYGB or SG. Could these patients benefit from another type of surgery such as biliopancreatic diversion with duodenal switch? Even the most recent information from a RCT by Mingrone *et al*[24] with the largest follow-up (10 years), exhibited maintained diabetes remission in only 37,5% of the patients when compared to conventional medical therapy.

BPD/DS is an under-utilized surgical procedure which has been associated with enhanced weight loss and resolution of comorbid disease[31], though postoperative complications are increased when compared to RYGB or SG[32]. Numerous studies, including our predictive model, have demonstrated that this procedure is related to increased weight loss and remission of diabetes and other comorbidities. Yet, its low implementation fails to show its benefits on a wide scale.

The discussion is no longer whether metabolic surgery achieves remission of diabetes or not, as this has broadly been demonstrated. Debate arises on which procedure is best for each individual patient. Predictive models are warranted to be improved once they succeed in including a large, diverse population, addressing duration of diabetes and insulin use, who are submitted to any of the surgical

Table 2 Predictors of diabetes mellitus remission following bariatric surgery

	Diarem	Diarem2	IMS	ABCD	Duke diabetes remission
Procedure	Rygb	RYGB	RYGB or SG	RYGB or mini-gastric	RYGB, SG, AGB, BPD/DS
Number of patients (n)	690	307	659	63	602
Variables	Insulin use	Insulin use	Insulin use	Diabetes duration	Age Sex
	Age	Age	Duration of diabetes	Age	Race Insulin use
	Hba1c	Hba1c	Hba1c	Baseline BMI	Hba1c BMI
	Type of antidiabetic drugs	Duration of diabetes	Number of diabetic medications	C-peptide level	Preop asthma, GERD, hypertension, hyperlipidemia, anticoagulation medication status Type of antidiabetic drugs
Scale	0-22 (5 groups)	0-25 (High-Intermediate-Low remission)	3 stages (Mild-Moderate-Severe)	0-10	Odds of remission according to preoperative variables and type of surgery
Recommendation on procedure of choice	No	No	Yes	No	No

RYGB: Roux-en-Y gastric bypass; SG: Sleeve gastrectomy; BPD-DS: Biliopancreatic diversion with duodenal switch; AGB: Adjustable gastric banding; HbA1c: Glycosylated hemoglobin; GERD: Gastroesophageal reflux disease.

procedures available (AGB, SG, RYGB, distal bypass, BPD-DS *etc.*).

The following steps are yet to be determined. Large multicentric studies are awaited to test and improve the existing scores, in order to ultimately develop a calculator able to predict individualized surgical outcomes. Yet, there is still a feeling of uncertainty and apprehension surrounding the fate of patients who experience diabetes relapse or weight regain after metabolic surgery.

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Basic Study

Decarboxylated osteocalcin, a possible drug for type 2 diabetes, triggers glucose uptake in MG63 cells

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Abstract

BACKGROUND

Uncarboxylated osteocalcin (GluOC) has been reported to improve glucose metabolism, prevent type 2 diabetes, and decrease the severity of obesity in mice with type 2 diabetes. GluOC can increase glucose uptake in a variety of cells. Glucose metabolism is the main source of energy for osteoblast proliferation and differentiation. We hypothesized that decarboxylated osteocalcin (dcOC), a kind of GluOC, can increase glucose uptake in MG63 cells (osteoblast-like osteosarcoma cells) and influence their proliferation and differentiation.

AIM

To investigate the effects of dcOC on glucose uptake in human osteoblast-like osteosarcoma cells and the possible signaling pathways involved.

METHODS

MG63 cells (human osteoblast-like osteosarcoma cells) were treated with dcOC (0, 0.3, 3, 10, or 30 ng/mL) for 1 and 72 h, and glucose uptake was measured by flow cytometry. The effect of dcOC on cell proliferation was measured with a CCK-8 assay, and alkaline phosphatase (ALP) enzyme activity was measured. PI3K was inhibited with LY294002, and hypoxia-inducible factor 1 alpha (HIF-1 α) was silenced with siRNA. Then, GPRC6A (G protein-coupled receptor family C group 6 subtype A), total Akt, phosphorylated Akt, HIF-1 α , and glucose transporter 1 (GLUT1) levels were measured by Western blot to elucidate the possible pathways by which dcOC modulates glucose uptake.

RESULTS

The glucose uptake of MG63 cells was significantly increased compared with that

human beings or animals, the study was not reviewed and approved by any institutional review board.

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of the paired control cells after short-term (1 h) treatment with dcOC at different concentrations (0.3, 3, and 10 ng/mL groups, $P < 0.01$; 30 ng/mL group, $P < 0.05$). Glucose uptake of MG63 cells was significantly increased compared with that of the paired control cells after long-term (72 h) treatment with dcOC at different concentrations (0.3, 3, and 10 ng/mL groups, $P < 0.01$; 30 ng/mL group, $P < 0.05$). DcOC triggered Akt phosphorylation in a dose-dependent manner, and the most effective stimulatory concentration of dcOC for short-term (1 h) was 3 ng/mL ($P < 0.01$). LY294002 abolished the dcOC-mediated (1 h) promotion of Akt phosphorylation and glucose uptake without affecting GLUT1 protein expression. Long-term dcOC stimulation triggered Akt phosphorylation and increased the protein levels of HIF-1 α , GLUT1, and Runx2 in a dose-dependent manner. Inhibition of HIF-1 α with siRNA abolished the dcOC-mediated glucose uptake and substantially decreased GLUT1 protein expression. DcOC intervention promoted cell proliferation in a time- and dose-dependent manner as determined by the CCK-8 assay. Treatment with both 3 ng/mL and 10 ng/mL dcOC affected the ALP activity in MG63 cells after 72 h ($P < 0.01$).

CONCLUSION

Short- and long-term dcOC treatment can increase glucose uptake and affect proliferation and ALP activity in MG63 cells. This effect may occur through the PI3K/Akt, HIF-1 α , and GLUT1 signaling factors.

Key Words: Decarboxylated osteocalcin; Osteoblast; Glucose uptake; Glucose transporter 1; Type 2 diabetes

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Core Tip: Uncarboxylated osteocalcin (GluOC) has been reported to improve glucose metabolism and prevent type 2 diabetes. GluOC can increase the glucose uptake in a variety of cells. In this study, MG63 cells were treated with different concentrations of decarboxylated osteocalcin (dcOC) for 1 h and 72 h to observe the changes in glucose uptake, proliferation, and alkaline phosphatase (ALP) activity, as well as possible signaling pathway. Short- or long-term intervention with dcOC *in vitro* can increase glucose uptake and promote the proliferation and ALP activity of MG63 cells. This effect may occur through the PI3K/Akt, hypoxia-inducible factor 1 alpha, and glucose transporter 1 signaling factors.

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INTRODUCTION

Osteocalcin (OC), synthesized by mature osteoblasts, is one of the most abundant noncollagen proteins in bone[1]. In the circulation, the concentration of OC is a measure of bone formation[2]. In osteoblasts, after protein translation in the endoplasmic reticulum, OC is posttranslationally modified by the addition of carboxyl groups at glutamyl (Glu) residues at positions 17, 21, and 24 *via* γ -Glu carboxylase, thereby facilitating its binding to hydroxyapatite in the bone matrix[1,3]. However, OC containing one or more uncarboxylated Glu residues (most commonly Glu17) is referred to as undercarboxylated OC (ucOC). Carboxylated OC can also be decarboxylated at Glu residues under acidic conditions and is thus converted to decarboxylated OC (dcOC). Together, ucOC and dcOC are referred to as uncarboxylated OC (GluOC) and are closely related to energy metabolism[4]. To date, studies have confirmed that G protein-coupled receptor family C group 6 subtype A (GPRC6A), the receptor for carboxylated OC and GluOC, participates in the physio-

logical response and glucose metabolism induced by GluOC[5-7].

Previous studies indicated that GluOC can improve glucose metabolism, prevent type 2 diabetes, and decrease the severity of obesity in mice with type 2 diabetes[8,9]. GluOC has great potential to become a new drug for the treatment of type 2 diabetes in the future. GluOC was also shown to promote glucose uptake in adipocytes, C2C12 myotubes, and muscles[10-13]. However, both the direct effects of GluOC on glucose uptake in bone tissues and the underlying mechanisms remain unexplored.

A previous study showed that the energy required for osteoblast proliferation and differentiation is produced mainly *via* glucose metabolism[14], and glucose transporter 1 (GLUT1) is the major glucose transporter[15]. GLUT1-mediated glucose uptake in osteoblasts occurs independently of insulin[14]. Moreover, GLUT1 may participate in osteosarcoma biology[16,17]. Activation of the PI3K/Akt and hypoxia-inducible factor 1 alpha (HIF-1 α) signaling pathways is closely related to glucose uptake mediated by GLUT1[18,19]. Idelevich *et al*[20] found that the glucose uptake rate of mouse chondrocyte precursor cells (ADTC5 cells) overexpressing OC was increased. The siRNA-mediated silencing of HIF-1 α abolished the effect of OC in upregulating the protein and mRNA expression of GLUT1, suggesting that HIF-1 α mediates the effect of OC on upregulating the expression of GLUT1 in ADTC5 cells[20].

Herein, we treated MG63 cells, a human osteoblast-like osteosarcoma cell line, with dcOC for 1 h and 72 h *in vitro* in the absence of insulin to confirm whether dcOC affects glucose uptake and to verify whether PI3K/Akt and HIF-1 α are involved in this process.

MATERIALS AND METHODS

Materials

MG63, HEK-293, and Jurkat cells were purchased from American Type Culture Collection. Synthetic human dcOC was purchased from Creative BioMart (United States). Antibodies specific for p-AKT (Ser473), AKT, HIF-1 α , GLUT1, and Runx2 were purchased from Cell Signaling Technology.

Cell culture and treatment

Synthetic human dcOC was freshly resuspended and diluted in phosphate-buffered saline to the desired final concentrations before the experiments. MG63, HEK-293, and Jurkat cells were cultured in low-glucose Dulbecco's modified Eagle's medium (L-DMEM; 1000 mg/L glucose, HyClone, United States), high-glucose Dulbecco's modified Eagle's medium (H-DMEM; 4500 mg/L glucose, HyClone), and complete RPMI 1640 medium (HyClone), respectively. All media were supplemented with 10% fetal bovine serum (FBS, HyClone, United States) and 1% Pen-Strep, and cultures were maintained at 37 °C in a humidified atmosphere with 5% CO₂. When the cells were 70% confluent, the medium was replaced with L-DMEM containing 4% FBS and different concentrations of dcOC (0, 0.3, 3, 10, and 30 ng/mL). When MG63 cells were treated with different concentrations of dcOC solution for 72 h, the culture medium was changed daily. After cells were treated for 1 h or 72 h, glucose uptake and Western blot analyses were performed to determine the optimal concentration of dcOC.

For the PI3K inhibition assay, cells were treated with the PI3K inhibitor LY294002 (10 μ mol/L, Cayman Chemical Inc., Michigan, United States) or 0.1% dimethyl sulfoxide as the vehicle control for 20 min and then treated with dcOC for 1 h.

Glucose uptake assay with 2-deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose

A glucose uptake assay was performed according to a previously described method with minor modifications[21]. MG63 cells were plated at a density of 1×10^6 cells per well (for the 1 h dcOC treatment) or 1×10^5 cells per well (for the 72 h dcOC treatment) in 6-well plates and used at subconfluence. After 24 h of incubation, the culture medium was replaced with 2.5 mL of culture medium containing various concentrations of dcOC (0, 0.3, 3, 10, or 30 ng/mL) and incubated for 1 h or 72 h. The medium was then removed, and the cells were washed twice with precooled Krebs Ringer buffer (KRB). Fresh culture medium containing 100 μ mol/L 2-deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose (2-NBDG, Creative BioMart Inc., New York, NY, United States), a fluorescent glucose analog, was added to the cells and incubated at 37 °C for 30 min in a humidified atmosphere with 5% CO₂. 2-NBDG uptake was stopped

by removal of the incubation medium, and the cells were washed twice with precooled KRB. The cells were trypsinized and resuspended in 2.0 mL of precooled fresh growth medium. For each measurement, data from 10000 single-cell events were recorded by flow cytometry (FACSCalibur, BD, United States). Second, cells were plated at a density of 1×10^5 cells per well in 6-well plates and used at subconfluence after 24 h of incubation. The culture medium was then removed from each well and replaced with 2.5 mL of culture medium containing dcOC (0, 0.3, 3, 10, or 30 ng/mL) for 72 h of preincubation. The subsequent steps were the same as those listed above. The optimal concentration at dcOC affected glucose uptake was determined by these experiments. The experiment was performed in triplicate, and the experimental data were analyzed using FlowJo software. The geometric mean was used to determine the mean fluorescence intensity (MFI). The average fluorescence intensity of each group was compared with that of the control group to obtain the normalized fluorescence intensity (AU), which indicated the glucose uptake ability of MG63 cells.

SiRNA-mediated silencing of HIF-1 α

MG63 cells were grown and transfected with either HIF-1 α siRNA (Sangon Biotech, Shanghai, China) or negative control siRNA using the transfection reagent Lipofectamine 2000 (Invitrogen, Carlsbad, CA, United States) according to the manufacturer's instructions. After transfection, the medium was replaced with regular medium, and the cells were treated with dcOC for 72 h. Glucose uptake and Western blot assays were then performed.

PI3K inhibition assay

MG63 cells were treated with the PI3K inhibitor LY294002 (10 μ mol/L) for 30 min and then with dcOC for 1 h. Then, glucose uptake and Western blot assays were performed in triplicate. The glucose uptake data were analyzed using FlowJo software. The geometric mean was used to determine the MFI.

Western blot analysis

The levels of GPRC6A, p-AKT (Ser473), AKT, HIF-1 α , GLUT1, and Runx2 in MG63 cells were determined. For analysis of GPRC6A expression, HEK-293 cells were used as the negative control[22], and Jurkat cells were used as the positive control. Cell samples were homogenized on ice in lysis buffer containing protease and phosphatase inhibitors. A bicinchoninic acid protein assay was used to determine the protein concentration according to the manufacturer's instructions (Beyotime Institute of Biotechnology, China). All steps were performed as previously described[23]. Immunoblotting was performed using primary antibodies against GPRC6A (Absin Bioscience Inc., China) and horseradish peroxidase-conjugated anti-rabbit and anti-mouse secondary antibodies (Cell Signaling Technology). Immunoreactions were visualized with enhanced chemiluminescence reagents (GE Healthcare, UK, Ltd.). The band intensities were determined using ImageJ analysis software (NIH).

Cell proliferation assay

A Cell Counting Kit-8 (CCK-8, Tongren, China) assay was used to assess the effects of dcOC on MG63 cell proliferation. In brief, cells were plated in 96-well plates (4000 cells per well) in L-DMEM supplemented with 4% serum containing normal (5.5 mmol/L) levels of glucose and treated with various concentrations of dcOC (0, 0.3, 3, 10, and 30 ng/mL) for 24, 48, or 72 h. The absorbance values were read at 450 nm using an automated microplate reader (Power Waves XS, BioTek, United States).

Alkaline phosphatase activity assay

The rate of p-nitrophenyl phosphate (Sigma) hydrolysis was analyzed to measure alkaline phosphatase (ALP) activity. Cells were plated in 24-well plates at a density of 1×10^5 cells per well and incubated overnight. Then, the cells were incubated with solutions containing various concentrations of dcOC for 72 h. The medium was removed, and 500 μ L of 0.1% Triton X-100 (Sigma) was added to each well. Cells were frozen at -70 °C, thawed at 37 °C, and centrifuged at 14000 g and 4 °C for 10 min. The supernatant was collected for ALP activity measurement. The absorbance values at 405 nm were read on a microplate reader (Power Waves XS, BioTek, United States). The Bradford method was used to determine the protein concentration.

Statistical analysis

Every experiment was performed at least three times. Data are presented as the mean \pm SD. The results were analyzed by one-way analysis of variance (ANOVA) followed

by the LSD method for multiple comparisons using the statistical software SPSS 22.0. A *P* value of < 0.05 was considered statistically significant.

RESULTS

Evidence of GPRC6A receptor expression in MG63 cells

Previous studies have indicated that GPRC6A is expressed in bones and osteoblasts [24] of mice. We examined the expression of GPRC6A in MG63 cells by Western blot. Because previous experiments confirmed that HEK-293 cells lack GPRC6A expression [5], they were selected as the negative control, while Jurkat cells served as the positive control. Western blot analysis confirmed that MG63 cells expressed the GPRC6A receptor (Figure 1), thereby indicating that the roles of dcOC in MG63 cells could be examined.

DcOC increases glucose uptake in MG63 cells

The normalized fluorescence intensity (AU) of MG63 cells was significantly increased compared with that of the paired control cells after short-term (1 h) treatment with dcOC at different concentrations (0.3, 3, and 10 ng/mL groups, *P* < 0.01; 30 ng/mL group, *P* < 0.05; Figure 2A and B). In addition, 3 ng/mL was determined to be the optimal concentration for short-term (1 h) stimulation. Treatment with 3 ng/mL dcOC (1 h) increased glucose intake by 79% compared with that in the control group (*P* < 0.01; Figure 2B). In addition, the normalized fluorescence intensity (AU) of MG63 cells was significantly increased compared with that of paired control cells after long-term (72 h) treatment with dcOC at different concentrations (0.3, 3, and 10 ng/mL groups, *P* < 0.01; 30 ng/mL group, *P* < 0.05; Figure 2C and D). Additionally, 10 ng/mL was determined to be the optimal concentration for long-term (72 h) stimulation. Treatment with 10 ng/mL dcOC (72 h) increased glucose intake by 81% compared with that in the control group (*P* < 0.01; Figure 2D).

Involvement of the PI3K/Akt pathway in the promotional effect of dcOC on glucose uptake after short-term stimulation

As shown in Figure 3A and B, dcOC triggered Akt phosphorylation in a dose-dependent manner, and the most effective stimulatory concentration was 3 ng/mL in the short term (1 h) (*P* < 0.01). The protein expression of p-Akt (Ser473) in the 3 ng/mL group was increased by 2.99-fold compared to that in the 0 ng/mL group, as assessed relative to the level of Akt, after 1 h of dcOC stimulation (*P* < 0.01; Figure 3B). However, no significant changes were observed in the expression levels of GPRC6A, HIF-1 α , GLUT1, or Runx2 as assessed relative to the level of β -actin (Figure 3B). Moreover, inhibition of PI3K with LY294002 abolished the dcOC-mediated promotion of Akt phosphorylation (Figure 3C and D) and 2-NBDG uptake (Figure 3E and F) without affecting GLUT1 protein expression (Figure 3C and D), indicating that PI3K/Akt signaling is involved in the enhancement of dcOC-induced glucose uptake for a short period (1 h).

Involvement of HIF-1 α in the promotional effect of dcOC on glucose uptake after long-term stimulation

Long-term dcOC stimulation not only triggered Akt phosphorylation but also increased the protein levels of HIF-1 α , GLUT1, and Runx2 in a dose-dependent manner (Figure 4B), whereas no increase in the expression level of GPRC6A was observed (Figure 4A and B). The most effective stimulatory concentration of dcOC was 10 ng/mL. The Western blot results indicated that the protein expression of p-Akt in the 10 ng/mL group was increased by 1.93-fold compared to that in the 0 ng/mL group, as assessed relative to the level of Akt, after 72 h of dcOC stimulation (*P* < 0.01, Figure 4B). The protein expression of HIF-1 α , GLUT1, and Runx2 in the 10 ng/mL group was increased by 2.32-fold (*P* < 0.01, Figure 4B), 1.40-fold (*P* < 0.05, Figure 4B), and 2.06-fold (*P* < 0.01, Figure 4B), respectively, compared to that in the 0 ng/mL group, as assessed relative to the level of β -actin. Then, HIF-1 α siRNA was used to decrease the HIF-1 α protein levels in MG63 cells (*P* < 0.05, *vs* the control group, Figure 4D). Inhibition of HIF-1 α with siRNA abolished dcOC-mediated 2-NBDG uptake (Figure 4E and F) and substantially decreased the GLUT1 protein expression (Figure 4C and D), indicating that HIF-1 α signaling is involved in the promotional effect of dcOC on glucose uptake *via* GLUT1 modulation.

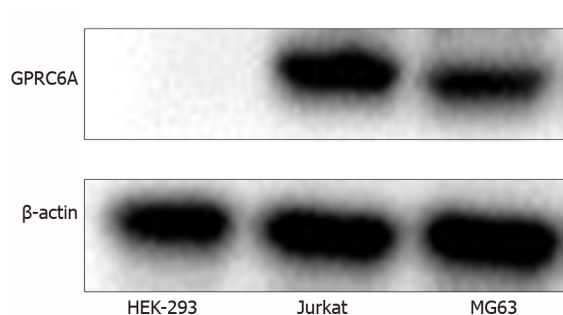


Figure 1 Western blot analysis demonstrating the protein expression of G protein-coupled receptor family C group 6 subtype A in MG63 cells. HEK-293 cells were selected as the negative control cells, and Jurkat cells were used as the positive control cells. GPRC6A: G protein-coupled receptor family C group 6 subtype A.

Biological effect of dcOC on MG63 cells

According to the cell proliferation assay results, the average cell counts for each day were plotted as a histogram. In the presence of dcOC, the number of cells was increased at 24, 48, and 72 h (Figure 5A). These results demonstrate that dcOC enhances MG63 cell proliferation in a time- and dose-dependent manner. DcOC had the most marked effect on proliferation at a concentration of 10 ng/mL ($P < 0.01$, Figure 5A). The ALP activity assay results showed that treatment with either 3 ng/mL or 10 ng/mL dcOC affected ALP activity in MG63 cells after 72 h ($P < 0.01$, Figure 5B).

DISCUSSION

An increasing number of studies have shown that GluOC is closely related to energy metabolism[25,26]. *In vitro* experiments showed that different doses of GluOC could increase glucose uptake in various cells with or without insulin[11,12]. Glucose uptake is mediated by transmembrane GLUT proteins in cells[27]. Among these transporters, GLUT1 is closely related to the energy metabolism of tumor cells. The increase in glucose uptake by tumor cells is closely related to their proliferation[28]. Previous studies have shown that the expression of GLUT1 affects the prognosis of patients with osteosarcoma[29,30]. In addition, Fan *et al*[31] reported that interfering with GLUT1 expression may inhibit the proliferation of MG63 cells *in vitro*. Our study explored the relationship between dcOC, a type of GluOC, and glucose uptake in osteoblastic sarcoma cells *in vitro* and the possible association of this effect with GLUT1. Although MG63 cells synthesize GluOC, the level of GluOC synthesized by MG63 cells without retinoic acid intervention and $1\alpha,25$ -dihydroxycholecalciferol [$1\alpha,25(\text{OH})_2\text{D}$], as shown in previous studies[32], was negligible compared with the level of exogenous dcOC in our study. In addition, the concentration of dcOC used in our study was confirmed to increase glucose uptake in the previous study[11].

As the receptor for GluOC, GPRC6A plays an important role in the regulation of glucose metabolism by GluOC in histiocytes[6,10]. The expression of GPRC6A in human osteoblasts was confirmed by scholars as early as 1998[33]. In the present study, we confirmed the expression of GPRC6A in MG63 cells (Figure 1), which provided a basis to study the effect of dcOC on the metabolic response. In our study, both short- and long-term dcOC intervention altered the glucose uptake by MG63 cells but did not change the protein level of GPRC6A. We speculate that dcOC may affect the signaling pathway downstream of GPRC6A by altering the protein conformation of GPRC6A, thereby affecting the glucose uptake of MG63 cells. However, further investigation is needed to confirm this hypothesis.

Hill *et al*[11] showed that short-term intervention with carboxylated osteocalcin in adipocytes could increase the glucose uptake and transport in a cell-based system (in an insulin-independent manner). GLUT1 is the main glucose transporter in osteoblasts[15]. Activation of the PI3K/Akt signaling pathway has been confirmed to be necessary for GLUT1 translocation, cell glucose uptake, and maintenance of cell surface GLUT1 Levels[18]. Application of a PI3K inhibitor can effectively inhibit the expression of GLUT1 on the cell membrane, thereby affecting the uptake of glucose in cells[34]. A previous study showed that ucOC could increase the phosphorylation of Akt in adipocytes in an insulin-independent manner[12]. In our study, short-term incubation (1 h) of MG63 cells with dcOC promoted glucose uptake under

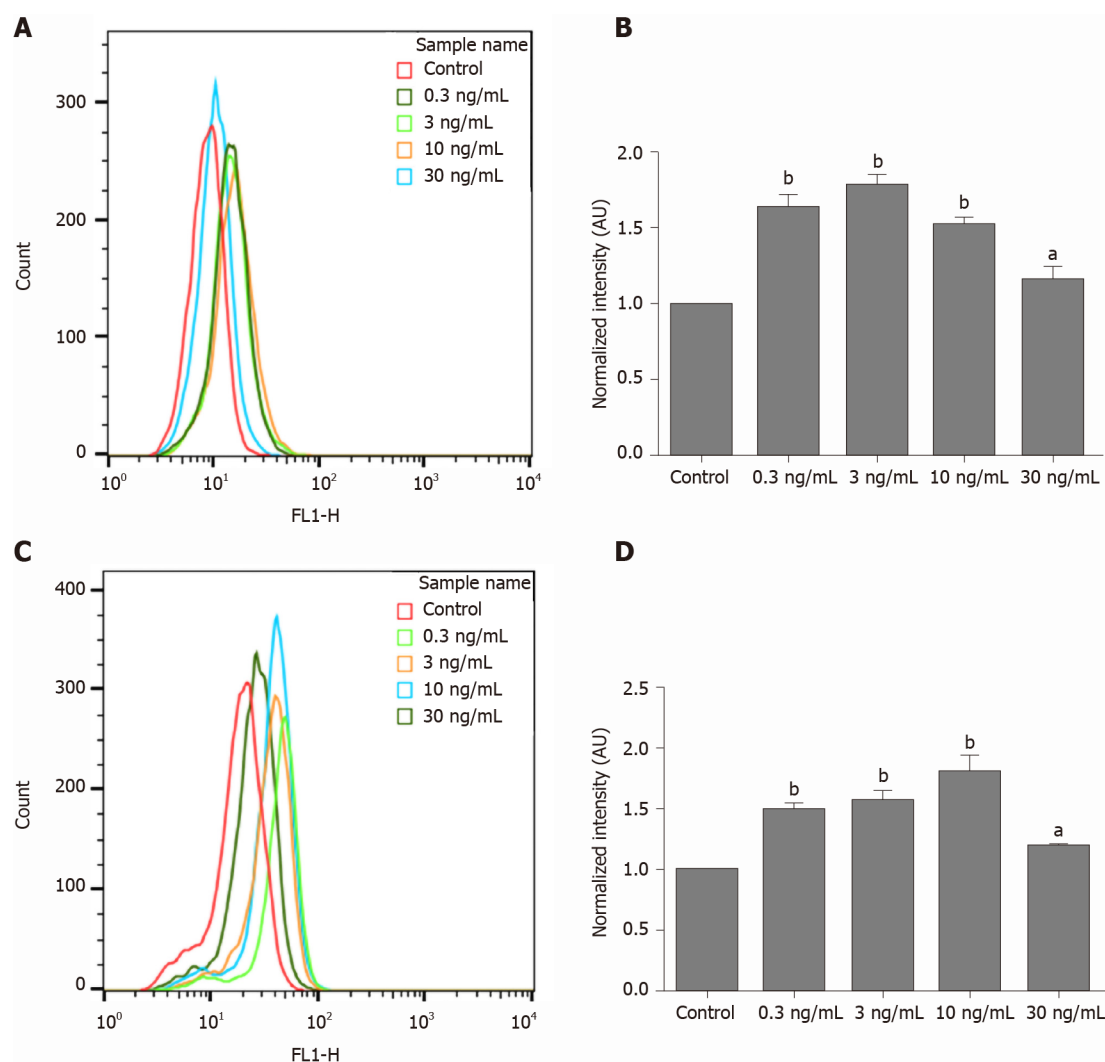


Figure 2 Flow cytometric analyses of 2-deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose uptake by MG63 cells after decarboxylated osteocalcin stimulation. A: The distribution of fluorescence intensities which represented 2-Deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose (2-NBDG) uptake after decarboxylated osteocalcin (dcOC) stimulation for 1 h; B: The normalized fluorescence intensities corresponding to 2-NBDG uptake after dcOC stimulation for 1 h; C: Distribution of fluorescence intensities which represented 2-NBDG uptake after dcOC stimulation for 72 h; D: The normalized fluorescence intensity corresponding to 2-NBDG uptake after dcOC stimulation for 72 h. The red lines in the histograms in A and C indicate the control group (0 ng/mL), while the other lines indicate the groups treated with dcOC at different concentrations. The data are representative of three independent experiments performed in triplicate. ^a $P < 0.05$, ^b $P < 0.01$ vs the control group.

physiological glucose conditions in an insulin-independent manner (Figure 2A and B). In addition, the phosphorylation of AKT was increased significantly in MG63 cells incubated with dcOC for a short time, although the GLUT1 expression was not affected (Figure 3A and B), suggesting that short-term dcOC treatment increases the glucose uptake rate, probably by regulating GLUT1 activity and transport *via* PI3K/Akt rather than by increasing the protein expression of GLUT1. Then, we used the PI3K inhibitor LY294002 to reduce the phosphorylation of Akt and found that the effect of dcOC on increasing glucose uptake was abolished (Figure 3C-F). This result confirmed that the PI3K/Akt signaling pathway participates in dcOC, promoting glucose uptake in MG63 cells. In addition to GLUT1, GLUT3 and GLUT4 have also been reported to be expressed in osteoblasts[15]. The increase in Akt phosphorylation is related to increases in GLUT3 and GLUT4 translocation and protein expression levels[35,36]. DcOC may increase glucose uptake by increasing the GLUT3 or GLUT4 translocation or protein expression in MG63 cells after short-term intervention, but further research is needed to confirm this hypothesis. Moreover, the expression of GPRC6A was not altered by short-term treatment with dcOC, suggesting that short-term dcOC intervention induces glucose uptake in MG63 cells by altering the activity or configuration of the receptor GPRC6A rather than its expression.

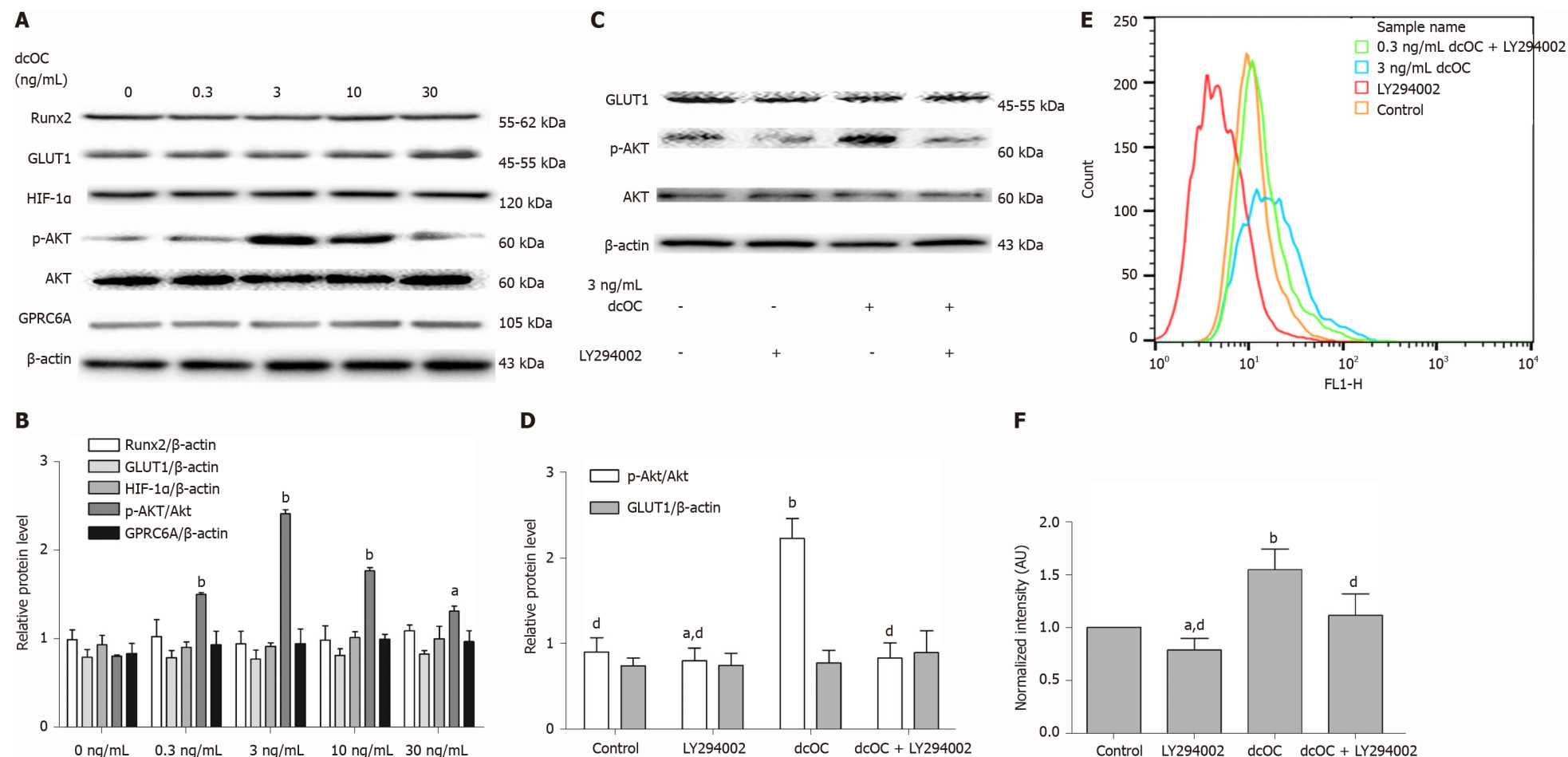


Figure 3 Promotional effect of decarboxylated osteocalcin on glucose uptake after short-term stimulation (1 h) in MG63 cells. A: Protein bands; B: Relative protein levels of GPRC6A (G protein-coupled receptor family C group 6 subtype A), p-Akt (Ser473)/Akt, hypoxia-inducible factor 1 alpha, glucose transporter 1 (GLUT1), and Runx2 after decarboxylated osteocalcin (dcOC) stimulation for 1 h at different concentrations. C: Protein bands; D: Relative protein levels of p-Akt (Ser473)/Akt and GLUT1. E: The distribution of fluorescence intensities which represented 2-Deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose (2-NBDG) uptake; F: The normalized fluorescence intensity corresponding to 2-NBDG uptake. The MG63 cells in C-F were treated with dcOC (3 ng/mL) for 1 h and (or) LY294002 (10 μmol/L) for 30 min. The data are representative of three independent experiments performed in triplicate. B: ^a*P* < 0.05, ^b*P* < 0.01 vs untreated cells; D and F: ^a*P* < 0.05, ^b*P* < 0.01 vs the control group; ^c*P* < 0.05, ^d*P* < 0.01 vs the dcOC-only group. dcOC: Decarboxylated osteocalcin; HIF-1α: Hypoxia-inducible factor 1 alpha; GLUT1: Glucose transporter 1; GPRC6A: G protein-coupled receptor family C group 6 subtype A.

Next, we validated the effect of glucose uptake on MG63 cells with long-term dcOC intervention (72 h). Similar to the short-term stimulation, the long-term stimulation of MG63 cells with dcOC also promoted glucose uptake under physiological glucose conditions in an insulin-independent manner (Figure 2C and D), accompanied by a

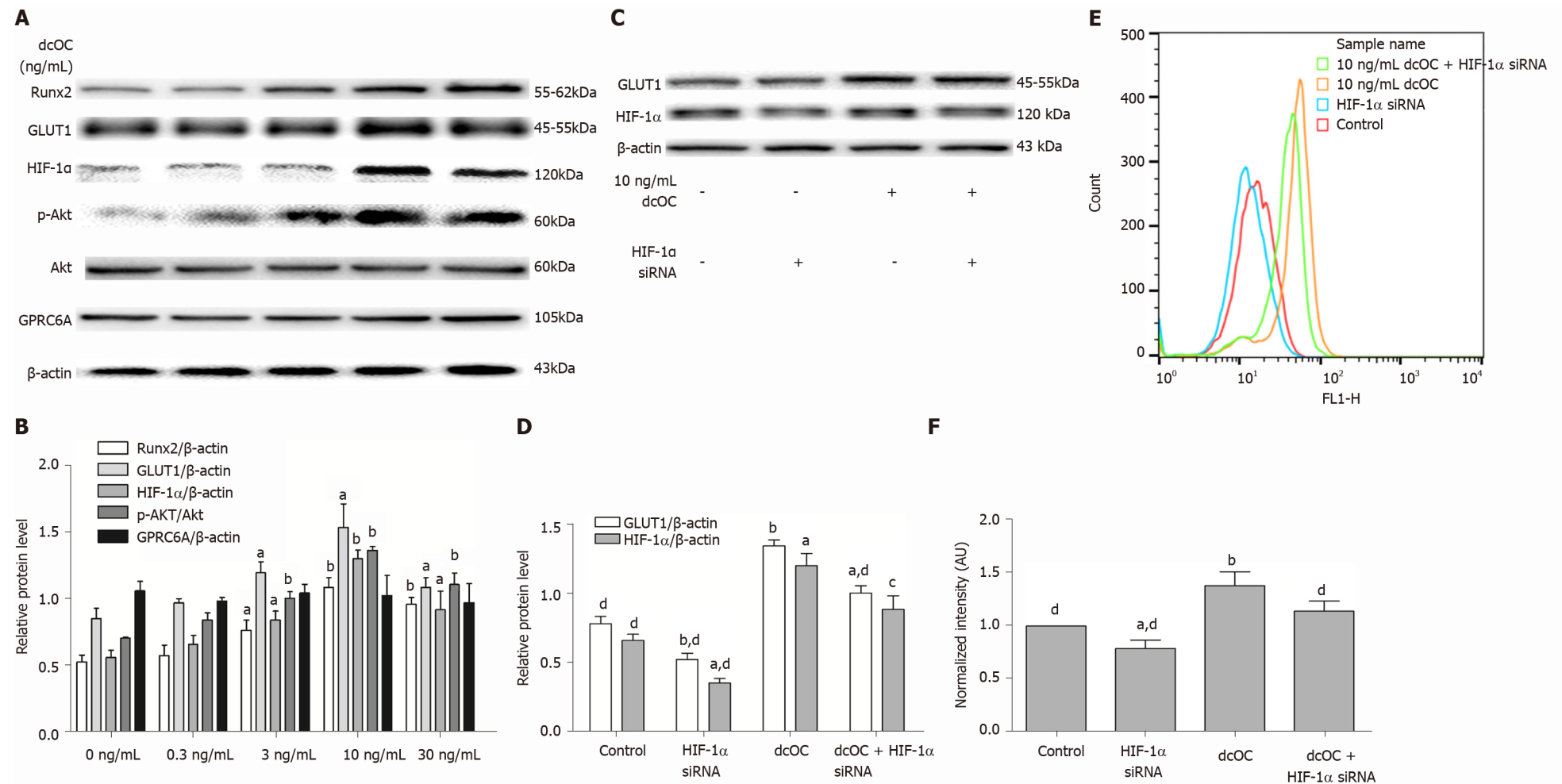


Figure 4 Promotional effect of decarboxylated osteocalcin on glucose uptake after long-term stimulation (72 h) in MG63 cells. A: Protein bands; B: Relative protein levels of GPRC6A (G protein-coupled receptor family C group 6 subtype A), p-Akt (Ser473)/Akt, hypoxia-inducible factor 1 alpha (HIF-1α), glucose transporter 1 (GLUT1), and Runx2 after decarboxylated osteocalcin (dcOC) stimulation for 72 h at different concentrations; C: Protein bands; D: Relative protein levels of HIF-1α and GLUT1; E: The distribution of fluorescence intensities which represented 2-Deoxy-2-[(7-nitro-2,1,3-benzoxadiazol-4-yl)amino]-D-glucose (2-NBDG) uptake; F: The normalized fluorescence intensity corresponding to 2-NBDG uptake. The MG63 cells in C-F were treated with dcOC (10 ng/mL) 72 h and (or) were transfected with HIF-1α siRNA. The data are representative of three independent experiments performed in triplicate. B: ^a*P* < 0.05, ^b*P* < 0.01 vs untreated cells; D and F: ^a*P* < 0.05, ^b*P* < 0.01 vs the control group; ^c*P* < 0.05, ^d*P* < 0.01 vs the dcOC-only group. dcOC: Decarboxylated osteocalcin; HIF-1α: Hypoxia-inducible factor 1 alpha; GLUT1: Glucose transporter 1; GPRC6A: G protein-coupled receptor family C group 6 subtype A.

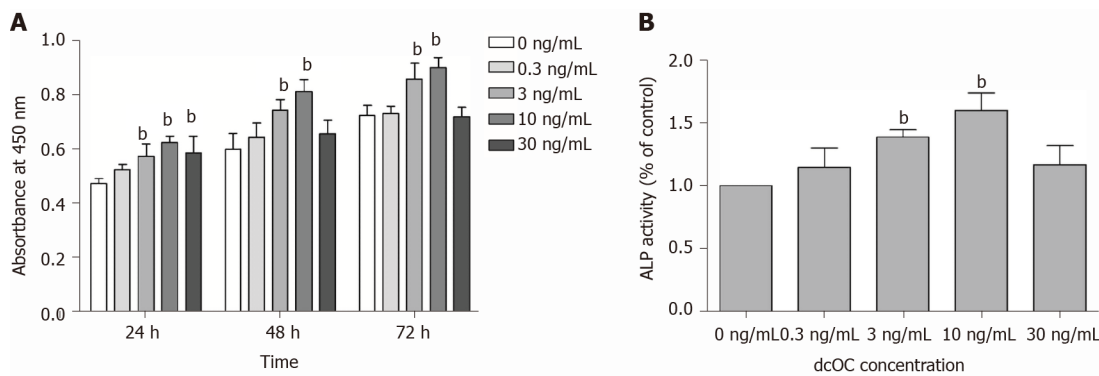


Figure 5 Effects of decarboxylated osteocalcin on the proliferation and alkaline phosphatase activity in MG63 cells. A: Histogram showing the effects of decarboxylated osteocalcin (dcOC) on MG63 cell proliferation. The absorbance value was measured at 24, 48, and 72 h; B: Alkaline phosphatase activity in MG63 cells after 72 h of incubation with different concentrations of dcOC. Significant differences ($P < 0.01$) were found between the dcOC treatment groups (3 ng/mL and 10 ng/mL) and the control group (0 ng/mL). The data are representative of three independent experiments performed in triplicate. ^a $P < 0.05$, ^b $P < 0.01$ vs the control group (0 ng/mL). dcOC: Decarboxylated osteocalcin; ALP: Alkaline phosphatase.

significantly increased p-AKT level (Figure 4A and B). However, long-term stimulation significantly increased the protein expression levels of HIF-1 α and GLUT1 in MG63 cells treated with different concentrations of dcOC, suggesting that dcOC can increase the glucose uptake rate, probably by regulating GLUT1 protein expression after incubation for an extended duration (Figure 4A and B). Then, we silenced HIF-1 α *via* siRNA and found that the effect of dcOC on increasing glucose uptake was abolished, with decreased expression of HIF-1 α and GLUT1 (Figure 4C-F). HIF-1 is a transcription factor that mediates the adaptive response, which enhances the energy metabolism of cancer cells. HIF-1 is composed of two subunits, HIF-1 α and HIF-1 β , among which HIF-1 α determines the activity of HIF-1. HIF-1 α is closely related to GLUT1 in tumor cells. For example, HIF-1 α can upregulate the protein expression of GLUT1[37], and silencing or inhibiting HIF-1 α in tumor cells can decrease the expression of GLUT1[38,39]. Previous studies have shown that HIF-1 α plays an important role in the growth of osteosarcoma[40,41]. The results of our study suggested that dcOC promotes the glucose uptake in MG63 cells after incubation for an extended duration by upregulating the protein expression of GLUT1. Using HIF-1 α siRNA, we demonstrated that GLUT1 expression induced by dcOC is dependent on HIF-1 α in MG63 cells. Therefore, these results support a new perspective on the modulation of GLUT1 expression by HIF-1 α in response to dcOC in MG63 cells.

Runx2 is an essential transcription factor for osteoblast differentiation, matrix production, and mineralization during bone formation[42]. It controls the expression of bone formation-related genes such as *OCN*, *ALP*, *BMP2*, and *BMP4*[43]. In this study, short-term intervention with dcOC in MG63 cells did not change the protein expression of Runx2 (Figure 3A and B), while long-term dcOC intervention significantly increased the protein expression of Runx2 (Figure 4A and B). The optimal concentration was consistent with that required to increase GLUT1 expression (10 ng/mL) (Figure 4A and B). Runx2 expression has been reported to be significantly increased in human osteosarcoma tissues and osteosarcoma cell lines[44]. Runx2 is closely related to osteosarcoma metastasis, and downregulation of Runx2 was found to inhibit osteosarcoma metastasis and invasion[45]. Here, we speculated that long-term intervention with dcOC influenced osteoblastic osteosarcoma cell metastasis and invasion by increasing glucose uptake, which was achieved by increasing the expression of GLUT1.

In our study, dcOC promoted the proliferation of MG63 cells (Figure 5A). Bone formation and osteoblast proliferation are energy-expensive processes, and the energy for osteoblast proliferation is generated mainly *via* glucose metabolism[14]. Because GLUT1 is the key glucose transporter regulating glucose uptake[46], we speculated that the ability of dcOC to increase MG63 cell proliferation is closely related to its ability to improve glucose metabolism.

ALP is a major enzyme expressed during the early maturation of osteoblasts. UcOC has been reported to increase ALP activity in bone marrow mesenchymal stem cells (BMSCs)[47]. In our study, the ALP activity in MG63 cells was increased after dcOC treatment for 72 h (Figure 5B), consistent with the results of a previous study. Moreover, previous studies have shown that increased serum ALP concentrations are indicative of a worse prognosis in osteosarcoma, correlating with shorter survival

times and disease-free intervals[48-50]. The results of our study indicated that dcOC might affect the prognosis of osteosarcoma patients by increasing the ALP activity in osteoblast-like osteosarcoma cells. However, the specific mechanism by which dcOC increases ALP activity is not clear and needs to be further investigated.

GluOC has been suggested to be closely related to energy metabolism and can increase glucose uptake in various cells[10-13]. In animal experiments, GluOC has been proven to reduce blood glucose levels and visceral fat in mice with type 2 diabetes[8,9]. GluOC is considered a potential agent for the treatment of type 2 diabetes and insulin resistance. The present study clearly showed that dcOC, a type of GluOC, promoted glucose uptake in MG63 cells *in vitro*. dcOC may affect the invasion and migration of MG63 cells and the prognosis of osteosarcoma patients by affecting the ALP activity and Runx2 expression in osteoblastic sarcoma cells. Thus, while considering dcOC as a potential treatment for type 2 diabetes, it is also necessary to be aware of its possible adverse effects on osteoblastic osteosarcoma.

CONCLUSION

DcOC can promote glucose uptake in MG63 cells *in vitro*. DcOC may affect the invasion and migration of MG63 cells and the prognosis of osteosarcoma patients by affecting ALP activity and Runx2 expression.

ARTICLE HIGHLIGHTS

Research background

Uncarboxylated osteocalcin (GluOC) has been reported to improve glucose metabolism, prevent type 2 diabetes, and decrease the severity of obesity in mice with type 2 diabetes. GluOC can increase glucose uptake in a variety of cells. GluOC has great potential to become a new drug for the treatment of type 2 diabetes in the future.

Research motivation

Glucose metabolism is the main source of energy for osteoblast proliferation and differentiation. However, both the direct effects of GluOC on glucose uptake in bone tissues and the underlying mechanisms remain unexplored.

Research objectives

To investigate the effects of decarboxylated osteocalcin (dcOC), a kind of GluOC, on glucose uptake in human osteoblast-like osteosarcoma cells and the possible signaling pathways involved.

Research methods

MG63 cells (human osteoblast-like osteosarcoma cells) were treated with dcOC (0, 0.3, 3, 10, or 30 ng/mL) for 1 and 72 h, and glucose uptake was measured by flow cytometry. The effect of dcOC on cell proliferation was measured with a CCK-8 assay, and alkaline phosphatase (ALP) enzyme activity was measured. PI3K was inhibited with LY294002, and hypoxia-inducible factor 1 alpha (HIF-1 α) was silenced with siRNA. Then, the G protein-coupled receptor family C group 6 subtype A, total Akt, phosphorylated Akt, HIF-1 α , and glucose transporter 1 (GLUT1) levels were measured by Western blot to elucidate the possible pathways by which dcOC modulates glucose uptake.

Research results

The glucose uptake of MG63 cells was significantly increased compared with that of the paired control cells after short-term (1 h) treatment and long-term (72 h) treatment with dcOC at different concentrations. LY294002 abolished the dcOC-mediated (1 h) promotion of Akt phosphorylation and glucose uptake without affecting GLUT1 protein expression. Long-term dcOC stimulation triggered Akt phosphorylation and increased the protein levels of HIF-1 α , GLUT1, and Runx2 in a dose-dependent manner. Inhibition of HIF-1 α abolished the dcOC-mediated glucose uptake and substantially decreased GLUT1 protein expression. DcOC intervention promoted cell proliferation in a time- and dose-dependent manner. Treatment with dcOC affected the ALP activity in MG63 cells.

Research conclusions

DcOC can promote glucose uptake in MG63 cells *in vitro*. DcOC may affect the invasion and migration of MG63 cells and the prognosis of osteosarcoma patients by affecting ALP activity and Runx2 expression.

Research perspectives

DcOC can promote glucose uptake in human osteoblast-like osteosarcoma cells. It is necessary to be aware of its possible adverse effects on osteoblastic osteosarcoma while considering dcOC as a potential treatment for type 2 diabetes.

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Basic Study

Expression and role of P-element-induced wimpy testis-interacting RNA in diabetic-retinopathy in mice

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Abstract

BACKGROUND

As one of the major microvascular complications of diabetes, diabetic retinopathy (DR) is the leading cause of blindness in the working age population. Because the extremely complex pathogenesis of DR has not been fully clarified, the occurrence and development of DR is closely related to tissue ischemia and hypoxia and neovascularization. The formation of retinal neovascularization (RNV) has great harm to the visual acuity of patients.

AIM

To investigate the expression of P-element-induced wimpy testis-interacting RNA (piRNA) in proliferative DR mice and select piRNA related to RNV.

METHODS

One hundred healthy C57BL/6J mice were randomly divided into a normal group as control group (CG) and proliferative DR (PDR) group as experimental group (EG), with 50 mice in each group. Samples were collected from both groups at the same time, and the lesions of mice were evaluated by hematoxylin and eosin staining and retinal blood vessel staining. The retinal tissues were collected for second-generation high-throughput sequencing, and the differentially expressed piRNA between the CG and EG was detected, and polymerase chain reaction (PCR) was conducted for verification. The differentially obtained piRNA target genes and expression profiles were enrichment analysis based on gene annotation (Gene Ontology) and Kyoto Encyclopedia of Genes and Genomes.

RESULTS

In the CG there was no perfusion area, neovascularization and endothelial nucleus broke through the inner boundary membrane of retina. In the EG, there

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were a lot of nonperfused areas, new blood vessels and endothelial nuclei breaking through the inner boundary membrane of the retina. There was a statistically significant difference in the number of vascular endothelial nuclei breaking through the inner retinal membrane between the two groups. High-throughput sequencing analysis showed that compared with the CG, a total of 79 piRNAs were differentially expressed in EG, among which 43 piRNAs were up-regulated and 36 piRNAs were down-regulated. Bioinformatics analysis showed that the differentially expressed piRNAs were mainly concentrated in the signaling pathways of angiogenesis and cell proliferation. Ten piRNAs were selected for PCR, and the results showed that the expression of piR-MMU-40373735, piR-MMU-61121420, piR-MMU-55687822, piR-MMU-1373887 were high, and the expression of piR-MMU-7401535, piR-MMU-4773779, piR-MMU-1304999, and piR-MMU-5160126 were low, which were consistent with the sequencing results.

CONCLUSION

In the EG, the abnormal expression of piRNA is involved in the pathway of angiogenesis and cell proliferation, suggesting that piRNAs have some regulatory function in proliferative diabetic-retinopathy.

Key Words: P-element-induced wimpy testis-interacting RNA; P-element-induced wimpy testis protein; High-throughput sequencing; Neovascularization; Diabetic retinopathy in mice; Bioinformatics

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Core Tip: As one of the major microvascular complications of diabetes, diabetic retinopathy is the leading cause of blindness in the working age population. In the diabetic retinopathy model, the abnormal expression of P-element-induced wimpy testis-interacting RNAs (piRNAs) are involved in angiogenesis and cell proliferation pathways, suggesting that piRNAs have a certain regulatory function in diabetic retinopathy.

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INTRODUCTION

As one of the major microvascular complications of diabetes, diabetic retinopathy (DR) is the leading cause of blindness in working age population. Because the extremely complex pathogenesis of DR has not been fully clarified, the occurrence and development of DR is closely related to tissue ischemia and hypoxia and neovascularization[1,2]. The formation of retinal neovascularization (RNV) has great harm to the visual acuity of patients. Patients who are refractory to treatment may experience serious complications, such as neovascular glaucoma, vitreous hemorrhage, and retinal detachment which can lead to permanent blindness. RNV is a key link in proliferative DR (PDR) and is a complex pathological process. Intravitreal injection of anti-vascular endothelial growth factor (VEGF) is an effective method for treating ocular neovascular diseases. However, the procedure can result in complications, side effects, and only short-term effects. Previous studies reported that anti-VEGF treatment cannot prevent the formation of RNV in some patients[3,4]. Therefore, it is particularly important to find other VEGF-independent pathways that promote angiogenesis to identify safe therapeutic targets against DR.

P-element-induced wimpy testis (PIWI)-interacting RNA (piRNA) was first found in the ovarian germ cells of *Drosophila melanogaster* in 2006. This novel short non-coding small RNA has an average length of 26-31 nucleotides[5] and functions by binding with PIWI protein to form a piRNA-induced silencing complex (PIRISC)[6-8]. piRNA plays an important role in transposon silencing, epigenetic regulation, protein

regulation of genome rearrangement, spermatogenesis, and germ stem cell maintenance[9,10]. Additionally, piRNA participates in tumor formation, human aging, and neural axon regeneration[11-13]. Based on existing studies and literature reports, which highlight the role of piRNA in neovascularization-related diseases[14, 15], piRNA may play an important role in the formation and development of DR. However, to the best of our knowledge, no previous study has explored this hypothesis. In the present study, the role of piRNA in RNV diseases was evaluated by sequencing of RNA obtained from the retinal tissues of mice with PDR mice and normal mice. The study aimed to provide theoretical support for the possible alternative clinical treatment of DR.

MATERIALS AND METHODS

Experimental animals and models

We used 100 7-d-old C57 mice of either sex in this study. All experimental animals were purchased from Changsheng Biology Co., Ltd. (Shenyang, China). The animals were fed and related operations were conducted in the animal laboratory of Shengjing Hospital in a stable, specific pathogen-free environment; the temperature was maintained at $23 \pm 2^{\circ}\text{C}$, with a 12 h light cycle. The experimental study was approved by the animal ethics committee of Shengjing Hospital of China Medical University (2020PS078K).

The animals were randomly divided into two groups, each consisting of 50 animals: normal group as control group (CG) and PDR group as experimental group (EG). Mice in CG were fed with mice and their mothers under normal conditions without any treatment. Briefly, 7-d-old EG mice and their mothers were housed and fed in a closed glass container with an oxygen concentration of $75\% \pm 2\%$ for 5 d. Next, 12-d-old mice were fed under normal conditions, and the closed container was opened once per day to replace the bedding material, add water, and replace the mother mice[16,17]. All animals were euthanized at the age of 17 d for subsequent histopathological examination and total RNA extraction.

Retinal patch staining

Mice aged 17 d from the two groups were anesthetized and sacrificed, after which their eyeballs were removed. The eyeballs were fixed in 4% paraformaldehyde for 12 h. The contents of the anterior segment and vitreous cavity were removed, and the retina was carefully separated. The retinas were incubated in isolectin B4-594 (Invitrogen, Carlsbad, CA, United States) in a shaker at 4°C overnight. Next, the glass slide was covered with an anti-radiation agent, and this agent was also applied to the retina[18]. The retinas were observed under a microscope (Eclipse NI, Nikon, Tokyo, Japan) and images were collected.

Hematoxylin and eosin staining

After the eyeballs of mice were removed, they were fixed in 4% paraformaldehyde for 12 h. Next, they were embedded in paraffin and cut along the sagittal plane of the optic nerve to obtain serial sections with a thickness of $4\text{ }\mu\text{m}$. Non-continuous sections were acquired from each eye for hematoxylin and eosin (HE) staining, and sections containing the optic nerve were excluded. The number of endothelial cells breaking through the inner limiting membrane in the vitreous cavity was counted, and the average of this number was calculated in each section[19]. Only the vascular nuclei located closely to the retina were counted; thus, vascular nuclei not close to the internal limiting membrane in the vitreous cavity were excluded[20,21].

High-throughput sequencing

The total RNA of each retinal tissue sample was extracted using Trizol reagent according to the manufacturer's instructions (Takara, Japan). The quality of RNA was analyzed using NanoDrop ND-2000 (Thermo Fisher Scientific, United States). A small RNA library was constructed by real-time polymerase chain reaction (RT-PCR) using 5' and 3' linkers. Agilent 2100 and Applied Biosystems StepOnePlus Real-Time PCR systems were used to assess the quality and yield of the constructed library (Life Technologies). Finally, the RNA was sequenced by Illumina Hiseq 2000 (Illumina, San Diego, CA, United States).

Sequencing result analysis

After standardization and quality control of the sequencing data, 26-31 nt piRNAs were selected from small RNA reads, and the differential expression of piRNA was analyzed. Fold change in piRNA expression ≥ 1.5 ($P < 0.05$) was used as the threshold for determining gene upregulation or downregulation. Gene Ontology (GO) enrichment (<http://www.geneontology.org/>) was used to analyze the abnormal expression of genes, and KO enrichment (<https://www.genome.jp/kegg/pathway>) was utilized to determine the biological function of the differentially expressed piRNA and investigate its possible involvement in the disease mechanism[22].

RT-PCR

RT-PCR was performed on total RNA extracted from retina samples using Trizol reagent (Takara, Shiga, Japan) according to the manufacturer's instructions.

Statistical analysis

SPSS 22.0 software (SPSS, Inc., Chicago, IL, United States) was used for all statistical analyses. The mean \pm SD of relative piRNA expression in PCR analyses was calculated. Student's *t*-test was used to analyze the difference between the two groups. $P < 0.05$ indicated a statistically significant difference.

RESULTS

Evaluation of fluorescence imaging

The samples obtained from the normal control and EGs of mice were stained with isolectin B4-594 to observe the retinal vascular structure. In the normal CG, the retinal blood vessels were intact and clear, and large blood vessels were characterized by an even radial distribution around the optic disc reaching the periphery of the retina. In the DR group, there was no perfusion in the large vessel area and no decomposition of the perfusion area. The large vessels near the optic disc were tortuous and irregular, and they were mainly visible in the middle and periphery. A large number of disordered new vessels and new vascular buds were detected at the retina boundary along with vascular leakage (Figure 1).

Quantitative analysis of retinal vascular endothelial cells

HE staining images were used to quantitatively analyze the number of retinal vascular endothelial nuclei. In the CG, the structure of the retinal internal limiting membrane was intact and smooth with occasional vascular endothelial nuclei breaking through the internal limiting membrane on the vitreous side (average number 1.163 ± 0.31). In the EG, the morphology of the internal limiting membrane was irregular, and cells under the internal limiting membrane proliferated and were arranged in a disorderly manner. A large number of clusters of vascular endothelial cells broke through the inner limiting membrane and formed the neovascular lumen (average number 29.42 ± 1.07). There was a significant difference in the number of retinal vascular endothelial cells that broke through the inner limiting membrane between the two groups ($P < 0.01$) (Figure 2).

High-throughput sequencing results

There were 79 piRNAs differentially expressed in EG compared to in CG mice, among which 43 were upregulated and 36 were downregulated (Figure 3).

Verification of results indicating differential gene expression

We selected 10 differentially expressed genes according to their gene expression levels determined by high-throughput sequencing and verified the expression levels in two groups of retina samples by RT-PCR. The primer sequences used in this study are shown in Table 1. The results of quantitative verification by RT-PCR are shown in Figure 4.

GO analysis

To further analyze the biological functions of differentially expressed genes in EG and CG mice, the GO and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses was performed. The results showed that the differentially expressed piRNAs were involved in many biological processes, such as sensory development, G-protein-coupled receptor signaling pathway, regulation of inflammatory factors, and visual

Table 1 Real-time polymerase chain reaction verification results of piRNA expression and list of primer sequences used

Gene ID	Fold-change	Up/down	Primer (5'-3')
piR-mmu-40373735	17.4426	Up	F: CCGGACCTCAAGCAGCC; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-61121420	17.5967	Up	F: GGCCAGCCGGGGTACA; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-55687822	17.5982	Up	F: CGCACTGCTTCACITGACCAG; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-1373887	18.0930	Up	F: AATGATGAACCTTTTGACGGG; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-52367843	18.4806	Up	F: CGAGGACAGCCTGGTCTACACA; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-7401535	-18.5696	Down	F: CAGCCCTCGACACAAGGG; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-4773779	-18.2665	Down	F: GCACCATGATGACGGAAATT; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-1304999	-17.8006	Down	F: GCATGCAGGAGCATCAGTAGAC; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-7422255	-17.5913	Down	F: CCACATGATGATCCATAACGAGAT; R: AGTGCAGGGTCCGAGGTATT
piR-mmu-5160126	-17.4335	Down	F: GCTGAGACAGGAGGATCGCT; R: AGTGCAGGGTCCGAGGTATT

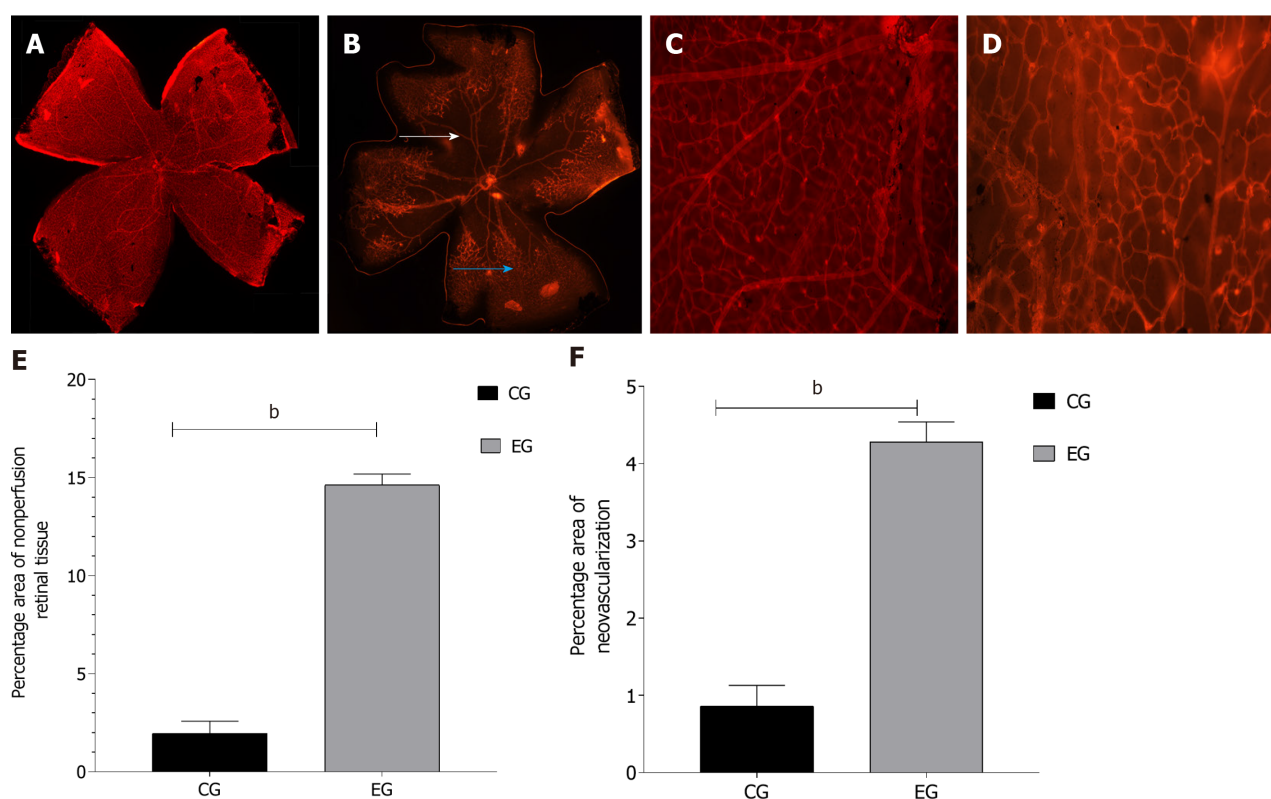


Figure 1 Evaluation of retinal neovascularization. A: Retina patch morphology of control group (CG); B: Retina tissue morphology of experimental group (EG) (white arrow indicates no perfusion area, blue arrow indicates neovascularization); C: Retina local enlarged map of CG; D: Retina local enlarged map of EG; E: Retina no perfusion area statistical map; F: Retina neovascularization cluster area statistical map. $^bP < 0.01$.

development, which are potentially related to RNV (Figure 5).

KEGG analysis

KEGG analysis of differentially expressed genes and proteins showed that the enriched pathways were mainly related to angiogenesis and cell proliferation and were strongly correlated with RNV (Figure 6).

Analysis of protein-protein interaction network

We obtained piRNA-target gene pairs correlated with expression level to construct the network analysis diagram. We selected the *EPO*, *HIF-1a*, *IGF1*, and *TGF- β 2* genes, which are potentially related to RNV, to construct the interaction analysis diagram (Figure 7).

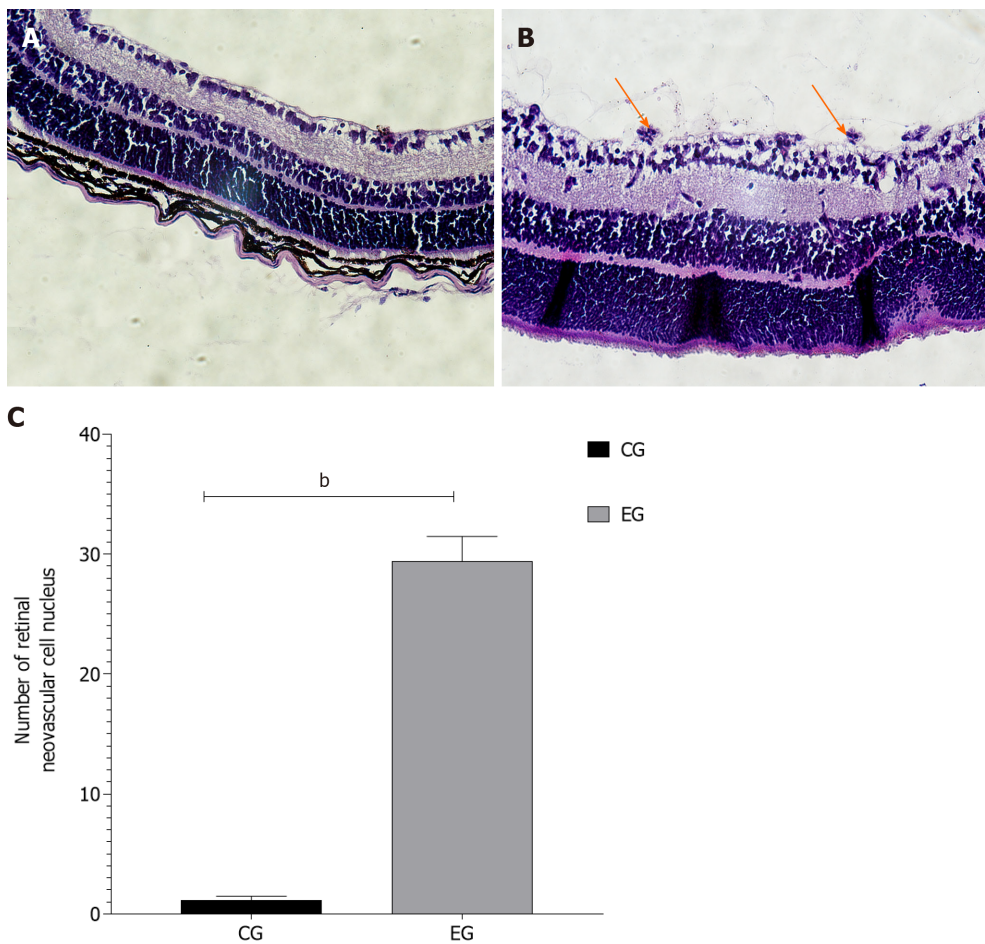


Figure 2 Quantitative analysis of vascular endothelial cells. A: Hematoxylin and eosin (HE) staining of paraffin-embedded retina sections in the control group (CG) (200 ×); B: HE staining of paraffin-embedded retina sections in the experimental group (EG) (200 ×, orange arrow indicates that endothelial cell nucleus breaks through the inner limiting membrane); C: Number of nuclei breaking through the inner limiting membrane in the two groups. $^bP < 0.01$.

DISCUSSION

Non-coding RNA is involved in the occurrence and development of several diseases. Numerous studies have shown that non-coding RNA is an important factor in the pathophysiological changes leading to malignant tumors and vascular diseases[23]. piRNA is a type of small non-coding RNA with an important role in animal development, reproduction, and gene regulation[10,24]. To date, 23439 piRNAs have been identified in the human genome, which is equivalent to the number of proteins encoded by mRNA (about 20000) and more than the number of miRNAs. These numbers indicate that piRNAs play an important role in regulating gene transcription [25,26].

After transcription, PIWI protein cleavage and amplification as well as piRNA clusters eventually form mature piRNAs having biological activity by forming PIRISC [27]. PIRISC, a silencing complex formed by piRNA and PIWI protein, can inhibit its target by transcriptional gene silencing and post-transcriptional gene silencing to maintain the genomic integrity of the germline[27,28]. PIRISC regulates transposon expression at the transcriptional level by inducing epigenetic repression *via* histone H3K9me3 and DNA methylation[29]. Some studies report a larger number of allowed mismatches between target mRNA and piRNA as opposed to between target mRNA and miRNA[30]. siRNA and miRNA are easily and rapidly degraded by nucleases, whereas piRNA is relatively stable in the serum, and thus has the potential to serve as a marker for diagnosis and prediction of disease progression[31].

piRNAs are presently thought to act mainly in somatic cells and cancer tissues and are involved in cell proliferation, apoptosis, cell cycle arrest, angiogenesis, invasion, and metastasis[32]. Moreover, studies have shown that PIRISC may participate in tumorigenesis by inducing abnormal DNA methylation, which leads to genomic silencing[33]. Further, the piRNA-30473/WTAP/HK2 axis promotes the occurrence of breast cancer by regulating the methylation of m6A RNA in diffuse large B-cell

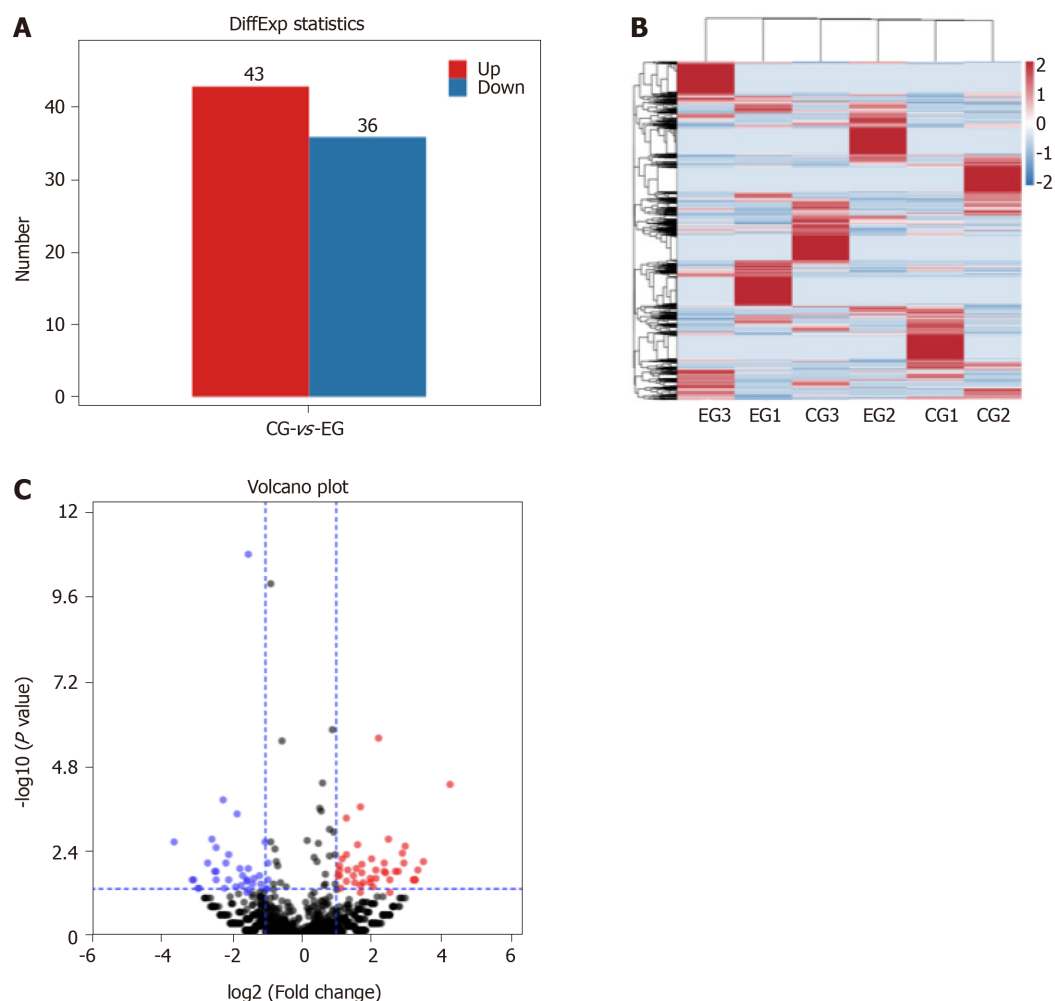


Figure 3 Screening results of differentially expressed genes. A: Number of differentially expressed piRNAs between experimental group (EG) and control group (CG); B: Clustering analysis of differentially expressed piRNAs; C: Volcano map of differentially expressed piRNAs.

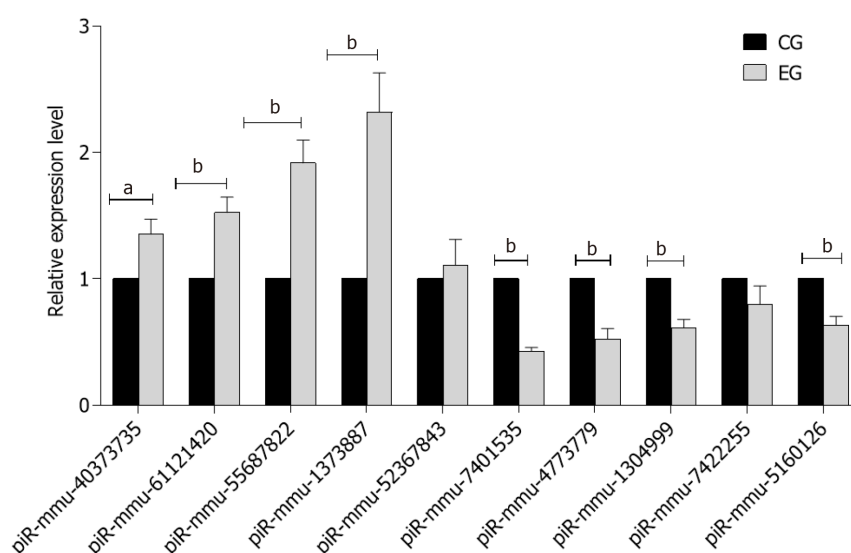
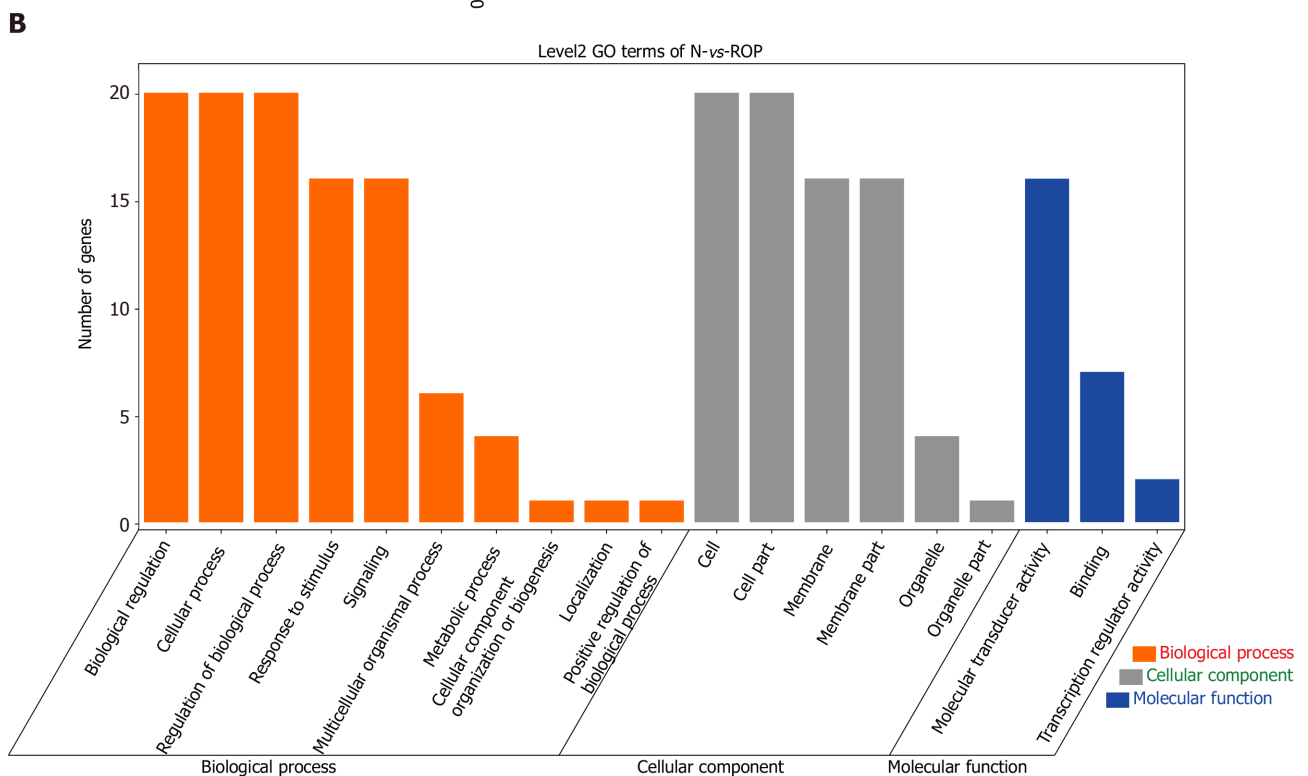
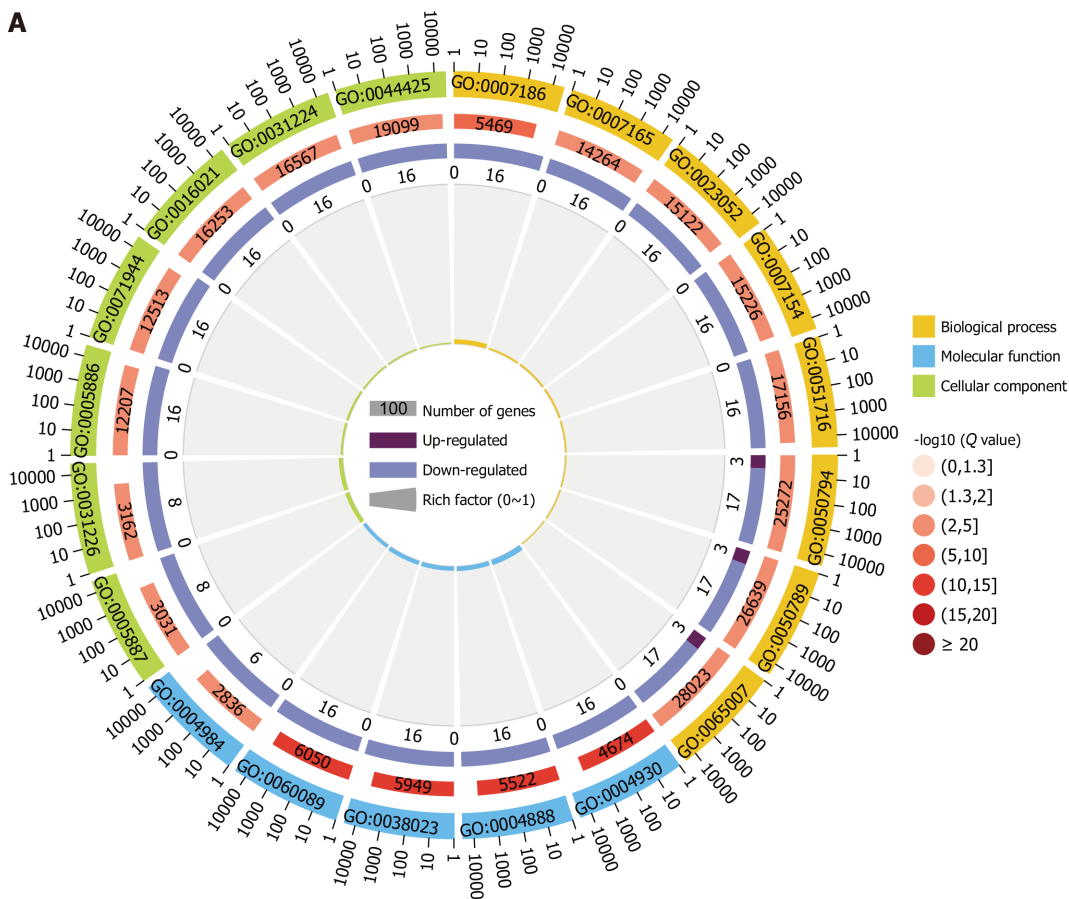


Figure 4 Statistics of ten piRNA validation results. ^a $P < 0.05$; ^b $P < 0.01$. CG: Control group; EG: Experimental group.

lymphoma[34]. piRNA-19166 inhibits cell migration and metastasis through the cortactin/mitochondrial membrane potential pathway in prostate cancer[35]. piRNA-823 promotes the angiogenesis of endothelial cells by promoting the secretion of VEGF and interleukin -6. It also enhances the invasion of endothelial cells by inducing the



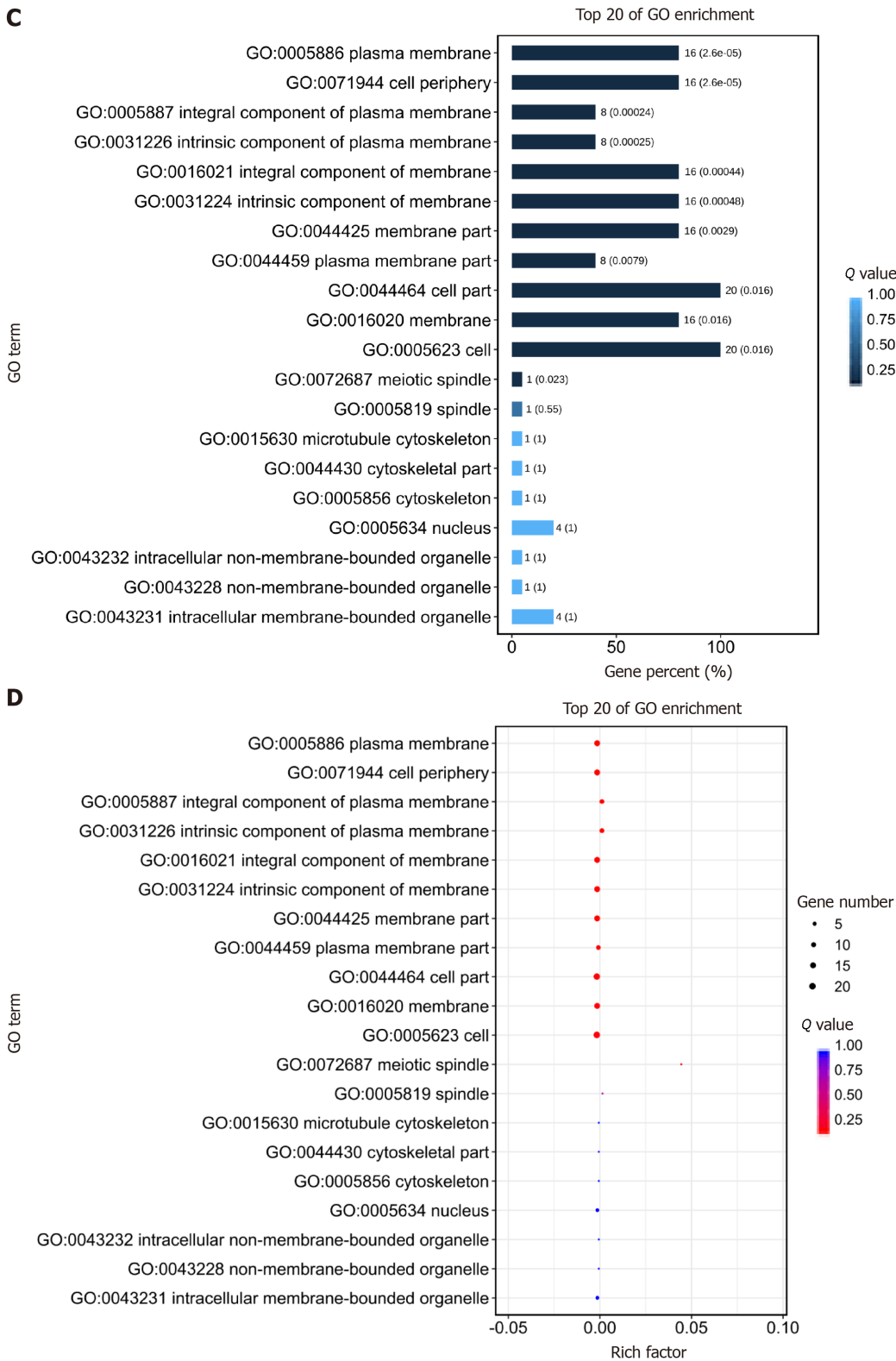


Figure 5 Gene Ontology analysis results. A: Gene Ontology (GO) enrichment circle diagram (first circle: top 20 GO terms, the coordinate scale of gene number is presented outside the circle. Second circle: number and Q value of the GO term in the background gene. Third circle: number of GO term piRNA target genes. Fourth circle: rich factor value of each GO term piRNA); B: Bar graph of GO enrichment (abscissa shows the level 2 GO term, whereas the ordinate shows the number of genes in the term); C: Bar graph of GO enrichment (a darker color, results in a smaller Q value; the value in the column is the number and Q value of the GO term); D: GO enrichment bubble chart (size indicates the quantity; a redder color leads to a smaller Q value).

expression of ICAM-1 and CXCR4[36]. Downregulation of piRNA-36712 expression is known to result in upregulation of SEPW1 expression, which in turn inhibits the expression of its downstream gene p53 and therefore it suppresses the formation of malignant tumors[37]. In addition, piRNA plays an important role in gastric cancer,

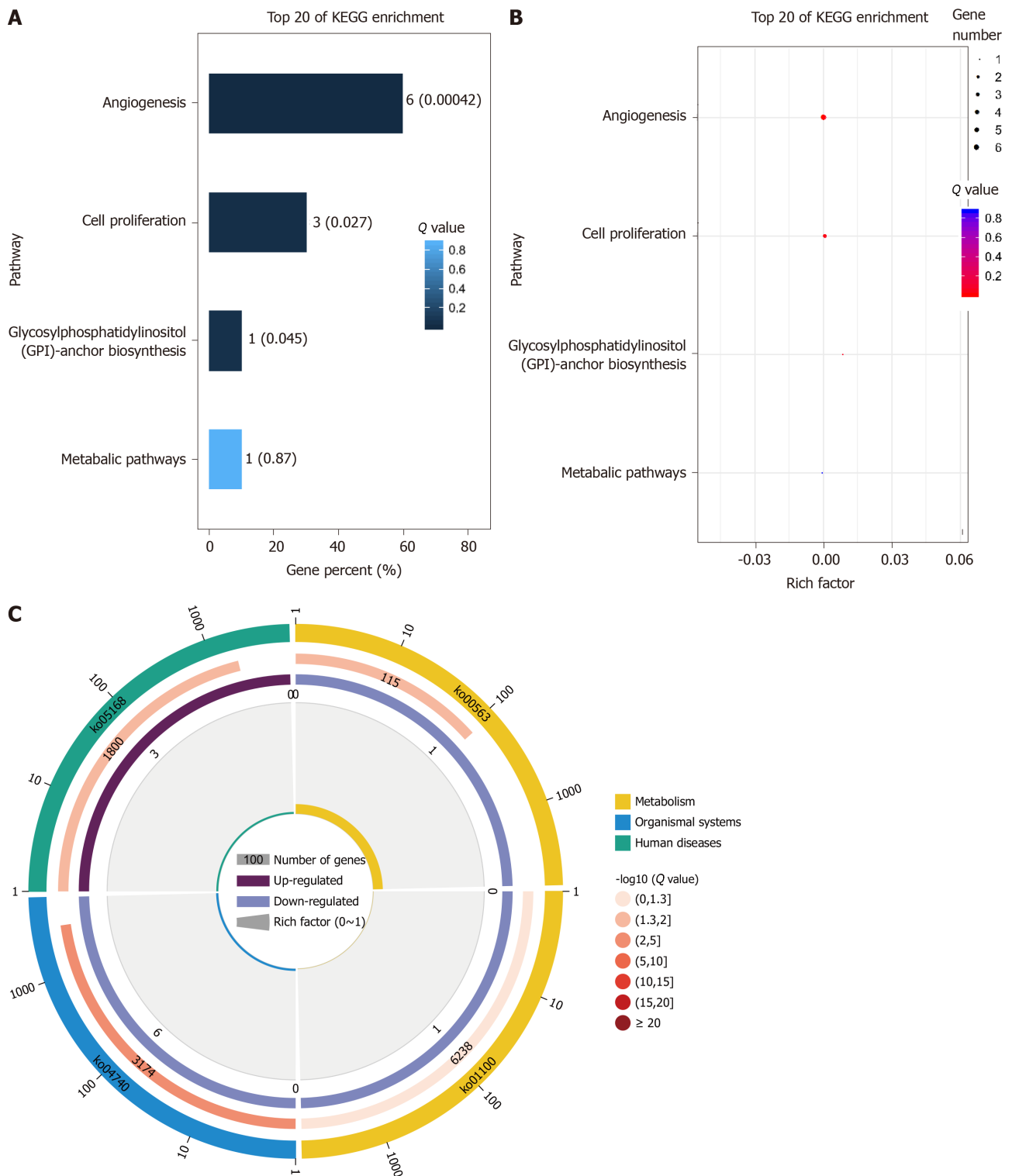


Figure 6 KO analysis results. A: KO enrichment bar chart (top 20 pathways with the lowest Q value were used to draw the chart. The ordinate represents the pathways, whereas the abscissa shows the percentage of the number of pathways in all piRNA target genes; a darker color correlates with a smaller the Q value. The value in the column is the number and Q value of the pathways); B: KO enrichment bubble chart [top 20 pathways with the lowest Q value were used to plot. The ordinate shows the pathway, whereas the abscissa shows the enrichment factor (the number of piRNA target genes in the pathway divided by all numbers). The size indicates the number; a redder color indicates a smaller Q value]; C: KO enrichment circle diagram [first circle: top 20 enriched pathways; outside the circle is the coordinate scale of gene number, and different colors represent different classes. Second circle: number and Q value of the pathway in the background gene; the more the number of genes, a longer bar and smaller Q value leads to a redder color. Third circle: number of piRNA target genes in the pathway. Fourth circle: rich factor value of each pathway (number of piRNA target genes in the pathway divided by all numbers); background grid line, each grid represents 0.1].

liver cancer, glioma, and other diseases. Based on these correlations, piRNA is expected to serve as a new target for cancer treatment[6,10,38].

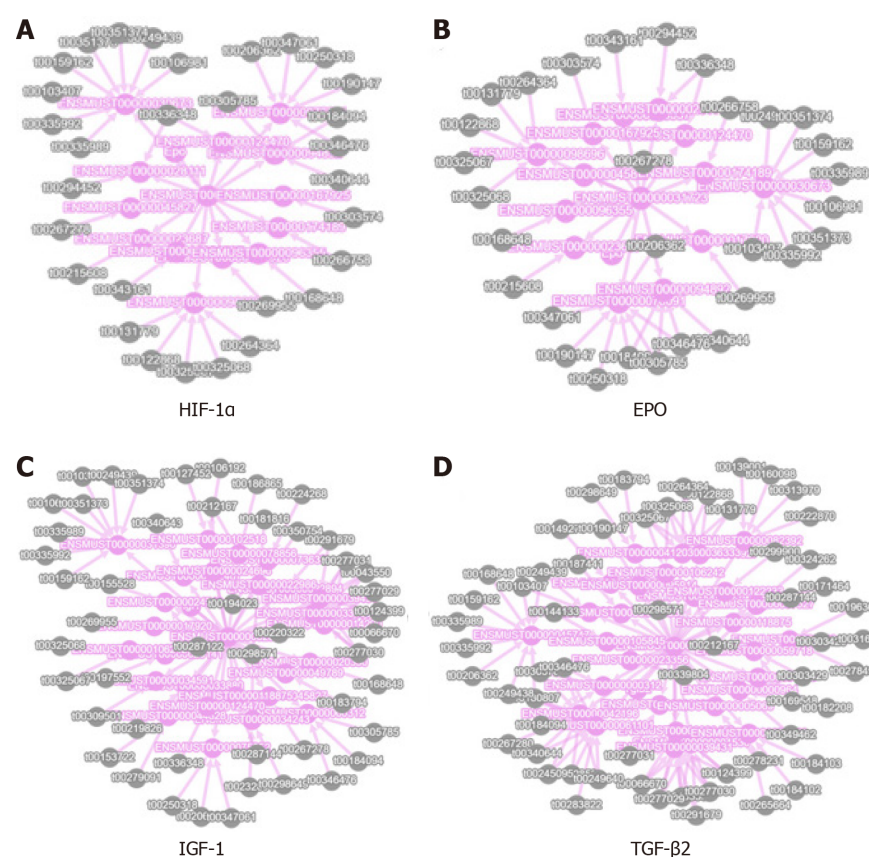


Figure 7 Protein interaction network analysis. A-D: Stand for differential expression results of piRNA and *EPO* (B), *HIF-1α* (A), *IGF1* (C), *TGF-β2* (D) which are associated with retinal neovascularization

There are many models for the study of DR. At present, the model of RNV and vascular leakage without hyperglycemia has been applied. This model simulates PDR or the process to be developed from non-PDR (NPDR) to PDR. The retinopathy injury caused by hypoxia is due to the occurrence of the release of angiogenesis actors, presented with microhemangiomas, vascular leakage, venous occlusion, capillary in perfusion, neovascularization, and even vitreous hemorrhage, and retinal detachment [16]. There are notable nonperfusion areas in the center of the retina, the central great vessels are tortuous, and the number of vascular nuclei breaking through the inner limiting membrane is significantly increased, which are important factors indicating the success of the EG[39]. HE staining of retinal slices and paraffin sections of EG samples showed that there were large areas of nonperfusion, neovascularization, and vascular endothelial cells breaking through the inner limiting membrane in the retina.

DR is one of the most common microvascular diseases of diabetes and also the main cause of blindness in diabetic patients[40]. Studies have shown that DR occurs in both type 1 diabetes and type 2 diabetes[41]. With the increase in the number of diabetic patients, DR has become the main cause of visual impairment in diabetic patients[42]. The whole pathological process of DR includes important pathological changes such as loss of retinal capillary pericytes, thickening of basement membrane, loss of endothelial barrier function, destruction of blood-retinal barrier, and lead to retinal ischemia, which will increase the level of VEGF. Studies have shown that overexpression of VEGF is associated with RNV, which can cause retinal hemorrhage, macular edema, retinal detachment, and neovascularization glaucoma, *etc.*, leading to severe visual impairment and eventually blindness.

The development of DR involves two stages: early NPDR and advanced PDR. The former is mainly characterized by increased retinal permeability and intraretinal hemorrhage, while the latter is mainly manifested by RNV. In NPDR, high glucose induced retinopathy mainly includes loss of capillary pericytes, thinning of the vascular layer and destruction of the blood-retinal barrier, which further leads to retinal ischemia and hypoxia. When the disease progresses to PDR, neovascularization occurs and eventually leads to severe visual impairment. RNV is a common pathological change in many retinopathies, including DR, retinopathy of prematurity, and age-related macular degeneration.

The common feature of clinical treatment of RNV as well as malignant tumors is treatment with targeted drugs, mainly anti-VEGF drugs. However, targeted drugs against RNV have short action time and require multiple intraocular injections, creating safety risks. Based on the findings of previous studies on the role of piRNA in cancers and neovascularization-related diseases, we compared piRNA expression levels between the DR model and CGs. The results revealed 79 piRNAs with differential expression in EG and CG. Through GO and KEGG analysis, we established that the mRNA of the differentially expressed piRNAs was involved in processes such as angiogenesis, optic nerve development, inflammation, and proliferation of cells. Among them, *EPO*, *HIF-1 α* , *IGF1*, *TGF- β 2*, and other genes are closely related to angiogenesis. Interestingly, a change in *EPO* expression is considered as an important factor affecting the retinopathy of prematurity. *EPO* treatment can effectively protect the nervous system and optic nerve development of premature infants[42,43]. *HIF-1 α* is stably expressed under hypoxia; it can regulate *EPO* and VEGF expression and promote RNV[44,45]. Inhibiting the VEGF/VEGFR2 and HIF-1 α /VEGF signaling pathways can prevent angiogenesis[46]. TGF- β 2 is a pro-inflammatory cytokine precursor related to the pathogenesis of DR. IGF1 has been identified as the direct target of miR-142-5p. It can reduce the level of miR-142-5p by activating the IGF1/IGF1R median signaling pathway (involving p-PI3K, p-ERK, p-Akt, and VEGF activation), eventually leading to cell proliferation and is involved in the pathological process of DR[47,48].

piRNA plays an important role in various diseases. By interacting with PIWI protein, piRNA can participate in cancer formation and neovascularization through DNA methylation. It can also affect the expression of target genes. We examined the differential expression of piRNA in an oxygen-induced retinopathy mouse model and the potential cellular pathways involved in this process. The study identified a set of target genes that can enhance the theoretical understanding of the role of piRNA in RNV. Because the specific mechanism of action has not been studied in detail, studies are needed to explore its mechanism in a larger sample size. Moreover, it can drive further research on new strategies for clinical treatment. We plan to predict the downstream targets of each differentially expressed piRNA and verify the predicted targets using molecular biology methods. These results provide a foundation for further exploration of the molecular mechanism underlying the development of PDR.

CONCLUSION

Abnormal expression of the piRNAs are involved in pathways of angiogenesis and cell proliferation, which suggests that piRNAs may regulate some functions in proliferative DR.

ARTICLE HIGHLIGHTS

Research background

Retinal neovascularization is caused by the progression of ischemic retinal diseases, including diabetic retinopathy, retinopathy of prematurity, age-related macular degeneration, and retinal vein occlusion. Complications of retinal neovascularization can severely impair vision or lead to permanent blindness.

Research motivation

To explore the upstream molecules of vascular endothelial growth factor or rate-limiting steps of angiogenesis, and to reveal new approaches to the treatment of diabetic retinal.

Research objectives

The research on the role of piRNAs (p-Element-induced wimpy testis-interacting RNAs) in retinal neovascularization disease is expected to provide theoretical support for the clinical treatment of diabetic retina.

Research methods

A diabetic retinopathy model was established. The differentially expressed piRNA

was screened by high-throughput sequencing, and the differentially expressed piRNA was selected according to the sequencing results, and verified by polymerase chain reaction.

Research results

A total of 79 piRNAs were differentially expressed in experimental group, of which 43 were upregulated and 36 were down-regulated.

Research conclusions

piRNAs were differentially expressed in DR model. Differentially expressed piRNAs is involved in the formation of retinal neovascularization. Differentially expressed piRNAs can regulate retinal development and retinal angiopathy through a variety of signaling pathways.

Research perspectives

Drugs targeting piRNAs may be novel candidates for the treatment of diabetic retinopathy.

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Observational Study

Fasting biochemical hypoglycemia and related-factors in non-diabetic population: Kanagawa Investigation of Total Check-up Data from National Database-8

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Abstract

BACKGROUND

In healthy people, the lowest daily blood glucose concentration is usually observed in the early morning, after overnight fasting. However, the clinical relevance and the prevalence of fasting biochemical hypoglycemia (FBH) are poorly understood in people who do not have diabetes, although the clinical implications of such hypoglycemia have been extensively studied in patients with diabetes. FBH can be influenced by many factors, including age, sex, body mass, smoking, alcohol drinking, exercise levels, medications, and eating behaviors, such as breakfast skipping and late-night eating.

AIM

To determine the prevalence of FBH and investigated its association with potential risk factors in a population without diabetes.

METHODS

Clinical parameters and lifestyle-related factors were assessed in a cross-sectional study of 695613 people aged 40-74 years who had undergone a health check-up (390282 men and 305331 women). FBH was defined as fasting plasma glucose < 70 mg/dL (3.9 mmol/L) after overnight fasting, regardless of any symptoms. The absence of diabetes was defined as HbA1c < 6.5%, fasting plasma glucose < 126 mg/dL (7.0 mmol/L), and no pharmacotherapy for diabetes. Multivariate logistic

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regression analysis, with adjustment for confounding factors, was used to identify associations.

RESULTS

FBH was present in 1842 participants (0.26%). There were significantly more women in the FBH group (59.1%) than in the non-FBH group (43.9%). Values of most of the clinical parameters, but not age, were significantly lower in the FBH group than in the non-FBH group. Logistic regression analysis showed that a body mass index of ≤ 20.9 kg/m² (reference: 21-22.9 kg/m²) and current smoking were significantly associated with FBH, and this was not altered by adjustment for age, sex, and pharmacotherapy for hypertension or dyslipidemia. Female sex was associated with FBH. When the data were analyzed according to sex, men in their 60s or 70s appeared more likely to experience FBH compared with their 40s, whereas men in their 50s and women aged ≥ 50 years appeared less likely to experience FBH. The relationships of FBH with other factors including alcohol drinking and pharmacotherapies for hypertension and dyslipidemia also differed between men and women.

CONCLUSION

FBH occurs even in non-diabetic people, albeit at a very low frequency. FBH is robustly associated with low body mass and smoking, and its relationship with lifestyle factors varies according to sex.

Key Words: Hypoglycemia; Body mass index; Age; Smoking; Women; Breakfast skipping

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Core Tip: The clinical relevance of fasting biochemical hypoglycemia (FBH) is poorly understood in people who do not have diabetes. Therefore, we determined the prevalence of FBH and its relationships with other parameters in approximately 700000 people who did not have diabetes. FBH was identified in 0.26% of the participants and women were over-represented among these (59.1%). Low body mass and smoking were associated with FBH in both men and women. Women and men in their 60s and 70s were more likely to experience FBH, and the relationships of FBH with other factors differed between men and women.

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INTRODUCTION

Hypoglycemia is one of the most serious complications during the treatment of diabetes, whether it be type 1, type 2, or another type[1-4]. Hypoglycemia is associated with high mortality due to cardiovascular events and impaired cognitive function. The prevalence and severity of hypoglycemia, which is particularly frequent in diabetic patients who are administering insulin[1-4], are affected by multiple factors, including medication, diet, exercise, and the presence of comorbidities. However, the clinical relevance of hypoglycemia is poorly understood in people who do not have diabetes, and its prevalence has been determined in only a few small studies[5-7]. In apparently healthy people, blood glucose concentration tends to be lowest under fasting conditions in the early morning, after overnight fasting.

We therefore aimed to determine the prevalence of fasting biochemical hypoglycemia (FBH), which was assessed using a sample of plasma instead of finger-stick blood, and to identify the associated factors from among age, sex, body mass, smoking, alcohol drinking, exercise status, and breakfast skipping in a general population of people without diabetes, using healthcare data provided by the Japanese

Ministry of Health, Labour, and Welfare.

MATERIALS AND METHODS

Study design and participants

The overarching study was a composite multidisciplinary study that consisted of the secondary use of annual health check-up data collected in Japan (Kanagawa Investigation of the Total Check-up Data from the National Database) that aimed to determine the clinical factors associated with cardiometabolic diseases. Details of the study concept and design have been published elsewhere[8]. The present study was performed using data from individuals who underwent specific health check-ups and were living in Kanagawa Prefecture between April 2012 and March 2013. The study protocol was approved by the Ethics Committee of Kanagawa University of Human Services (10-43) and the Ministry of Health, Labour, and Welfare of Japan (No. 121).

We received digitally recorded anonymous data from the Ministry of Health, Labour, and Welfare of Japan in 2017, as part of its nationwide program for the provision of medical data to third parties[9]. To protect against the identification of specific individuals, their ages had been categorized as 40-44, 45-49, 50-54, 55-59, 60-64, 65-69, or 70-74 years. However, for the purposes of the present study, to evaluate age as a single numeric value, we transformed the age groups into substituted ages (stage), corresponding to the median for each age group (42, 47, 52, 57, 62, 67, and 72 years, respectively).

We initially reviewed data collected from 1623399 non-hospitalized people aged 40-74 years who had attended health check-ups. As shown in Figure 1, individuals who were undergoing pharmacotherapy for diabetes and/or had an HbA1c of $\geq 6.5\%$, regardless of their type of diabetes, were excluded ($n = 95664$; 5.9%). Individuals with a fasting plasma glucose (FPG) ≥ 126 mg/dL (7.0 mmol/L) were also excluded ($n = 34336$). After the further exclusion of those for whom incomplete clinical and lifestyle data were available ($n = 797786$), data from 695613 individuals remained for analysis (390282 men and 305331 women).

Measurements

Anthropometric and laboratory measurements were performed in the morning following an overnight fast. Overnight fasting for > 10 h was individually confirmed and recorded by a staff member[8]. Body mass, waist circumference at the level of the navel, and height were measured by trained staff members. Body mass index (BMI) was calculated as mass (kg) divided by the square of height (m^2). The participants were then placed into eight BMI groups: ≤ 16.9 , 17-18.9, 19-20.9, 21-22.9, 23-24.9, 25-26.9, 27-28.9, and ≥ 29.0 kg/ m^2 .

Fasting plasma glucose was measured (approximately 54% of samples) mainly by spectrophotometric or potentiometric (approximately 30%) method[8]. FBH was defined as an FPG < 70 mg/dL (3.9 mmol/L), regardless of the presence or absence of symptoms[4,10]. Laboratory measurements were performed using standard automated methods. Habitual breakfast skipping was defined as a positive response to the question: "Do you skip breakfast at least three times per week?"[8].

Biostatistics

Data are expressed as mean \pm SD or medians (interquartile range). Differences in continuous and categorical datasets between FBH and non-FBH groups were evaluated using Student's *t*-test or the χ^2 test, respectively. Trends in the prevalence of FBH with increasing alcohol consumption and age (three groups were defined: people in their 40s, 50s, and 60s + 70s) were evaluated using Cochran-Armitage tests. Because the number of participants in their 70s was relatively low, those in their 70s were grouped with those in their 60s for the analysis.

A logistic regression model was used to evaluate the relationships between FBH and plausibly related factors, with adjustment for potential confounding factors (age, sex, pharmacotherapy for hypertension or dyslipidemia, smoking status, alcohol consumption, and exercise status), yielding adjusted odds ratios (ORs) and 95% CIs. As in our previous study[11], a BMI range of 21.0-22.9 kg/ m^2 was used as the reference.

Statistical analyses were performed using SAS-Enterprise Guide (SAS-EG 7.1) in SAS software, version 9.4 (SAS Institute, Cary, NC, United States). $P < 0.05$ was considered to represent statistical significance. The statistical methods of this study were reviewed by Dr. Hiroto Narimatsu from the Kanagawa Cancer Center Research Institute, Yokohama, Japan.

RESULTS

The clinical characteristics of the participants, grouped according to the absence or presence of FBH, are shown in [Table 1](#). FBH was experienced by 1842 participants (0.26% of the total). Women were significantly over-represented in the FBH group and the prevalence of FBH was significantly higher in women (0.35%, $n = 1,088$) than in men (0.18%, $n = 754$) (χ^2 test, $P < 0.001$).

BMI, systolic blood pressure, serum triglyceride, and HbA1c were significantly lower in the FBH group than in the non-FBH group ($P < 0.001$). No difference in st-age was found, but the plasma high-density lipoprotein-cholesterol concentration was significantly higher in the FBH group ($P < 0.001$). The prevalence of current smoking and breakfast skipping was significantly higher in the FBH group, whereas that of pharmacotherapy for hypertension, late-night dining, and high alcohol consumption was lower in the FBH group.

[Figure 2](#) shows the results of logistic regression analysis, with adjustment for all the listed potential confounding factors (covariates) in the 695613 participants. Low BMI (≤ 20.9 kg/m²) was significantly associated with FBH, compared with the reference BMI category of 21-22.9 kg/m². The OR of BMI ≤ 16.9 kg/m² for FBH was almost four, compared with the reference BMI. By contrast, BMI ≥ 23.0 kg/m² was inversely associated with FBH. Female sex, current smoking, a history of cardiovascular disease, pharmacotherapy for dyslipidemia, habitual exercise, and breakfast skipping were also significantly associated with FBH. Being in one's 50s and mild-to-moderate alcohol consumption (23-68 g ethanol/day), but not heavy consumption, were inversely associated with FBH, compared with being in one's 40s and a small amount of alcohol consumption (< 23 g ethanol/day), respectively.

However, the relationships of FBH with several of these factors were changed when data from men and women were analyzed separately. Among the men ([Figure 3](#)), those in their 60s and 70s were more likely to have FBH. Pharmacotherapy for either hypertension or dyslipidemia was associated with FBH. Additionally, the inverse association of FBH with mild-to-moderate alcohol consumption was also present in men alone. By contrast, among women ([Figure 4](#)), those aged ≥ 50 were less likely to have FBH. A history of cardiovascular disease was significantly associated with FBH. However, mild-to-moderate alcohol consumption was not significantly associated with FBH in women. Finally, the associations of FBH with habitual exercise and breakfast skipping almost disappeared when data from men and women were analyzed separately ([Figures 3 and 4](#)), although both associations were marginally significant in women.

DISCUSSION

Hypoglycemia frequently occurs in diabetic patients undergoing pharmacotherapy and is difficult to predict[1-4]. In the present study, we have demonstrated that FBH also occurs in non-diabetic people, although the prevalence was very low (less than 1.0% of the total) in the general population studied, in contrast to that in diabetic patients[12,13]. This prevalence of FBH is not dissimilar to that of hypoglycemia (0.2%-0.5%) in non-diabetic people[3,5]. Among the potential confounding factors considered, low body mass and smoking were robustly associated with FBH in both men and women, and across the entire group, women appeared more likely to experience FBH than men. However, when data from each sex were analyzed separately, older women were found to be less likely to have FBH, whereas older men were more likely. The relationships of FBH with other factors (pharmacotherapy, a history of cardiovascular disease, and alcohol consumption) also differed between men and women. Habitual exercise and breakfast skipping were associated with FBH across the entire group, although these associations disappeared when men and women were analyzed separately, probably due to the lower statistical power.

Consistent with our findings, many previous studies have shown associations between low body mass and hypoglycemia in patients with diabetes[14-16]. Additionally, severe hypoglycemia has been shown to be prevalent in people with diabetes who are habitual smokers[17,18]. Therefore, common mechanisms may mediate the relationships between hypoglycemia, low body mass, and habitual smoking, regardless of the type of diabetes present.

FBH can occur as a reactive hypoglycemia in the non-diabetic population[19,20]. For example, reactive hypoglycemia caused by the dumping syndrome, with an incretin-driven insulin hypersecretory response occurs within a few hours of eating a meal in

Table 1 Characteristics of the participants, categorized according to the presence or absence of fasting biochemical hypoglycemia

	No FBH	FBH
<i>n</i> (% of total)	693771 (99.7)	1842 (0.26)
st-Age (yr)	54.7 ± 10.1	54.7 ± 10.7
40s, <i>n</i> (%)	269439 (99.7)	758 (0.28)
50s, <i>n</i> (%)	185374 (99.8)	418 (0.22)
60s + 70s, <i>n</i> (%)	238958 (99.7)	666 (0.28)
Women, <i>n</i> (%)	304243 (43.9)	1088 (59.1)
BMI (kg/m ²)	22.9 ± 3.3	21.2 ± 3.4 ^c
Systolic blood pressure (mmHg)	122 ± 16.8	118 ± 17.8 ^c
High-density lipoprotein-cholesterol (mg/dL)	64.2 ± 16.8	70.6 ± 19.0 ^c
Triglyceride, IQR (mg/dL)	90 (64-131)	71 (49-108) ^c
Fasting plasma glucose (mg/dL)	94.3 ± 10.0	64.7 ± 5.6
HbA1c (%)	5.5 ± 0.4	5.4 ± 0.6 ^c
Pharmacotherapy for hypertension, <i>n</i> (%)	120461 (17.4)	282 (15.3) ^a
Pharmacotherapy for dyslipidemia, <i>n</i> (%)	77208 (11.1)	213 (11.6)
Cardiovascular disease, <i>n</i> (%)	21410 (3.1)	71 (3.9)
Current smoking, <i>n</i> (%)	146253 (21.1)	492 (26.7) ^c
Habitual exercise, <i>n</i> (%) ¹	217322 (31.3)	597 (32.4)
Breakfast skipping, <i>n</i> (%) ³	102669 (14.8)	309 (16.8) ^a
Late night dinner, <i>n</i> (%) ⁴ , N = 689639	205062 (29.8)	482 (26.3) ^b
Alcohol consumption per day (g ethanol)		
< 23 g	379830 (54.8)	1167 (63.4)
23-45 g	193102 (27.8)	421 (22.9)
46-68 g ²	88021 (12.7)	173 (9.4)
≥ 69 g ²	32818 (4.7)	81 (4.4) ^c

Differences in continuous and categorical variables between the two groups were evaluated using Student's *t*-test or the χ^2 test, as appropriate. The trends with increasing alcohol consumption were evaluated using the Cochran-Armitage test.

^a*P* < 0.05.

^b*P* < 0.01.

^c*P* < 0.001.

¹Defined as habitual exercise to a light sweat for over 30 min per session twice weekly.

²Defined as a daily alcohol consumption of ≥ 46 g ethanol.

³Defined as skipping breakfast at least three times per week.

⁴Defined as eating dinner within the 2 h preceding bedtime at least three times per week. st-Age: Substituted age; BMI: Body mass index; IQR: Interquartile ratio; FBH: Fasting biochemical hyperglycemia.

people who have undergone gastric or esophageal surgery[21,22]. However, because we excluded individuals from the present study who ate within the 10 h preceding blood sampling, which was established using individual questionnaires, the FBH of the individuals in the present study is unlikely to represent this type of reactive hypoglycemia, which often accompanies hyperinsulinemia[19,20]. However, hypoglycemia in the early morning may be caused by hepatic dysfunction and low gluconeogenesis, both in non-diabetic and diabetic individuals[23,24].

Many conditions and diseases are considered to contribute to the incidence of hypoglycemia in non-diabetic people[24,25]. For example, adrenal insufficiency, use of pain-relieving medication, malnutrition or low food intake, infection, low hepatic gluconeogenic capacity, and low glycogen storage have all been implicated.

The reasons why women and older men were more likely to have FBH are unknown. A plausible explanation for the former is that the insulin sensitivity of women is higher, whereas their hepatic gluconeogenesis is lower because of higher

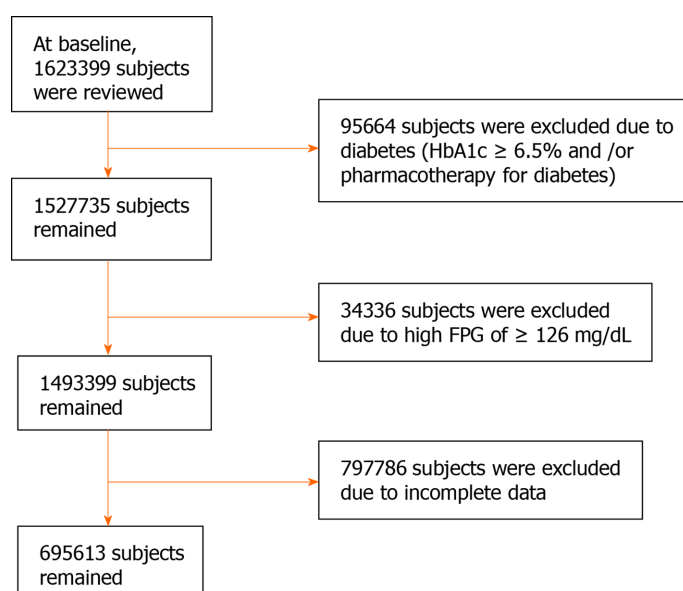


Figure 1 Exclusion criteria and participant disposition. The exclusion criteria and participant flow chart are shown. FPG: Fasting plasma glucose.

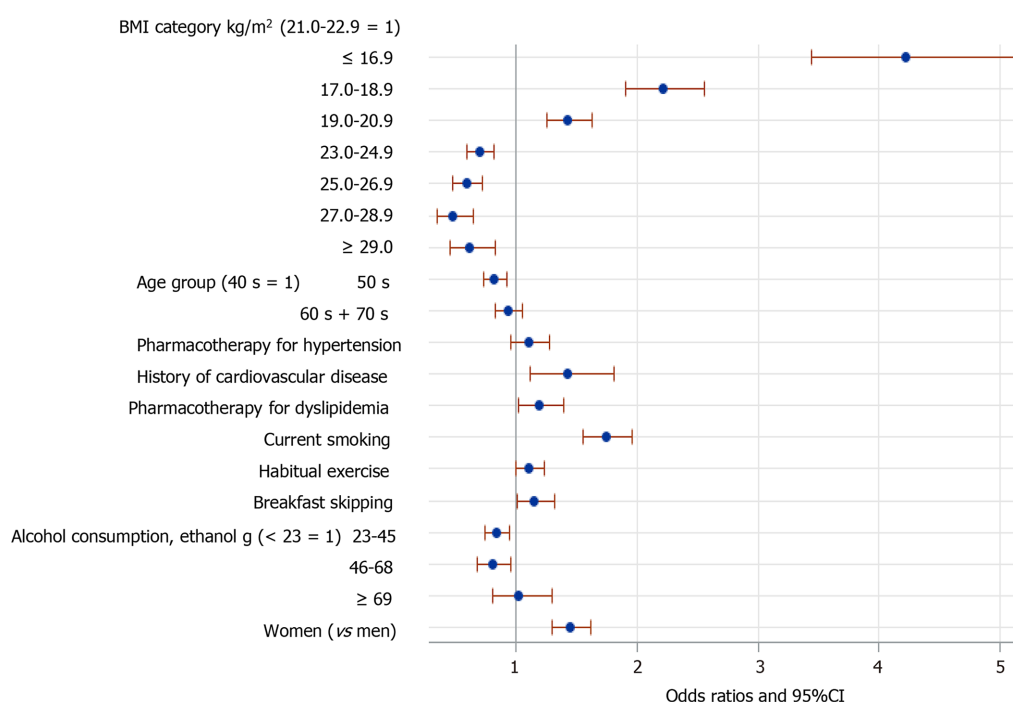


Figure 2 Odds ratios and 95% confidence interval for the relationships between various parameters and fasting biochemical hypoglycemia across the entire group. BMI: Body mass index; CI: Confidence interval.

circulating 17β -estradiol concentrations in women than men[26,27]. Furthermore, older men may have a lower gluconeogenic capacity than younger men[28,29], which would result in an inadequate supply of blood glucose in the early morning before breakfast. The insulin sensitivity of individuals who habitually exercise may also be higher, possibly contributing to lower blood glucose concentrations. However, it is unknown whether such factors specifically influence the incidence of FBH.

Acute alcohol consumption increases the risk of hypoglycemia through the suppression of gluconeogenesis in the liver, which is more likely to occur in the fasting state in both diabetic and non-diabetic people[30-32]. However, the long-term effect of alcohol consumption is poorly understood[32].

In the present study, heavy alcohol consumption (≥ 69 g ethanol/day) was not associated with FBH, whereas mild-to-moderate consumption was inversely associated with FBH, particularly in men. A plausible explanation for this is that

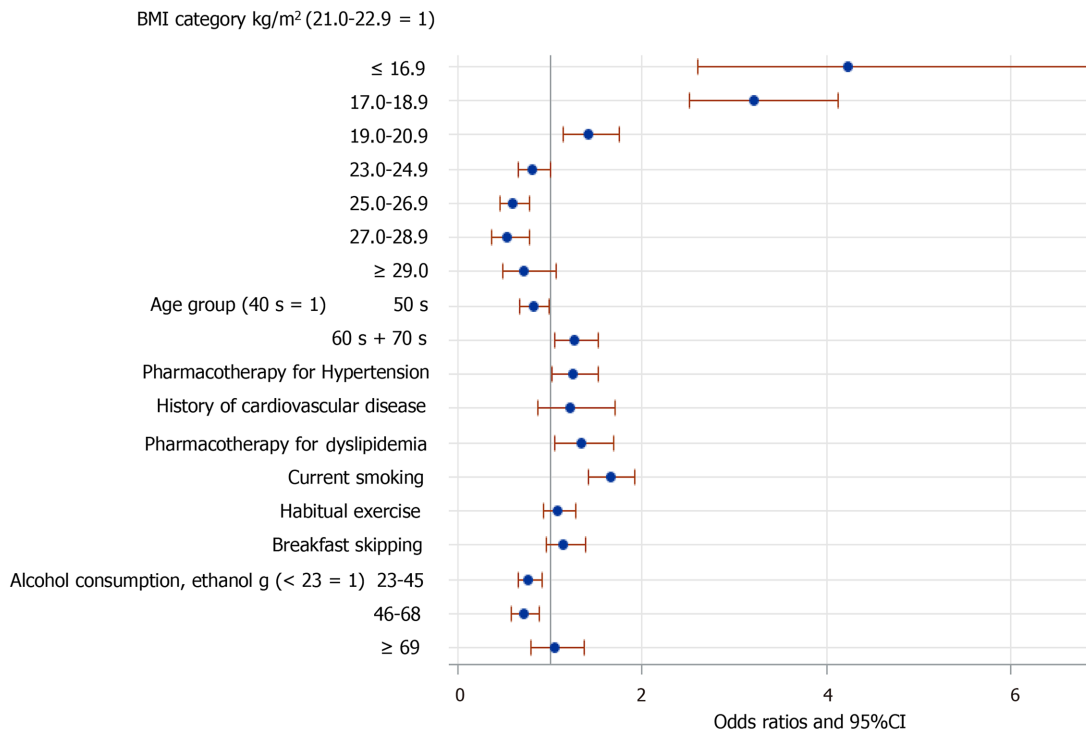


Figure 3 Odds ratios and 95% confidence interval for the relationships between various parameters and fasting biochemical hypoglycemia in men. BMI: Body mass index; CI: Confidence interval.

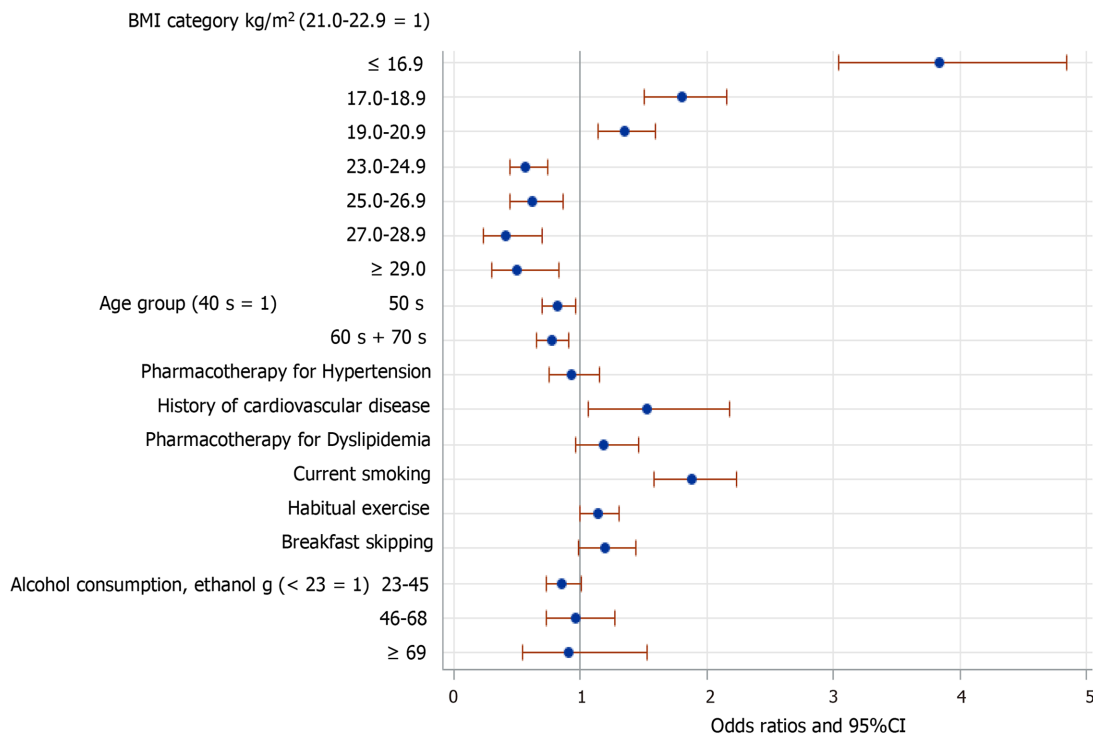


Figure 4 Odds ratios and 95% confidence interval for the relationships between various parameters and fasting biochemical hypoglycemia in women. BMI: Body mass index; CI: Confidence interval.

individuals who drink mild-to-moderate amounts of alcohol may concurrently consume an inadequate amount of food, predisposing toward subsequent hypoglycemia. In heavy drinkers, carbohydrate intake and glycogen storage may be inadequate, which could result in hypoglycemia several hours later, in addition to their lower renal and hepatic gluconeogenesis[31,32].

The reasons why breakfast skipping and pharmacotherapy for hypertension and dyslipidemia tended to be associated with FBH are unknown. A plausible reason for the former is that the sensitivity to hypoglycemia may be low, such that it does not elicit hunger and consequently removes the perceived need for the consumption of breakfast. In contrast, the lower prevalence of late-night dining in the FBH group (Table 1) may be less prevalent because the consumption of carbohydrates before sleep prolongs the peak blood glucose concentration until early morning.

Although we have shown that FBH occurs even in non-diabetic people, its clinical relevance in this group remains to be more fully determined. Although higher mortality in hospital[6,33], traffic accidents due to cognitive dysfunction[34], and fatal arrhythmias such as QT prolongation[35] are more prevalent in non-diabetic individuals who experience hypoglycemia, it is unknown whether these problems are also more common in non-diabetic people who experience FBH, and this deserves further study.

The main strength of the present study was that the FPG concentration was measured using a standard laboratory method, rather than using portable glucose meters, which can sometimes be inaccurate[36,37]. Furthermore, we were unable to conduct the present analysis until we had collected data from hundreds of thousands of people because of the very low prevalence of FBH. To the best of our knowledge, this study is the first to determine the prevalence of FBH and identify the associated factors in a non-diabetic population.

The present study also had several limitations. First, the assessment of hypoglycemia was conducted just once, using plasma samples obtained after overnight fasting. Therefore, it is unknown whether the prevalence of calculated FBH represents a transient or persistent phenomenon. Furthermore, the prevalence of hypoglycemia, including reactive hypoglycemia, during the daytime was not assessed during the present study. Second, the diet of the participants was not assessed in the present study, which prevented investigation of the relationships between the amounts of carbohydrates and energy consumed with FBH. Finally, we cannot draw conclusions with respect to cause and effect using the data collected because the study was cross-sectional. To identify causal relationships, a prospective, large-scale study of non-diabetic people should be conducted in the future.

CONCLUSION

We have shown that FBH occurs even in non-diabetic people, albeit very infrequently. FBH appears to be robustly associated with low body mass and smoking. Women and men in their 60s and 70s were more likely to experience FBH, and the relationships between FBH and other factors also differed between men and women.

ARTICLE HIGHLIGHTS

Research background

The clinical relevance and the prevalence of fasting biochemical hypoglycemia (FBH) are poorly understood in a general population without diabetes.

Research motivation

FBH can be influenced by many factors, including age, sex, body mass, smoking, alcohol drinking, exercise levels, medications, and eating behaviors.

Research objectives

We determined the prevalence of FBH and investigated its association with potential risk factors in a population who did not have diabetes.

Research methods

In a cross-sectional study of 695613 people aged 40-74 years who had undergone a health check-up, clinical parameters and lifestyle-related factors were reviewed. FBH was defined as a fasting plasma glucose < 70 mg/dL (3.9 mmol/L) after overnight fasting, regardless of any symptoms.

Research results

The prevalence of FBH was very low (0.26%) in this study. A body mass index of ≤ 20.9 kg/m² and current smoking were significantly associated with FBH, which was not altered by adjustment for age, sex, and pharmacotherapy for hypertension or dyslipidemia. When the data were analyzed according to sex, men in their 60s or 70s appeared more likely to experience FBH compared with their 40s, whereas men in their 50s and women aged ≥ 50 years appeared less likely to experience FBH.

Research conclusions

FBH was observed even in non-diabetic people, albeit at a very low frequency. FBH is robustly associated with low body mass and smoking, and its relationship with lifestyle factors varies according to sex.

Research perspectives

To identify causal relationships between FBH and relevant factors (underweight, smoking, men in their 60s and so on), a prospective, large-scale study of non-diabetic people should be conducted in the future.

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