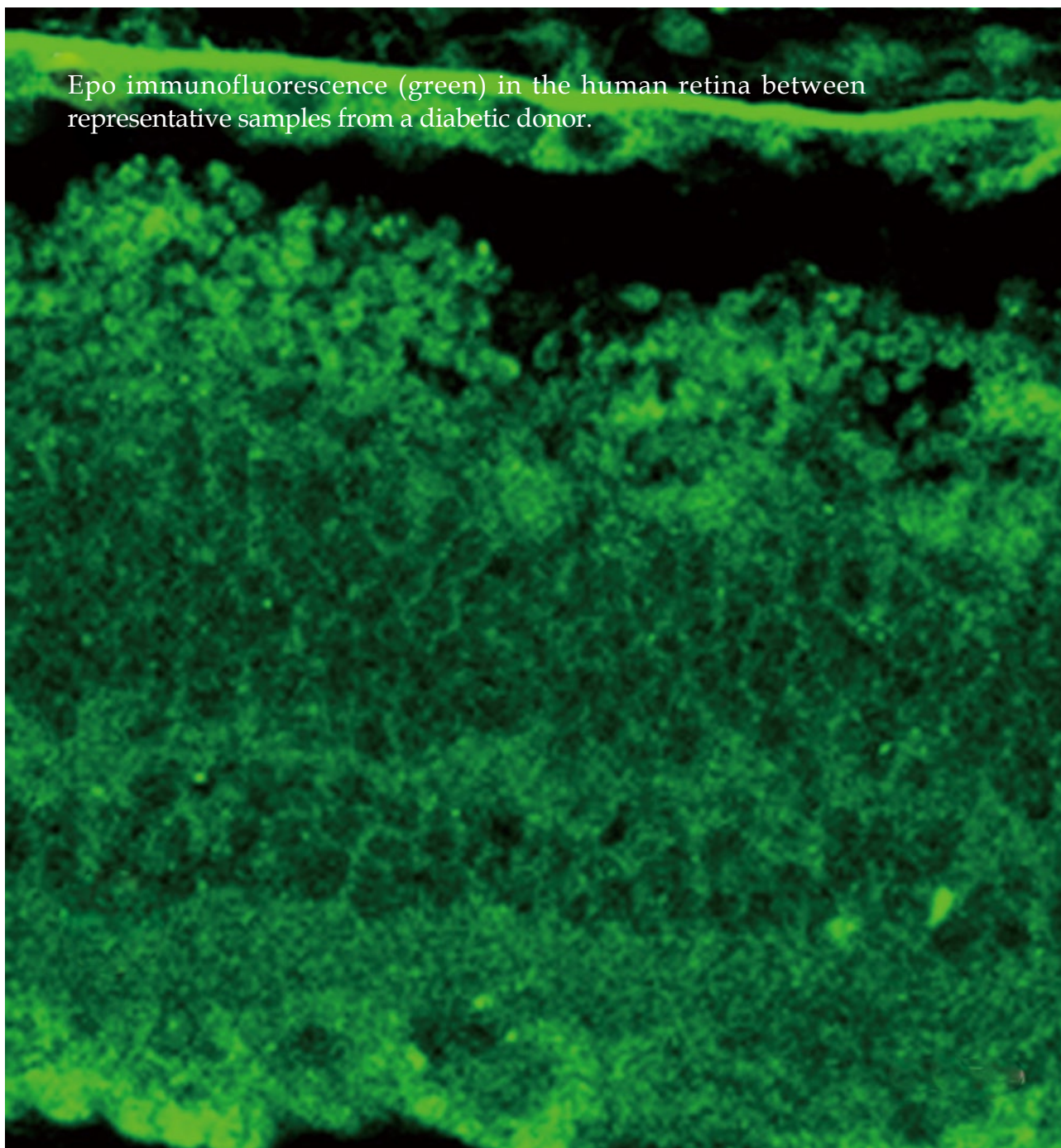


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Epo immunofluorescence (green) in the human retina between representative samples from a diabetic donor.



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Exacerbation of chronic inflammatory diseases by infectious agents: Fact or fiction?

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Abstract

Chronic inflammatory diseases caused by obesity represent critical public health concerns worldwide. In these diseases such as metabolic syndrome, diabetes and atherosclerosis, adipose tissue acts as an endocrine organ that releases large quantities of inflammatory mediators into circulation. Besides classically recognized effectors on the development of obesity and resultant conditions, infection has attracted attention as an enhancer of chronic inflammatory diseases. Infectious diseases have long been associated with obesity, metabolic syndrome, diabetes and atherosclerosis. However, the infectious hypothesis for chronic inflammatory diseases has been challenged by inconclusive clinical trials. Nevertheless, the large body of evidence accumulated over decades on the association of infectious diseases with obesity, diabetes and cardiovascular disease should not be disregarded. Instead, re-formulation of hypotheses

of the mechanisms by which microbes affect obesity-associated diseases may be required with an emphasis on the early events in the progression of such diseases and the multifactorial nature of pathogen-host interactions. This review focuses on pathogens that directly promote obesity and on pathogens that cause chronic infections and thereby enhance metabolic diseases in obese patients. A new perspective on the interaction between infections and obesity-related diseases may improve management of chronic inflammatory diseases that rank high among global threats to human health.

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Key words: Chronic inflammatory diseases; Obesity; Diabetes; Adenovirus-36; *Chlamydia pneumoniae*

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INTRODUCTION

The incidence of obesity has dramatically increased during the recent decades worldwide. Currently, two-thirds of adults in the USA are overweight and around 32% are obese with obesity still trending upwards^[1,2]. Worldwide, over 1 billion adults are overweight and more than 300 million are clinically obese (body mass index $\geq 30 \text{ kg/m}^2$)^[3]. Alarming, obesity has also increased markedly in children^[2]. It has only been recognized over

the last 15 years that obesity is an endocrine disease in which particularly white abdominal adipose tissue secretes large amounts of inflammatory mediators^[4]. The chronic release of these mediators called adipocytokines in patients with high body mass index results in a combination of clinical symptoms characterized by high blood pressure, resistance to intracellular uptake of glucose such that glucose homeostasis requires increased insulin secretion (insulin resistance) and perturbation of the blood lipid profile (high total cholesterol and low-density lipoprotein). The cluster of these clinical symptoms is termed metabolic syndrome.

Obesity and its associated conditions such as metabolic syndrome, diabetes and atherosclerosis are now considered chronic inflammatory diseases^[5]. Inflammation is the key characteristic of obesity and metabolic syndrome and production of pro-inflammatory cytokines such as TNF- α is essential to enhance the development of type 2 diabetes and atherosclerosis. For example, TNF- α induces insulin resistance by stimulating stress hormone production and decreasing tyrosine phosphorylation of insulin-induced insulin receptor substrate 1^[6]. Similarly, inflammation is also a key characteristic of the host response to infectious agents^[7].

While inflammation is a shared and key characteristic of both chronic inflammatory diseases and infections, infectious diseases have long been associated directly with obesity [i.e. Canine distemper virus (CDV), Rous-associated virus-7 (RAV-7), Borna disease virus (BDV), Scrapie agent and adenoviruses SMAM-1 and 36] as well as the consequences of obesity such as metabolic syndrome, diabetes and atherosclerosis [i.e. *Helicobacter pylori* (*H. pylori*), *Chlamydia pneumoniae* (*C. pneumoniae*), *Porphyromonas gingivalis* (*P. gingivalis*), hepatitis C virus (HCV) and human immunodeficiency virus (HIV)]. Clinical experience clearly shows that infectious diseases worsen glycemic control in diabetic patients^[8-10]. Conversely, diabetic patients are also known to be at increased risk for infectious diseases and for higher severity of such diseases^[8,11]. Obesity and exposure to infectious agents overlap in large population segments and therefore may mutually influence each other. Thus, profound practical medical benefits may result from a rational comprehensive approach to the management of chronic inflammatory diseases if therapy of either metabolic syndrome or infectious disease would also mitigate the respective other conditions.

This review focuses first on pathogens that directly promote obesity and, as a downstream consequence of obesity, the development of metabolic syndrome and its associated conditions. Subsequently, the review will focus on a second set of pathogens that cause chronic infections and subsequent release of inflammatory mediators and, *via* this mechanism, induce or exacerbate metabolic syndrome. A new perspective on the connection between infections and obesity-related diseases will better the management of these chronic inflammatory diseases that now rank very highly among the global threats to human health.

OBESITY-ENHANCING PATHOGENS

CDV

CDV is a lymphotropic and neurotropic negative-stranded RNA virus belonging to the genus *Morbillivirus*^[12,13]. It affects mainly dogs and related mammals by invading the nervous system and replicating in neurons and glial cells of the white cell subgroup resulting in a frequently fatal disease^[13]. Even though CDV is not considered a human pathogen, a suggestive association with human disease has been described^[14]. CDV is antigenically closely related to human measles virus with both of them belonging to the same family of *Paramyxoviridae* viruses.

CDV was reported as the first obesity-promoting pathogen in 1982 when Lyons *et al.*^[15] published the landmark article in *Science*, "A virally induced obesity syndrome in mice" that reported that CDV infection induced obesity in Swiss Albino mice. CDV-inoculated mice showed increased body weight as well as an increased number and size of fat cells^[15]. Anatomical damage and altered neurochemistry in the hypothalamus was subsequently demonstrated in CDV-infected mice^[16-21]. The hypothalamus plays a well-documented role in appetite regulation, energy consumption and neuroendocrine function^[18]. CDV-infected mice showed down-regulated leptin receptors in the hypothalamic area of the brain, explaining their inability to generate a proper response to leptin in the brain^[18]. With lower number of leptin receptors, hunger may be induced despite high leptin plasma levels that signal satiety. In addition, CDV also down-regulates melanin-concentrating hormone^[21], expression levels of neuropeptides and catecholamine^[15,22] and production of proinflammatory cytokines^[20]. Collectively, these data suggest that persistent CDV infection of the hypothalamus specifically alters satiety-signaling pathways and thereby induces excessive food consumption and eventually obesity.

RAV-7

RAV-7, an avian leukosis virus, was the second microbe reported to induce obesity. RAV-7 (avian leukosis virus subgroup C) is the most common poultry retrovirus associated with neoplastic disease^[23]. RAV-7 causes obesity in chickens combined with growth stunting, hypertriglyceridemia, hypercholesterolemia as well as enlarged fatty liver, anemia and immunosuppression^[23]. The lipid content of the diet did not influence the RAV-7-mediated induction of obesity^[24]. By 20 d after hatching, infected chickens were smaller than uninfected hatch mates and developed ataxia and obesity over the next 30 d. These chickens also developed mild anemia and lipemia and had high levels of plasma uric acid. RAV-7 infection also induced a marked decrease in the weight of thymus and bursa of Fabricius^[23]. The histological appearance of obesity is characterized in the liver by a diffuse panlobular accumulation of fat in microdroplets and by a lymphoblastoid cellular infiltrate in thyroid gland and pancreas. Carter *et al.*^[24] (1983) hypothesized that RAV-7 infection induces obesity by reducing thyroid hormone levels.

Carter *et al.*^[25] also investigated the specificity of obesity induction by RAV-7. Avian leucosis viruses of the subgroups A [RAV-1 and MAV-1 (O) causing osteopetrosis], B [MAV-2 (O) and MAV-2 (N) causing nephroblastoma], D (RAV-50) and F (RAV-61 and ring-necked pheasant virus) did not induce obesity^[25].

BDV

Borna disease virus is an enveloped, non-segmented, negative-stranded RNA virus of the order *Mononegavirales* with replication and transcription inside the nucleus of the host cells^[26-28]. BDV infection is found worldwide and induces fatal disease in numerous animals such as horse, sheep, cat and dog^[29,30] and there is also evidence that BDV may affect humans^[31,32]. Chalmers *et al.*^[32] (2005) reported between 0% to 48% BDV seropositivity and 0% to 82% BDV antigen prevalence in humans. Narayan *et al.*^[33] and Gosztonyi *et al.*^[34,35] described an obesity syndrome in rats apparently induced by BDV in an age-, genetic background- and virus strain-dependent manner. Infected obese rats showed massive visceral fat deposition with elevated serum glucose levels and hypertriglyceridemia^[34]. Several investigators hypothesized that BDV infection induces obesity through inflammatory lesions and viral antigen expression in the brain, particularly in the hypothalamus, similar to CDV infection^[36].

Scrapie agent

The causative agent of scrapie is thought to be a prion^[37]. Scrapie agent causes a fatal neurodegenerative disease with a long incubation period in sheep and goats^[38]. Scrapie agent is not known to infect humans. In the laboratory, many other animals such as hamster, mice, rats, voles, gerbils, mink, cattle and monkeys have been successfully infected with scrapie agent^[37]. This disease is classified as transmissible spongiform encephalopathy, similar to human Creutzfeldt-Jacob's disease and related TSEs caused by prions^[39-40].

Kim *et al.*^[41] reported that the ME-7 scrapie strain induced obesity and vacuolization in the forebrain of mice but other strains did not. Since adrenalectomy prevented obesity, it was suggested that this scrapie agent induces obesity *via* the hypothalamic-pituitary-adrenal axis^[42]. Scrapie agent was also confirmed to cause hyperglycemia, hyperinsulinemia and diabetes by inducing pancreatic lesions and a significant decrease of the glucose transporter GLUT-1 in the brain^[43,44].

Adenovirus-SMAM-1

Adenoviruses are non-enveloped DNA viruses with icosahedral symmetry and a diameter of 65-80 nm^[45]. Adenoviruses were first isolated in 1953 during establishment of cell lines from pediatric adenoidal tissues obtained by tonsillectomy^[46]. Adenoviruses infect a wide range of hosts such as birds, mammals and humans. Approximately 8% of the world-wide reported virus infections were caused by adenoviruses which can cause serious respiratory disease of epidemic proportions

reported with a group of military recruits^[47]. There are 5 major subgroups of human adenoviruses and each subgroup is also subdivided into several serotypes. The viral genome consists of 5 early transcription units (E1A, E1B, E2, E3, and E4), 2 delayed early units (IX and Iva2) and one major late unit to generate mRNAs (L1-L5)^[38]. Adenoviruses produce a variety of serious diseases in people of all ages.

SMAM-1 is a strain of avian adenovirus responsible for a poultry epidemic in India during the 1980s^[48] and is serologically related to another poultry adenovirus, chick embryo lethal orphan virus (CELO). SMAM-1-inoculated 3 wk-old chickens showed 53% greater visceral fat 3 wk post inoculation compared to uninfected controls. Paradoxically, the increased adiposity in SMAM-1 infected chickens was accompanied by reduced body weight and lower blood concentrations of cholesterol and triglycerides than in controls^[49]. Livers of the SMAM-1 infected chickens were significantly heavier and showed severe congestion, fatty infiltration and presence of intranuclear inclusion bodies under histopathological examination. The infected chickens showed also atrophied bursae, spleen and thymus^[49]. Dhurandhar *et al.*^[50] (1997) reported an association between SMAM-1 seropositivity and human obesity. SMAM-1 antibody-positive humans showed significantly higher BMI and significantly lower blood cholesterol and triglycerides compared to the antibody-negative subjects.

Adenovirus-36

The Adenovirus-36 strain of adenoviruses was first identified in 1978 in Germany from the feces of a 6-year-old girl with diabetes and enteritis^[51]. Accumulated evidence from animal models, *in vitro* experiments and human epidemiology strongly suggest a positive association between adenovirus-36 and human obesity. Atkinson *et al.* showed that 11%-30% of Americans are seropositive against adenovirus-36^[52]. Dhurandhar *et al.*^[53] (2000) explored the influence of adenovirus-36 infection on the development of obesity in chickens. Adenovirus-36 challenged chickens showed 100% greater visceral fat and total body weight than the control group inoculated with sterile cell culture medium and these conclusions were confirmed by the subsequent studies^[54]. Adenovirus-36 inoculated male marmoset monkeys showed an astonishing 3-fold weight gain compared to uninfected controls^[55]. *In vitro* studies showed that adenovirus-36 promotes the proliferation, differentiation and lipid accumulation in 3T3-L1 preadipocytes^[38]. Atkinson *et al.* screened the sera of 360 obese (BMI ≥ 30 kg/m²) and 142 non obese (BMI ≤ 30 kg/m²) subjects in Wisconsin, Florida and New York for adenovirus-36 antibodies. Adenovirus-36 antibodies were 30% and 11% prevalent in obese and non-obese subjects respectively and obese and non obese subjects with adenovirus-36 antibodies had significantly greater BMI than their respective seronegative counterparts^[52]. The authors concluded that the influence of adenovirus-36 seropositivity on obesity

was highly significant independent of age, sex and origin of the human subjects^[38,52]. *In vitro* studies shed light on the mechanisms of adenovirus-36-inducing obesity. Adenovirus-36 infected human preadipocytes showed increased replication, differentiation, lipid accumulation as well as reduced leptin secretion in fat cells^[38,54,56]. This effect is specific for adenovirus-36 and is not observed with nonadipogenic adenovirus (Ad-2). It is likely that adenovirus-36 infection increases the number of fat cells, glucose uptake by adipocytes and promotes lipogenesis^[56]. Na *et al*^[57] and Atkinson *et al*^[58] reported a positive association between human adenovirus-36 and obesity in children. However, two recent epidemiological surveys^[59,60] indicated that human adenovirus-36 did not play a direct role in the development of obesity in both Western Europe and the US.

Adenovirus type 5 has been widely used for gene therapy because it is a safe and efficient vector and accommodates large antigen-encoding structures^[61]. So *et al*^[62] (2005) showed that adenovirus-5 infected mice attained significantly greater body weight and higher adiposity than control group 22-23 wk post inoculation. The same mechanisms as found in adenovirus-36, i.e. increased preadipocyte differentiation, also apply for adenovirus-5 infection^[56]. Human adenovirus-37 was first isolated by de Jong *et al*^[63]. Adenovirus-37 caused adiposity in chickens and the visceral fat pads were three times heavier in adenovirus-37-inoculated chickens than in controls. Different from adenovirus-36, adenovirus-37 infections did not induce reduced concentrations of serum cholesterol. Among over 50 strains of adenoviruses among five subgroups maintained by ATCC, strains adenovirus-36 and adenovirus-37, adenovirus-5 are adipogenic and adenovirus-2 and adenovirus-31 are not adipogenic. The potential of other human adenoviruses on the development of obesity remains unknown.

PATHOGENS ENHANCING HUMAN CHRONIC INFLAMMATORY DISEASES AND OBESITY

H. pylori

H. pylori is a spiral-shaped gram-negative flagellated bacterium and causes highly prevalent chronic infections worldwide^[64]. *H. pylori* is the etiology of diseases such as gastritis and stomach cancer but most *H. pylori* infections are “silent” and produce no clinical symptoms and in particular are asymptomatic in childhood. Worldwide, up to 10% of children and 80% of adults show laboratory evidence of *H. pylori* infection. Aydemir *et al*^[65] (2005) provided the first association between chronic *H. pylori* infection and insulin resistance. The homeostasis model assessment of insulin resistance was significantly higher in 36 *H. pylori*-positive subjects than in 27 *H. pylori*-negative ones^[65]. Epidemiological evidence also supports the association of *H. pylori* seropositivity with cardiovascular diseases and elevated parameters of metabolic syndrome^[66,67].

C. pneumoniae

C. pneumoniae, an intracellular respiratory bacterium, causes acute or chronic bronchitis and pneumonia^[68] and is responsible for 10% of the cases of community-acquired pneumonia and approximately 5% of cases of bronchitis and sinusitis in adults^[68-70]. Many epidemiological surveys, experimental studies and clinical trials have provided strong evidence for the association between *C. pneumoniae* infection and metabolic syndrome, insulin resistance and cardiovascular disease^[70-82]. The current concept of the influence of *C. pneumoniae* on atherosclerosis is that *C. pneumoniae*-infected macrophages traffic to secondary organs including arterial endothelium, induce persistent infection and lead to the local upregulation of proinflammatory molecules (Figure 1A). Subsequently, infected macrophages and smooth muscle cells transform into foam cells and result in plaque destabilization, thrombus formation and myocardial infarction in arterial endothelium^[75,85]. Ased on this notion, antibiotic treatment would reduce cardiovascular events by eliminating *C. pneumoniae* persistent infection and preventing re-infection. However, clinical trials with antibiotic treatment based on this concept failed. This failure to reduce cardiovascular events by antibiotic treatment requires the reformulation of the current mechanistic understanding of the association between *C. pneumoniae* and metabolic syndrome and cardiovascular disease^[83].

Wang *et al*^[84] examined the influence of *C. pneumoniae* infection on progression of insulin resistance in dependence of host genetic background and dietary fat concentration in an obese mouse model. They concluded that murine *C. pneumoniae* infection enhances insulin resistance and diabetes in a genetically and nutritionally restricted manner *via* circulating inflammatory mediators such as TNF- α ^[84] and proposed a new mechanism of *C. pneumoniae*-induced exacerbation of insulin resistance developed in this investigation (Figure 1B). By quantifying the levels of *C. pneumoniae* and TNF- α transcripts in different organs, they concluded that the dispersal of a small number of *C. pneumoniae* organisms to secondary tissues was irrelevant to progression of insulin resistance and the early onset of type 2 diabetes. In contrast, the bulk infection of the lung caused an increase in circulating cytokines that drove the long-term exacerbation of insulin resistance (Figure 1B) and accelerated the onset of type 2 diabetes^[84]. It was reported that combined pathogen burden^[82] and positive serology for both *H. pylori* and *C. pneumoniae*^[66] showed the strongest association with insulin resistance. These data suggest that exposure to multiple pathogens may potentiate chronic low-grade inflammation and insulin resistance and that the mechanisms whereby the pathogens affect chronic inflammatory diseases are shared.

P. gingivalis

A national survey with 9 689 subjects from 1988 to 1994 showed that periodontal disease is prevalent in the U.S. adult population^[86]. Approximately 35% of the adults

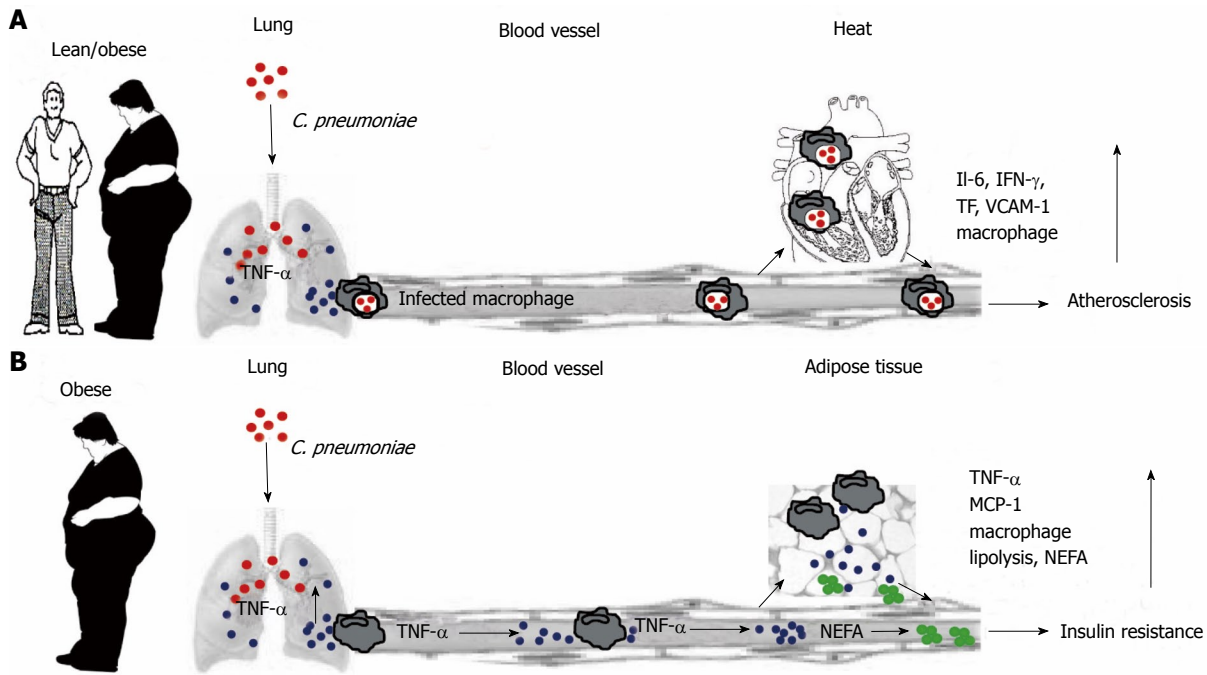


Figure 1 Schematic representation of *C. pneumoniae*-mediated acceleration of inflammatory diseases associated with metabolic syndrome. **A:** Current concept of the influence of *C. pneumoniae* on atherosclerosis. After respiratory infection, *C. pneumoniae* (red) is endocytosed by alveolar macrophages of infected lean or obese individuals. Infected macrophages re-enter circulation and traffic to secondary organs including arterial endothelium. Disseminated *C. pneumoniae* organisms infect other cell types, leading to up-regulation of pro-inflammatory molecules such as IL-6, IFN- γ , tissue factor and vascular-cell-adhesion molecule 1. These cytokines, in particular IFN- γ , retard chlamydial replication and induce persistent infection. In arterial endothelium, infected macrophages and smooth muscle cells transform into foam cells, affecting atheroma biology and leading to plaque destabilization, thrombus formation or myocardial infarction^[85]. **B:** Concept of *C. pneumoniae*-induced exacerbation of insulin resistance developed by Wang *et al.*^[84]. *C. pneumoniae* infection results in lung colonization, thereby increasing TNF- α release (blue). Circulating TNF- α induces insulin resistance by inhibiting the function of insulin receptor substrate-1 in peripheral tissues and further exacerbates insulin resistance by promoting lipolysis and increased NEFA (green) production in adipose tissue. TNF- α and NEFA promote further macrophage infiltration and excess production of pro-inflammatory molecules in adipose tissue. In contrast to the atherosclerosis concept, the perpetuation of adipose tissue inflammation is driven by circulating pro-inflammatory cytokines rather than by in situ production stimulated by infected macrophages. Sustained by continuous high-fat nutrition, the inflammatory condition of adipose tissue maintains the vicious cycle of insulin resistance in the absence of *C. pneumoniae* organisms.

in the USA have periodontitis, an inflammation that involves the periodontal ligament and alveolar bone, while about 75% have gingivitis, an inflammation of the gingival tissues surrounding the teeth^[8,86]. Periodontal diseases are initiated by gram-negative and anaerobic bacteria such as *P. gingivalis* residing in biofilms on gingival tissues and teeth^[87]. Periodontal diseases had been thought of as localized conditions of concern only to dental health professionals. Emerging evidence now suggests that periodontal diseases also exacerbate systemic conditions such as metabolic syndrome and diabetes^[88,89]. The oral infection causes elevated circulating IL-1 β and TNF- α which lead to hyperlipidemia and development of diabetes^[88,90].

HCV

HCV infection is a worldwide problem with approximately 200 million infected individuals^[1,2]. Chronic HCV infection may result in liver cirrhosis and hepatocellular carcinoma and is associated with multifaceted disease such as porphyria cutanea tarda, membranoproliferative glomerulonephritis and cryoglobulinemia. While epidemiological studies suggested a linkage between HCV infections and type 2 diabetes^[91-95], Shintani *et al.*^[91] confirmed the direct involvement of HCV infection in the

development of insulin resistance in a mouse model using mice with the HCV core gene inserted in their genome. They showed that a high level of TNF- α was the main factor to induce insulin resistance in HCV-transgenic mice and insulin sensitivity was restored by administration of anti-TNF- α antibody.

HIV

Insulin resistance is common in HIV-infected people and the prevalence of hyperglycemia and diabetes is significantly higher in people with HIV infection treated with antiretrovirals as compared with the general population^[96]. The prevalence of insulin resistance in HIV subjects is around 35% and up to 47% when they received protease inhibitor therapy, while the incidence of insulin resistance is only around 5% in the general population^[97]. Presumably, HIV induces an increased inflammatory state, as evident in elevated levels of adiponectin and free fatty acids in HIV-infected individuals^[96].

CONCLUSION

Ranked as one of the three major challenges to human progress along with war and famine, infectious diseases remain among the leading causes of death and disability

Table 1 Pathogens associated with obesity

Pathogen	Effect	Mechanisms	Ref
CDV	Increased body weight in Swiss albino mice	Altered hypothalamic integrity; increased cytokine production, hyperinsulinemia and decreased leptin and neuropeptides	[15-17,21, 22]
RAV-7	Stunting, anemia and increased visceral fat in white leghorn chickens	Decreased thyroxine, hyperlipidemia and hyperinsulinemia	[23,24]
BDV	Obesity with increased visceral fat in Lewis rats	Inflammatory lesions in hypothalamus, increased triglyceride and blood glucose	[35,36]
SMAM-1	Stunting and increased visceral fat in white leghorn chickens	Impaired liver function and lipogenesis and glucagon deficiency	[49,50]
Scrapie agent	Increased body weight and fat accumulation in mice	Altered brain function and reduced GLUT-1	[43,44]
Adenovirus	Increased body weight in chickens, mice, rats and monkeys; seropositive subjects were heavier than seronegative counterparts	Increased replication, differentiation and lipid accumulation of preadipocytes	[51-60]

CDV: Canine distemper virus; RAV-7: Rous-associated virus-7; BDV: Borna disease virus; Ref: Reference.

worldwide^[98]. More than 25% of annual human deaths are the direct result of infectious diseases^[98,99]. Progress in diagnostic methodology now allows the consistent detection of low-number but widely-prevalent pathogens as well as sensitive and precise quantification that captures subtle elevations of inflammatory cytokines which are closely related to metabolism and the immune response. Application of these essential tools in epidemiological, pathological and experimental studies has strongly suggested an infectious influence on obesity, metabolic syndrome, diabetes and cardiovascular diseases.

Following Darwinian adaption in human evolution, thrifty genes have probably evolved to maximize food utilization during periods of mass starvation. This metabolic adaptation combines frugal use of nutrients with vigorous inflammatory responses to pathogens and thus maximizes survival^[100,101]. While advantageous under selective pressure of starvation and epidemic infectious diseases, this genetic makeup of large population segments has become a liability in times of food abundance and increased hygiene that eliminates epidemic but not endemic chronic infections. The evolved frugal metabolic characteristics increase obesity under conditions of over-nutrition and intensive inflammatory responses enhance the pathological consequences of obesity under constant stimulation by previously unrecognized ubiquitous but low-level chronic infections.

In summary, the dominant influence on chronic inflammatory diseases is anchored in human genetics and the

Table 2 Pathogens associated with increased chronic inflammatory diseases in humans

Pathogen	Effect	Mechanisms	Ref
<i>H. pylori</i>	Affected subjects showed increased insulin resistance	Increased concentrations of plasma glucose and lipids	[64-67]
<i>C. pneumoniae</i>	Increased metabolic syndrome, insulin resistance and cardiovascular disease	Increased production of proinflammatory and circulating cytokines	[68-72]
<i>P. gingivalis</i>	Adults with dental infections demonstrated higher chance of insulin resistance and diabetes	Increased oxidative stress, advanced glycation end-products and altered immune function	[86-90]
HCV	Infected patients showed increased chance to develop insulin resistance and diabetes	Increased production of TNF and IL-6	[92-95]
HIV	HIV patients showed higher insulin resistance (35%) compared to normal subjects (5%)	Impaired glucose tolerance and significant hyperinsulinaemia	[96-97]

H. pylori: *Helicobacter pylori*; *C. pneumoniae*: *Chlamydia pneumoniae*; *P. gingivalis*: *Porphyromonas gingivalis*; HCV: Hepatitis C virus; HIV: human immunodeficiency virus; Ref: Reference.

outcome is driven by food supply and consumption. In this cause-effect network with tightly integrated metabolic and immune response pathways, infections likely play a heretofore underappreciated role in modulating intensity and pathological consequences, thus potentially decisively modulating the cause-effect network in the pathogenesis of chronic inflammatory diseases. Confirmation of the infectious modulation of obesity (Table 1) and chronic inflammatory diseases (Table 2) will facilitate prevention and management of such diseases. Very likely, vaccinations against multiple infectious agents will be the sole effective and realistic approach to ameliorate pathogen-enhanced obesity and related conditions such as diabetes and atherosclerosis.

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Surrogate markers of insulin resistance: A review

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Abstract

Insulin resistance is a hallmark of obesity, diabetes, and cardiovascular diseases, and leads to many of the abnormalities associated with metabolic syndrome. Our understanding of insulin resistance has improved tremendously over the years, but certain aspects of its estimation still remain elusive to researchers and clinicians. The quantitative assessment of insulin sensitivity is not routinely used during biochemical investigations for diagnostic purposes, but the emerging importance of insulin resistance has led to its wider application research studies. Evaluation of a number of clinical states where insulin sensitivity is compromised calls for assessment of insulin resistance. Insulin resistance is increasingly being assessed in various disease conditions where it aids in examining their pathogenesis, etiology and consequences. The hyperinsulinemic euglycemic glucose clamp is the gold standard method for the determination of insulin sensitivity, but is impractical as it is labor- and time-intensive. A number of surrogate indices have therefore been employed to simplify and improve the determination of insulin resistance. The object of this review is to highlight various aspects and methodologies for current and upcoming measures of

insulin sensitivity/resistance. In-depth knowledge of these markers will help in better understanding and exploitation of the condition.

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Key words: Insulin resistance; Markers; Insulin; Homeostatic model assessment; Quantitative insulin sensitivity check index

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INTRODUCTION

Insulin is a key regulator of glucose homeostasis. Insulin resistance is established by genetic and environmental factors. Insulin resistance (IR) leads to impaired glucose tolerance, and plays an important pathophysiological role in the development of diabetes^[1]. In addition, IR leads to many of the metabolic abnormalities associated with metabolic syndrome/syndrome X. Patients with insulin resistance are likely to have impaired fasting plasma glucose levels, which in turn enhance the prevalence of more atherogenic, small dense low-density lipoprotein (LDL) particles. Central obesity and insulin resistance form the basis of the pathophysiology of dyslipidemia, lack of glucose tolerance, and the existence of chronic subclinical inflammation and hypertension in metabolic syndrome. IR has been described as a condition where a greater than normal amount of insulin is required to obtain a quantitatively normal response^[2]. Measuring

insulin resistance has progressed from its role in the pathogenesis of diabetes, to an even more important role.

IR: PATHOGENESIS

The mechanism underlying IR involves a complex network of metabolism of glucose and fat, with the inflammatory cascade playing an important role. The important actions of insulin are anti-lipolysis in adipose tissue and stimulation of lipoprotein lipase^[3]. Expanded adipose tissue mass associated with obesity mobilises free fatty acids (FFA) in circulation through the action of the cyclic-AMP dependent enzyme hormone sensitive lipase. FFA are also released through lipolysis of Triglyceride (TG)-rich lipoproteins in tissues by means of lipoprotein lipase^[4]. In insulin-sensitive tissue, excessive fatty acids create insulin resistance by means of the added substrate availability and by modifying down-stream signalling^[5]. When insulin resistance sets in, the increased lipolysis of stored TG in adipose tissue produces more fatty acids. The increased FFA concentration inhibits the anti-lipolytic action of insulin. The role of innate immunity and infection has also been postulated in the development of insulin resistance and can predict the development of diabetes mellitus type II^[6,7].

Insulin resistance, metabolic syndrome and atherosclerotic events share a common inflammatory basis. Presence of a low-grade systemic inflammation is the main mechanism that leads to impaired insulin action^[8].

DISEASE CONDITIONS ASSOCIATED WITH IR

IR is an important clinical and biochemical determinant, not only of diabetes but also of many other clinical states. There is a need to evaluate insulin resistance, since it is an underlying mechanism and predictor of cardio-vascular diseases, diabetes, hypertension, obesity and other consequences of metabolic syndrome and impaired insulin sensitivity. In nondiabetic individuals, the initial presentation associated with insulin resistance is hyperinsulinemia, impaired glucose tolerance, dyslipidemia [hypertriglyceridemia and decreased high-density lipoprotein (HDL) cholesterol] and hypertension^[9]. Insulin resistance contributes significantly to the pathophysiology of type 2 diabetes and is a hallmark of obesity, dyslipidemias, hypertension, and other components of the metabolic syndrome^[10,11]. The association between insulin resistance and subclinical or clinical cardio-vascular disease in both nondiabetic^[12-14] and diabetic subjects^[15,16] has been observed.

Insulin resistance has been an area of interest in recent times, as it has effects on wide array of diseases. The pathophysiological conditions coupled with insulin resistance have persistently increased and include small dense LDL particles^[17], augmented postprandial lipemia^[18], enhanced renal sodium retention and high uric acid

levels^[19], dysfibrinolysis^[20] increased resting heart rate^[21] and polycystic ovarian syndrome^[22]. In clinical practice, a family history of diabetes, a history of polycystic ovarian syndrome, gestational diabetes, impaired glucose metabolism, and obesity should be seen as a herald of the possibility of insulin resistance^[23].

ESTIMATION OF IR/MEASUREMENT OF IR

A marker is a measurable variable found in an available biological sample or detected by tissue imaging, which can reflect the underlying disease pathophysiology, predict future events and indicate the response to treatment. Markers serve as sensitive detectors of early target organ damage^[24]. Currently, validated risk-assessment tools do not satisfactorily account for the increased risk factors associated with metabolic syndrome^[25]. Hence the need to identify markers of this syndrome is imperative.

Estimation of insulin resistance is being studied widely in humans. It is of great importance to develop animal models that are appropriate to the investigation of the epidemiology, pathophysiological mechanisms, outcomes of therapeutic interventions, and clinical courses of patients with insulin resistance. Insulin resistance is an established independent predictor of a range of disorders. Resistance to insulin sets in long before any disease signs start appearing. It is important to categorize and treat individuals with insulin resistance as early as possible, because hyperinsulinemia might remain undiagnosed for a long period, thereby increasing the risk of the development of other components of the syndrome, and consequent diseases. Prompt recognition and management of this metabolic syndrome offers important preventive measures^[23].

In addition to maintaining whole body glucose homeostasis and promoting efficient glucose utilization^[26], there are many other important physiological targets of insulin, including the brain, pancreatic β -cells, heart and vascular endothelium, that help to coordinate and couple metabolic and cardiovascular homeostasis under healthy conditions^[26-29]. An accurate method for easily evaluating insulin sensitivity and following changes after therapeutic intervention is thus required.

NEED FOR SURROGATE MARKERS

Quantifying insulin sensitivity/resistance in humans and animal models is of great importance for basic science investigations and eventual use in clinical practice^[30].

Among the tools to characterize IR and measure whole-body insulin action, the euglycemic hyperinsulinemic clamp technique is the direct method of estimation of IR. As this requires insulin infusion and repeated blood sampling, there is a need for simple, accessible measures for the evaluation of insulin sensitivity. Most large scale epidemiological studies merely correlate fasting insulin levels with the concerned outcome.

Table 1 Various methods to measure insulin resistance

S No	Method	Comments	Advantages	Disadvantages
1	Hyperinsulinemic euglycemic glucose clamp	Gold standard method for quantifying insulin sensitivity	Direct measure of insulin under steady-state conditions	Laborious, involves intra venous infusion of insulin, frequent blood sampling
2	Oral glucose tolerance test	Clinically used to detect glucose intolerance	Helps in estimating other surrogate indices	Useful for glucose tolerance but not for IR
3	Fasting insulin	Most practical method to measure IR	Detects insulin resistance before clinical disease appears	Lack of standardization of the insulin assay procedure
4	Glucose/insulin ratio (G/I ratio)	comparable to insulin sensitivity measured by the FSIVGTTT	Highly sensitive & specific for insulin sensitivity	Does not aptly reveal the physiology of insulin sensitivity
5	Insulinogenic index (IGI)	index of β -cell function $\delta I (0-30 \text{ min}) / \delta G (0-30 \text{ min})$	Measure of first-phase insulin response to glucose challenge	Not broadly validated
6	Homeostasis model assessment	Assesses inherent β -cell function and insulin sensitivity $HOMA-IR = (G \times I) / 22.5$	Simple, minimally invasive, predicts fasting steady-state G and I levels	Insulin sensitivity in subjects treated with insulin needs further validation
7	Quantitative insulin sensitivity check index (QUICKI)	Mathematical transformation of FBG and insulin $QUICKI = 1 / [\log (I \mu U/mL) + \log (G \text{ mg/dL})]$	Consistent, precise index of insulin sensitivity, minimally invasive	Normal range to be established for each laboratory due to significant inter laboratory variations in insulin assay
8	Minimal model analysis of frequently sampled intravenous glucose tolerance test	Indirect measure of insulin sensitivity/resistance	Analysis using the computer program MINMOD	Multiple blood sampling
9	Glucose insulin (GI) product	Index of whole-body insulin sensitivity		
10	Fasting insulin resistance index (FIRI)	$(\text{fasting } G \times \text{fasting } I) / 25$		

G: Glucose; I: Insulin; IR: Insulin resistance; FBG: Fasting blood glucose.

IR can be assessed by various means. Most of the methods employed are difficult to apply in clinical practice. Since compensatory hyperinsulinemia is highly correlated with IR^[31], it has been observed that it may offer a better way to identify insulin-resistant patients than do measurements of glucose intolerance. On the other hand, analytic methods for insulin measurements are not standardized, thus making it hard to compare absolute values of plasma insulin concentrations from one laboratory to another^[32].

There has been an urgent need for the consideration of other parameters that can be used to assess IR, along with the development of novel surrogate markers of insulin resistance, which are more applicable for large population-based epidemiological investigations. Numerous such markers have been proposed on many occasions in the literature^[33-39].

More than 15 years ago, the mathematical model of the normal physiological dynamics of insulin and glucose produced the homeostasis model assessment (HOMA), which provided equations for estimating insulin resistance (HOMA-IR) and β -cell function from simultaneous fasting measures of insulin and glucose levels^[36]. In addition, the quantitative insulin sensitivity check index (QUICKI) derived from logarithmically-transformed fasting plasma glucose (FPG) and insulin levels has proven to be a first-rate index of insulin resistance in comparison with clamp-IR^[40].

The efficacy and implication of surrogate assessment of insulin resistance depends on the extent to which it correlates with the direct estimate of this variable.

Various methods to quantify insulin resistance have been described, and are shown below in Table 1.

Hyperinsulinemic euglycemic glucose clamp

The hyperinsulinemic euglycemic glucose clamp technique has been described as the gold standard method for quantifying insulin sensitivity^[41]. It is the reference method for quantifying insulin sensitivity in humans because it directly measures the effects of insulin in promoting glucose utilization under steady-state conditions *in vivo*^[41]. Direct estimation of IR by means of the euglycemic clamp technique and insulin suppression test (IST) is experimentally demanding, complicated, and impractical when large scale epidemiological studies are involved. These methods are laborious, painstaking and expensive, are therefore rarely used in larger-scale clinical research and, as such, are irrelevant for clinical practice. Consequently, over the years, a number of surrogate indices for insulin sensitivity or insulin resistance have been developed.

The glucose clamp is difficult to apply in large scale investigations because of the chaotic procedure, which involves intra-venous infusion of insulin, taking frequent blood samples over a 3 h period, and the continuous adjustment of a glucose infusion.

SURROGATE MARKERS

Oral glucose tolerance test

The oral glucose tolerance test (OGTT) is an easy test,

and is commonly used in medical practice to detect glucose intolerance as well as type 2 diabetes^[42]. It involves the administration of glucose to find out how rapidly it is cleared from the blood stream. It implicates the efficiency of the body to utilize glucose after glucose load.

During OGTT, after 8 to 10 h of fasting, blood glucose levels are determined at 0, 30, 60, and 120 min following a standard oral glucose load (75 g)^[42,43].

It imitates the normal physiology of the glucose and insulin flux more closely than conditions of the other methods such as the glucose clamp, IST, or the Frequently Sampled Intravenous Glucose Tolerance Test (FSIVGTT). Since glucose tolerance and insulin sensitivity are dissimilar conceptually, OGTT provides useful information about glucose tolerance but not insulin resistance. However, OGTT is also used to estimate other surrogate indices of insulin resistance. Impaired glucose tolerance offers few aberrations during OGTT. Firstly, rapid and continuous rise in plasma glucose concentration, and secondly, lack of decline below 140 mg/dL in plasma glucose at 2 h after attaining peak value. Subjects with impaired fasting glucose (IFG) have higher FPG than individuals with normal glucose tolerance or impaired glucose tolerance (IGT)^[44].

Fasting insulin

Measurement of the fasting insulin level has long been considered the most practical approach for the measurement of insulin resistance^[33]. It correlates well with insulin resistance. A considerable correlation has been found between fasting insulin levels and insulin action as measured by the clamp technique. A substantial overlap between insulin-resistant and normal subjects is a constraint, as there is a lack of standardization of the insulin assay procedure. Nevertheless, with a reliable insulin assay, insulin resistance can be detected early, before clinical disease appears^[45].

As glucose levels change rapidly in the postprandial state, the use of fasting insulin for estimating IR should be done after an overnight fast, since the variable levels of glucose confound the simultaneous measure of insulin.

In healthy subjects, increased fasting insulin levels (with normal fasting glucose levels) correspond to insulin resistance. In this population $1/(\text{fasting insulin})$ can substituted for insulin sensitivity that decreases as subjects become more insulin resistant (and fasting insulin levels rise)^[33]. However, it does not cover the inappropriately low insulin secretion in the face of hyperglycemia seen in diabetic subjects or glucose-intolerant subjects.

Use of fasting insulin levels for assessment of IR is limited because of a high proportion of false-positive results and by lack of standardization. To overcome this issue, standardization of insulin assay has been recommended by the ADA Task Force, to be certified by a central laboratory^[44].

A high plasma insulin value in individuals with normal glucose tolerance reflects insulin resistance, and high insulin levels presage the development of diabetes^[45].

Glucose/insulin ratio

The Glucose/insulin (G/I) ratio has been employed in a number of studies as an index of insulin resistance^[34,46,47]. Functionally, it will be equivalent to $1/(\text{fasting insulin})$ in non-diabetics as fasting glucose levels are all in the normal range, though it does not appropriately reflect the physiology underlying the determinants of insulin sensitivity^[48]. The fasting G/I ratio is a theoretically imperfect index of insulin sensitivity.

In a study conducted by Legro *et al.*^[35] fasting G/I ratio was compared to insulin sensitivity measured by the FSIVGTT. It was found that fasting G/I ratio is a highly sensitive and specific measurement of insulin sensitivity.

Insulinogenic index

The insulinogenic index (IGI) is a frequently used index of β -cell function. It is an index of insulin secretion derived from OGTT^[49].

$$\text{IGI} = \delta\text{insulin (0-30 min)} / \delta\text{glucose (0-30 min)}$$

Insulin is measured in microunits per millilitre, whereas glucose is measured in milligrams per decilitre^[49].

The insulinogenic index helps to estimate the level of insulin secretion with a more physiological route of glucose administration.

While it has not been extensively validated, the insulinogenic index during the first 30 min of the OGTT has commonly been used in epidemiological studies as a surrogate measure of first-phase insulin responses to a glucose challenge.

HOMA

HOMA was first developed in 1985 by Matthews *et al.*^[36]. It is a method used to quantify insulin resistance and β -cell function from basal (fasting) glucose and insulin (or C-peptide) concentrations. HOMA is a model of the relationship of glucose and insulin dynamics that predicts fasting steady-state glucose and insulin concentrations for a wide range of possible combinations of insulin resistance and β -cell function. Insulin levels depend on the pancreatic β -cell effect to glucose concentrations while, glucose concentrations are regulated by insulin-mediated glucose production via the liver. Thus, deficient β -cell function will echo a diminished response of β -cell to glucose-stimulated insulin secretion^[35,50,51]. Similarly, insulin resistance is reflected by the diminished suppressive effect of insulin on hepatic glucose production. The HOMA model has proved to be a robust clinical and epidemiological tool for the assessment of insulin resistance.

HOMA describes this glucose-insulin homeostasis by means of a set of simple, mathematically-derived nonlinear equations. The approximating equation for insulin resistance has been simplified, and uses a fasting blood sample. It is derived from the use of the insulin-glucose product, divided by a constant. The product of FPG \times FPI is an index of hepatic insulin resistance.

HOMA-IR = (glucose \times insulin)/22.5: Insulin concentration is reported in $\mu\text{U/L}$ and glucose in mmol/L .

The constant of 22.5 is a normalizing factor; i.e., the product of normal fasting plasma insulin of 5 $\mu\text{U/mL}$, and the normal fasting plasma glucose of 4.5 mmol/L typical of a "normal" healthy individual = 22.5. Whereas the β -cell function is also calculated by another equation using fasting insulin and glucose values.

HOMA1 - %B = $(20 \times \text{FPI})/(\text{FPG} - 3.5)$: On the other hand, HOMA β -cell is another calculated variable indicating the insulin activity. It is a marker of basal insulin secretion of pancreatic β -cells^[52].

HOMA β cell = $20 \times \text{fasting plasma insulin } (\mu\text{U/mL})/\text{FPG (mmol)}-3$: Estimation with the help of HOMA model parallels equally with that of the euglycemic clamp method ($r = 0.88$)^[51].

HOMA-IR has been observed to have a linear correlation with the glucose clamp and minimal model estimates of insulin sensitivity/resistance in various studies of distinct populations^[51,53]. Derived from a mathematical assessment of the interaction between β -cell function and IR, the HOMA model is used to compute steady-state insulin and glucose concentrations. C-peptide, a measure of insulin secretion (not insulin action), can be used in HOMA modelling of both β -cell function and IR.

QUICKI

QUICKI is an empirically-derived mathematical transformation of fasting blood glucose and plasma insulin concentrations that provides a consistent and precise index of insulin sensitivity with better positive predictive power^[41,54-56]. It is simply a variation of HOMA equations, as it transforms the data by taking both the logarithm and the reciprocal of the glucose-insulin product, thus slightly skewing the distribution of fasting insulin values.

QUICKI has been seen to have a significantly better linear correlation with glucose clamp determinations of insulin sensitivity than minimal-model estimates, especially in obese and diabetic subjects^[54]. It employs the use of fasting values of insulin and glucose as in HOMA calculations. QUICKI^[37] is virtually identical to the simple equation form of the HOMA model in all aspects, except that a log transform of the insulin glucose product is employed to calculate QUICKI.

$\text{QUICKI} = 1/[\log(\text{Insulin } \mu\text{U/mL}) + \log(\text{Glucose mg/dL})]$ ^[37].

QUICKI should not be considered, as a new model rather simply logs HOMA-IR, which explains the near-perfect correlation with HOMA. It has similar drawbacks to the use of the HOMA equations, compared with the computer model. Given the similarities between QUICKI and HOMA, the two methods compare well.

In conditions like diabetes, glucose intolerance, and hyperlipidemia associated with insulin resistance, or with various combinations of these metabolic disorders, QUICKI index values have been observed to be lower when compared to those of healthy volunteers. Adult patients with a QUICKI index below 0.357 (which is

at the lower limit of 95% confidence limits in healthy people) tend to have a higher risk or frequently present with typical manifestations of metabolic syndrome^[57]. Each laboratory should establish its own normal QUICKI range, since variations in insulin determinations of different laboratories is unavoidable.

Minimal model analysis of the frequently sampled intravenous glucose tolerance test

The minimal model is a method to obtain an indirect measurement of metabolic insulin sensitivity/resistance was developed by Bergman *et al*^[58] in 1979. Glucose and insulin values obtained during a FSIVGTT are used in this method.

The data collected by this method, which involves multiple blood sampling, is subjected to minimal model analysis, using the computer program MINMOD to generate an index of insulin sensitivity (IS). After an overnight fast, glucose is infused intravenously over 2 min, starting at time 0. Presently, a modified FSIVGTT is used where exogenous insulin is also infused after the intravenous glucose bolus^[59-61] followed by the extraction of blood samples for the estimation of plasma glucose and insulin measurements at -10, -1, 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 14, 16, 20, 22, 23, 24, 25, 27, 30, 40, 50, 60, 70, 80, 90, 100, 120, 160, and 180 min.

In contrast to the glucose clamp and IST, which depend on steady-state conditions, the minimal model approach employs the use of dynamic data. Minimal model analysis of the modified FSIVGTT being less demanding in terms of labour, as there are no intravenous infusions and not requirement for steady-state conditions, it is generally found to be easier than the glucose clamp method. The minimal model method^[62] is a simple method, but the complexity of the sampling procedure, the sophisticated data analysis, and the correspondingly higher cost make it unsuitable for clinical settings.

Glucose insulin (GI) product

Application of the product of the plasma glucose and insulin concentrations during the OGTT has also been supported by few researchers as an index of whole-body insulin sensitivity^[63,64]. IR can be envisaged by increased plasma insulin in spite of normal or increased plasma glucose concentrations. The product of the plasma glucose and insulin concentrations provides the better index of insulin sensitivity. Furthermore, the higher the plasma glucose level, along with a higher plasma insulin response, the more severe is the state of insulin resistance. The lower the GI product, the more responsive are the tissues of the body to insulin. Nonetheless, Matsuda and DeFronzo found that this measure correlated well with rate of insulin-mediated glucose disposal during the euglycemic insulin clamp^[50].

Fasting insulin resistance index

The fasting insulin resistance index (FIRI) was formulated

Table 2 Various derived surrogate markers of insulin resistance

S No	Method	Measurement	Comments
1	Matsuda index	$10\,000/\sqrt{(\text{fasting G} \times \text{fasting I}) (\text{mean G} \times \text{mean I})}$	Represents both hepatic and peripheral tissue sensitivity to insulin.
2	Gutt index	$75\,000 + (G_0 - G_{120}) (\text{mg/dL}) \times 0.19 \times \text{BW}/120 \times \text{Gmean}_{(0,120)} (\text{mmol/L}) \times \text{Log} [\text{Imean}_{(0,120)}] (\text{mU/L})$	Good to predict onset of type 2 diabetes
3	Stumvoll index	$0.156 - 0.0000459 \times I_{120} (\text{pmol/L}) - 0.000321 \times I_0 (\text{pmol/L}) - 0.00541 \times G_{120} (\text{mmol/L})$	Utilizes demographic data like age, sex and BMI along with plasma glucose and insulin to predict insulin sensitivity
4	Avignon index	$\text{Sib} = 10^8/[I_0 (\text{mU/L}) \times G_0 (\text{mmol/L}) \times \text{VD}]$ $\text{Si2h} = 10^8/[I_{120} (\text{mU/L}) \times G_{120} (\text{mmol/L}) \times \text{VD}]$	Determines glucose tolerance and insulin sensitivity in single test
5	Oral glucose insulin sensitivity index	G and I concentrations from a 75 g OGTT at 0, 2, and 3 h (3 h OGTT) or at 0, 1.5, and 2 h (2 h OGTT). The formula includes six constants	
6	Log (HOMA-IR)	Evaluates insulin resistance in insulin-resistant states like glucose intolerance and mild to moderate diabetes	

Sib: Derived from fasting plasma insulin and glucose; Si2h: Derived from fasting plasma insulin and glucose ant 2 h of OGTT; OGTT: Oral glucose tolerance test.

by Duncan *et al*^[37] in search of a distinct marker, as the use or ratio of glucose and insulin might not be reliable for the estimation of IR. Increased insulin secretion to restore a normal level of plasma glucose leads to persistent elevation of insulin and probably of glucose also.

FIRI is calculated as $\text{FIRI} = (\text{fasting glucose} \times \text{fasting insulin})/25$.

Derived surrogate markers

Clinical investigators have been in search of more practical indices that measure insulin sensitivity comparable to that of the euglycemic hyperinsulinemic clamp. Such indices of whole-body insulin sensitivity derived from plasma glucose and insulin concentrations during OGTT reflect both muscle and liver insulin sensitivity (see Table 2).

Matsuda index

Several methods have been described that derive an index of insulin sensitivity from the OGTT. In these methods, the ratio of plasma glucose to insulin concentration during the OGTT is used. A novel assessment of insulin sensitivity that is simple to calculate and provides a reasonable approximation of whole-body insulin sensitivity from the OGTT was developed by Matsuda and DeFronzo, and is referred to as the Matsuda index^[50]. Here the OGTT index of insulin sensitivity [ISI (composite)] was calculated using both the data of the entire 3 h OGTT and the first 2 h of the test.

The composite whole-body insulin sensitivity index (WBISI), developed by Matsuda and DeFronzo is based on insulin values given in microunits per millilitre ($\mu\text{U/mL}$) and those of glucose, in milligrams per decilitre (mg/dL) obtained from the OGTT and the corresponding fasting values^[50].

$\text{WBISI} = 10\,000/\sqrt{(\text{fasting glucose} \times \text{fasting insulin}) (\text{mean glucose} \times \text{mean insulin})}$

This index represents a composite of both hepatic and peripheral tissue sensitivity to insulin.

Gutt index

Gutt *et al*^[65] also explored the use of OGTT values in order to try and develop an easy measure of insulin

sensitivity. A formula for an insulin sensitivity index, ISI (0, 120), that used the fasting (0 min) and 120 min post-oral glucose (OGTT) insulin(I) and glucose(G) concentrations along with body weight (BW) was devised.

$\text{ISI}_{(0,120)} = 75\,000 + (G_0 - G_{120}) \times 0.19 \times \text{BW}/120 \times \text{Gmean}_{(0,120)} \times \text{Log} [\text{Imean}_{(0,120)}]$ Insulin concentration is expressed in mU/L and glucose concentration is expressed as mg/dL in the numerator and mmol/L in the denominator. It was shown to correlate well with the insulin sensitivity index obtained from the euglycemic hyperinsulinemic clamp.

Stumvoll index

It is now possible to calculate insulin sensitivity and insulin release from simple demographic parameters and values obtained during an OGTT with practical precision.

Stumvoll *et al*^[66] proposed use of demographic data like age, sex and basal metabolic rate (BMI) in addition to plasma glucose (mmol/L) and insulin (pmol/L) responses during the OGTT to predict insulin sensitivity and beta cell function.

$\text{ISI}_{\text{Stumvoll}} = 0.156 - 0.0000459 \times I_{120} - 0.000321 \times I_0 - 0.00541 \times G_{120}$

$\text{ISI}_{\text{Stumvoll}} = 0.222 - 0.00333 \times \text{BMI} - 0.0000779 \times I_{120} - 0.000422 \times \text{Age}$

The metabolic clearance rate of glucose and ISI calculated by this method included BMI, insulin (120 min), and glucose (90 min).

These parameters correlated better with the measured parameters than the homeostasis model assessment for secretion and resistance^[66].

Avignon index

Avignon *et al*^[67] tried to compare IS indices which were derived from plasma insulin (I) (mU/L), glucose (G) (mmol/L) and apparent glucose distribution volume in the basal state (Sib), and at the end of second hour OGTT (Si2h). Another insulin sensitivity index (SiM) was calculated by averaging Sib and Si2h.

Table 3 Imminent markers of insulin resistance

S No	Marker
1	Insulin growth factor binding protein-1 (IGFBP-1)
2	sCD36 (solubleCD36)
3	C-reactive protein (CRP)
4	Ferritin
5	Adiponectin
6	Tumour necrosis factor (TNF alpha)
7	Resistin
8	C3 complement
9	Glycosylated hemoglobin (Hb)A1c
10	Protein kinase C (PKC) in microangiopathy
11	Sex hormone-binding globulin (SHBG) in hyperandrogenic syndrome

$SiM = [(0.137 \times Sib) + Si2h]/2$, where $Sib = 10^8/(I_0 \times G_0 \times VD)$ and $Si2h = 10^8/(I_{120} \times G_{120} \times VD)$ (VD is an estimate of the apparent glucose distribution volume).

It was observed that the results obtained by computation of sensitivity indices from G and I concentrations in the basal state and during a conventional 2 h OGTT were useful for blending both a determination of glucose tolerance and an estimate of insulin sensitivity in a single and simple test.

Oral glucose insulin sensitivity index

Another group of researchers developed an index of insulin sensitivity which was calculated using a model-derived principle from the OGTT glucose and insulin concentration. This index was found to be equivalent to glucose clearance calculated during a clamp^[68].

The oral glucose insulin sensitivity index requires glucose and insulin concentrations from a 75 g OGTT at 0, 2, and 3 h (3 h OGTT) or at 0, 1.5, and 2 h (2 h OGTT). The formula includes six constants optimized to match the clamp results. This is validated against the clamp method in subjects with IGT and type 2 diabetes.

Log (HOMA-IR)

Log (HOMA-IR) is useful for the assessment of insulin resistance in insulin-resistant conditions like glucose intolerance and mild to moderate diabetes. In research studies where assessing insulin sensitivity/resistance is of secondary interest, it may be appropriate to use log (HOMA-IR) instead of the direct use of HOMA.

In the case of relentlessly deranged β -cell function, HOMA-IR may not give an apposite method to evaluate IR. The coefficient of variation for HOMA-IR varies greatly, depending upon the number of fasting samples obtained and the type of insulin assay used^[50,51,69,70]. Log (HOMA-IR) transforms the skewed distribution of fasting insulin values to determine a much stronger linear correlation with glucose clamp estimates of insulin sensitivity when extensive ranges of insulin sensitivity/resistance are being studied^[37].

Log (HOMA) is being applied broadly in large epidemiological studies, and in clinical research studies^[51,52,71].

Imminent markers

With the passing of time and ongoing intensified research, many newer particles are gaining attention as surrogate markers in assessment of IR. In recent times, inflammatory markers have gained popularity in terms of assessment of insulin resistance (Table 3).

Insulin growth factor binding protein-1

Current research has recommended insulin growth factor binding protein-1 (IGFBP-1) as a new potential plasma marker to assess insulin resistance^[72]. IGFBP-1 has been found to have a good correlation with FSIVGTT assessment of insulin sensitivity, mainly in children younger than 10 years^[72]. However, more studies are required to authenticate the usefulness of this marker. IGFBP-1 levels decline with obesity and IR. Although elevated fasting insulin is less sensitive but more specific, it has been suggested that in young subjects, IGFBP-1 might act as a convenient and susceptible marker of IR. It is an emerging marker which may be useful in this context.

SolubleCD36

Macrophage CD36 is a key proatherogenic molecule that scavenges oxidized low-density lipoprotein, leading to foam cell formation. Hyperglycemia and altered macrophage insulin signaling in insulin resistance leads to increased expression of CD36^[73]. SolubleCD36 has been reported to be distinctly elevated in patients with type 2 diabetes and insulin resistance^[73].

It is postulated that it might represent a potential marker of IR and its complications.

C-reactive protein

C-reactive protein (CRP) is one of the best studied markers for systemic subclinical inflammation, and may have prognostic value in predicting the future risk of cardiovascular events^[74]. In cross-sectional studies, highly sensitive - CRP has been found to correlate with increased triglyceride, decreased HDL, increased blood pressure and increased fasting plasma glucose concentrations, suggesting its association with increased prevalence metabolic syndrome associated with IR^[75,76]. Few studies have established the association of CRP with IR independent of obesity^[77].

In a recent study, CRP was found to significantly associate with several surrogate measures of IR like fasting insulin, the Raynaud index, the quantitative insulin sensitivity check index, and the McAuley index, HOMA, QUICKI, the Insulin: glucose ratio and the Avignon index in non-diabetics^[78]. Because of the simplicity of measurement, stability, and improved high-sensitivity method, CRP may be useful as a clinical measure for identifying individuals at risk for IR^[79].

Ferritin

Ferritin is the major intracellular iron storage protein. Recently it has been suggested that when markers of the iron metabolism are elevated, the incidence of the metabolic syndrome is increased^[80]. Ferritin has been associated with

both hyperinsulinemia and hypertriglyceridemia. Metabolic disorders are common among patients with high ferritin without genetic hemochromatosis, than among patients with genetic hemochromatosis. Iron deposition in various tissues affects insulin sensitivity and function, thereby leading to insulin resistance and inflammation.

A few studies have demonstrated a link between markers of insulin resistance (HOMA-IR, fasting insulin) and ferritin^[81]. Fumeron *et al.*^[82] also found that plasma ferritin concentrations positively correlate with fasting insulin and fasting glucose.

Adiponectin

Adiponectin is a multifunctional protein that exerts pleiotropic insulin-sensitizing effects and hence is considered as a key molecule in the pathogenesis of metabolic syndrome^[83,84]. It lowers hepatic glucose production^[85] and increases glucose uptake and fatty acid oxidation in skeletal muscle^[86]. Adiponectin levels are decreased in obesity and are inversely correlated to insulin-resistant states and high-sensitivity CRP levels^[87].

Deranged levels of adiponectin have been found to be related to insulin resistance. Adiponectin appears to have a stronger negative correlation with HOMA in individuals without the metabolic syndrome as compared to those with metabolic syndrome^[88].

Several prospective studies have confirmed that hypoadiponectinemia was associated with an increase in insulin resistance^[89] and an elevated risk of developing diabetes^[90,91].

Tumour necrosis factor alpha

Several studies have been conducted to explore the role and use of tumour necrosis factor (TNF) to aid in assessing the IR. TNF has been proven to have a relation to insulin resistance measured by HOMA-IR^[92] or insulin clamp^[93,94] and to metabolic syndrome status^[95].

Resistin

The association between resistin and insulin resistance in humans has not been fully established. Many studies have been unsuccessful in recognizing an association between resistin and measures of insulin resistance^[96,97]. On the other hand, a few studies have been conducted which have indeed discovered a significant relationship between IR (HOMA-IR) and resistin^[88,98-100].

C3 complement

The main activation fragment of C3, C3a desArg (acylation stimulating protein) favours glucose transmembrane transport and the synthesis of triglycerides in adipocytes. This suggests that it has insulin-like properties^[101]. C3 is strongly linked with insulin resistance (as defined according to the homeostasis model assessment (HOMA), independent of the components of the metabolic syndrome^[102]. The strong association of C3 with insulin action and fasting insulin has been reported in young adult Pima Indians^[103].

Glycosylated hemoglobin

Glycosylated hemoglobin (HbA1c) has been used to review long-term glycemic control in diabetics. However, its role and clinical worth in patients suffering from IR or metabolic syndrome in nondiabetic subjects is dubious. HbA1c has been proposed as a measure of surrogate assessment of metabolic syndrome, thereby estimating IR because of various factors. HbA1c reflects long-term glycemic control in diabetic patients and is a significant predictor of long-term complications of diabetes^[104,105]. Though HbA1c cannot be considered as a screening or diagnostic tool for diabetes, it has been demonstrated that HbA1c represents both fasting and postprandial glycemic states^[106-111].

Upper normal levels of HbA1c in the range of 5.7%-6.4% have been found to echo some components of insulin resistance syndrome or metabolic syndrome^[112]. A study conducted in the nondiabetic, obese, first-degree relatives of African-Americans who were genetically predisposed to type 2 diabetes^[112] showed significantly high HOMA IR, reduced insulin sensitivity and reduced glucose effectiveness in the nondiabetic study group. Insulin sensitivity and glucose effectiveness were calculated using Bergman's Minmod software program^[113,114].

It has been postulated that HbA1c can be considered predictive of insulin resistance.

Protein kinase C in microangiopathy

It has been speculated that activation of the protein kinase C β isoform (PKC β) which is mediated by hyperglycemia acts as a potential surrogate marker for microangiopathic diseases, and diabetic retinopathy in particular^[115]. A study conducted on diabetic patients correlated PKC activation with diabetic retinopathy. It was suggested that PKC activation in mononuclear cells may serve as a surrogate marker for diabetic microangiopathy^[115].

Sex hormone-binding globulin in hyperandrogenic syndrome

Sex hormone-binding globulin (SHBG) may serve as a predictive marker of IR in obese women suffering from hyperandrogenic syndrome. In a study conducted by Kajaia *et al.*^[116], IR was established by means of the Matsuda ISI in hyperandrogenic women, who were discovered to have significantly lower SHBG and HDL levels. SHBG may be regarded as an extrapolative marker in these types of cases.

CONCLUSION

To summarize, this article is an attempt to scrutinize a variety of methods currently available for estimating insulin sensitivity/resistance. Assessment of insulin resistance is increasingly being exploited in clinical situations, and this calls for the existence of relatively simple markers. The application of surrogate markers is a useful tool with which to gauge IR. These vary from intricate, time-consuming and invasive procedures, to simple tests

involving a single fasting blood sample. The glucose clamp method has been the reference standard for direct measurement of insulin sensitivity. With regard to simple markers, HOMA and QUICKI are among the best and most extensively validated surrogates that can give a more physiological estimate of glucose homeostasis. Other derived indirect indices have been recognised that correlate well with those derived from clamp studies. It is important to understand the concepts and relative merits and limitations underlying each method in order to correctly interpret the data for measuring insulin sensitivity. Several novel markers like the insulin growth factor binding protein-1, hs-CRP, adiponectin, ferritin, HbA1c, C3 complement, TNF alpha and sCD36 are now surfacing as surrogate markers of IR.

The use of surrogate markers to assess insulin resistance might thus help to use medical resources to fullest, while minimizing costs and inconvenient side effects.

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Renal function in diabetic nephropathy

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Abstract

Diabetic nephropathy is the kidney disease that occurs as a result of diabetes. Cardiovascular and renal complications share common risk factors such as blood pressure, blood lipids, and glycemic control. Thus, chronic kidney disease may predict cardiovascular disease in the general population. The impact of diabetes on renal impairment changes with increasing age. Serum markers of glomerular filtration rate and microalbuminuria identify renal impairment in different segments of the diabetic population, indicating that serum markers as well as microalbuminuria tests should be used in screening for nephropathy in diabetic older people. The American Diabetes Association and the National Institutes of Health recommend Estimated glomerular filtration rate (eGFR) calculated from serum creatinine at least once a year in all people with diabetes for detection of kidney dysfunction. eGFR remains an independent and significant predictor after adjustment for conventional risk factors including age, sex, duration of diabetes, smoking, obesity, blood pressure, and glycemic and lipid control, as well as presence of diabetic retinopathy. Cystatin-C (Cys C) may in future be the preferred marker of diabetic nephropathy due to differences in measurements of serum creatinine by various methods. The appropriate reference limit for Cys C in geriatric clinical practice must be defined by further research. Various studies have shown the importance of measurement of albuminuria, eGFR, serum creatinine

and hemoglobin level to further enhance the prediction of end stage renal disease.

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Key words: Chronic kidney disease; End stage renal disease; Glomerular filtration rate; Estimated glomerular filtration rate; Microalbumin; Cockcroft-Gault formula; Modification of diet; Renal disease; Cystatin-C

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INTRODUCTION

Diabetes mellitus is a group of metabolic diseases characterized by hyperglycemia resulting from defects in insulin secretion, insulin action, or both. The chronic hyperglycemia of diabetes is associated with long-term damage, dysfunction and failure of various organs, especially the eyes, kidneys, nerves, heart and blood vessels. Type 2 diabetes mellitus has quickly become a global health problem due to rapidly increasing population growth, aging, urbanization and increasing prevalence of obesity and physical inactivity. There is, therefore, an urgent need to prevent diabetes and its complications. Diabetes is the major cause of end-stage renal disease (ESRD) both in the U.S. and around the world and has enormous medical, social and economic consequences. Diabetes affects the kidney in stages. At the onset of diabetes, the kidney grows large and the glomerular filtration rate (GFR) becomes disturbed. Most recent basic and clinical research has pointed toward sclerosis and kidney failure. The morbidity and mortality

caused by diabetes mellitus can be reduced by regular screening, early detection, and appropriate treatment of chronic complications. Thus, this discussion will focus on development of kidney damage, the various markers available and approaches to development of future markers to enhance the detection of ESRD at the earliest possible stage.

EPIDEMIOLOGY OF RENAL FAILURE

The global prevalence of diabetes is expected to increase from 4% in 1995 to 5.4% by the year 2025^[1]. Currently, the countries with the largest number of diabetic patients are India, China and United States. The acute and chronic complications of diabetes mellitus are major causes of hospital admissions. Asian patients have shown evidence of macro and micro vascular disease at the time of diagnosis of diabetes when compared to Europeans^[2].

Diabetes is the most common cause of kidney failure, accounting for nearly 44 percent of new cases^[3]. Even when diabetes is controlled, the disease can lead to chronic kidney disease (CKD) and kidney failure. Kidney failure is the final stage of chronic kidney disease. Nearly 24 million people in the United States have diabetes and nearly 180 000 people are living with kidney failure as a result of diabetes^[4]. The prevalence of nephropathy in India was less (8.9% in Vellore, 5.5% in Chennai) when compared with the prevalence of 22.3% in Asian Indians in the UK^[5]. In chronic renal failure patients the prevalence of diabetic nephropathy was 30.3% followed by chronic interstitial nephritis (23%) and chronic glomerulonephritis (17.7%)^[6].

African Americans, American Indians, and Hispanics or Latinos develop diabetes, CKD, and kidney failure at rates higher than Caucasians. Scientists have not been able to explain these higher rates and the interplay of various risk factors.

RISK FACTORS FOR DEVELOPMENT OF DIABETIC COMPLICATIONS

Diabetic nephropathy is the kidney disease that occurs as a result of diabetes. Nephropathy is the leading cause of chronic renal failure worldwide and is responsible for renal failure in about one third of patients who undergo dialysis. It is suggested that patients with common risk factors including greater duration of diabetes, hypertension, poor metabolic control, smoking, obesity and hyperlipidemia are more prone to develop diabetic complications^[7]. In a retrospective study done by Klag *et al*^[8] it was found that elevations of blood pressure are a strong independent risk factor for end-stage renal disease and that interventions to prevent the disease need to emphasize the prevention and control of both high-normal and high blood pressure.

The "Asian Indian Phenotype" refers to certain unique clinical and biochemical abnormalities in Indians which include increased insulin resistance, higher waist

circumference despite lower body mass index, lower adiponectin and higher C-reactive protein levels. This phenotype makes Asians more prone to diabetes and premature complications. Asians show a trend towards higher systolic and diastolic blood pressures, possibly due to more patients with nephropathy, although this is not significantly different. Total cholesterol and LDL cholesterol levels were very similar between Europeans, Americans and Asians, but HDL cholesterol was significantly lower and triglycerides level was significantly higher in Asian patients^[9].

James Sowers *et al* reviewed aspects of the association of diabetes with renal disease, emphasizing that CKD and albuminuria are associated with increased rates of cardiovascular disease (CVD) and mortality^[10], and should be considered part of the cardiovascular risk factors in persons with diabetes. Lorenzo *et al*^[11], found that the development of glomerular filtration rate < 60 mL/min per 1.73 m² was associated with increased fasting insulin, triglycerides, free fatty acids, and uric acid and also with antihypertensive treatment, although not with waist circumference, controlling for age, sex, ethnicity, blood pressure, glucose, and C-reactive protein in nondiabetic persons. This points towards the association of CKD with the risk of development of diabetes.

PATHOGENESIS OF KIDNEY DAMAGE

There are various mechanisms of albuminuria which involve abnormalities of the glomerular endothelial barrier^[12], causing excessive filtration as well as reduction of renal tubular cell albumin degradation and reabsorption. Glomerular hypertension, inflammation, and oxidative stress worsen albuminuria, with angiotensin-II^[13] and mechanical stress factors contributing to these processes.

Renal disease in diabetes is found to be associated with abnormalities of vasodilatation and generates reactive oxygen species mediated by endothelial derived nitric oxide (NO), suggesting linkage between vascular and metabolic abnormalities. Angiotensin II and aldosterone, interacting with pulse pressure and increased systolic blood pressure, activate NADP oxidase, which acts as mediator of oxidative stress. Angiotensin II increases metabolism of NO to peroxynitrite^[13], which further impairs endothelial-derived vasodilation.

In another mechanism, decrease in the ability to produce endothelial progenitor cells (EPCs), which can be quantitated with the cellular marker CD 34, leads to increased CVD risk. These cells derived from bone marrow, play a role in replacing damaged endothelium and are reduced in people with decreased endothelium-dependent vasodilation^[14]. Both angiotensin II and aldosterone inhibit production of EPCs, while angiotensin converting enzyme inhibitors (ACEIs) increase their levels.

Sowers *et al*^[15] discussed the relationship between dyslipidemia and CKD, hypothesizing that the mechanism

Table 1 The various tests for chronic tubular dysfunction in diabetic nephropathy

Test name	Use
Blood urea nitrogen (serum or plasma) Method: Spectrophotometry	Initial diagnosis of acute or chronic kidney disease
Creatinine (serum or plasma) Method: Spectrophotometry	Initial diagnosis of acute or chronic kidney disease
Microalbumin (urine) Method: Immunoturbidimetric	May be used as a screening test Useful in diabetic patients to assess baseline renal function Useful in monitoring diabetic nephropathy in insulin-dependent diabetes mellitus
Creatinine based glomerular filtration rate (estimated) Method: Spectrophotometry	Estimate renal function and use as monitoring tool (Test reports serum creatinine reference intervals)
Cystatin-C based glomerular filtration rate (estimated) Method: Nephelometry	May be useful sensitive marker of renal disease; however, test lacks specificity due to reference range inavailability
Retinol-binding protein 4 (RBP4) Method: Non-commercial enzyme-linked immunosorbant assay (ELISA)	May be used as a marker for early diabetic nephropathy. Limited studies are available
Adiponectin Method: Competitive radioimmunoassay	Shown inverse correlation with renal dysfunction in type 2 diabetes
Connective tissue growth factor (CTGF) Method: ELISA	CTGF excretion is correlated inversely with GFRs
Alpha-1-microglobulin (urine) Method: Nephelometry	May indicate renal involvement in diabetic patients
Liver type fatty acid binding protein (L-FABP) Method: ELISA	Expressed in proximal tubular cells and may associated with severity of diabetic nephropathy. Larger conclusive studies are required

of action of statins is an increase in endothelial NO synthase transcription *via* the phosphatidylinositol 3-kinase (PI3K) pathway and statin-induced inhibition of the mobilization of small molecular weight G-proteins. Also, Sowers suggested that the direct renin inhibitor aliskiren has similar benefits in renal disease to those of angiotensin receptor binders.

Charles Heilig *et al*^[16] discussed the relationship of renal glucose transporter expression in relation to the development of diabetic nephropathy. Expression of GLUT1, the major mesangial glucose transporter, regulates extracellular matrix production. Mesangial cells overexpressing GLUT1 show increased production of both types I and IV collagen, as well as increased fibronectin and laminin production, leading to a phenotype similar to that of diabetes. In animal models, GLUT1 overexpression in glomeruli creates a nephropathy phenotype resembling that of diabetic renal disease with increased mean glomerular volume, mesangial expansion, and sclerosis.

DEVELOPEMENT OF KIDNEY DISEASE

Diabetic nephropathy takes many years to develop. In

some people, the filtering function of the kidneys is actually higher than normal in the first few years of their diabetes.

In people who are developing kidney disease small amounts of the blood protein albumin begin to leak into the urine, a condition called microalbuminuria. The kidney's filtration function usually remains normal during this period. As the disease progresses further, more albumin leaks into the urine, a stage known as macroalbuminuria or proteinuria. As the amount of albumin in the urine increases, the kidney's filtering function usually begins to drop, resulting in the body's retention of various wastes. As kidney damage develops, blood pressure also often rises or hypertension may attenuate the process of renal injury. Early detection of renal damage may help to delay the process.

As these processes are slow, kidney damage rarely occurs in the first 10 years of diabetes, and 15 to 25 years will usually pass before kidney failure occurs. For people who live with diabetes for more than 25 years without any signs of kidney failure, the risk of ever developing it decreases.

BIOMARKERS OF CHRONIC TUBULAR DYSFUNCTION

The early detection of diabetic nephropathy, resulting in timely intervention with particular attention to blood pressure control (thus limiting proteinuria), glycemic control, smoking cessation, and accentuation of cardiovascular risk, can improve long-term outcomes and retard progression to ESRD.

Tubular proteinuria results when glomerular function is normal but the proximal tubules have diminished absorbing capacity. The biomarkers of this process are as Table 1.

Blood urea nitrogen

Blood tests for Blood urea nitrogen (BUN) and creatinine are the simplest way to monitor kidney function. These substances are normal metabolic waste products that are excreted by the kidneys. Urea is a byproduct of protein breakdown. A test can be done to measure the amount of urea nitrogen in the blood. In kidney disease, these substances (as well as numerous others) are not excreted normally, and so they accumulate in the body thus causing an increase in blood levels of urea. The normal level of BUN is 7-20 mg/dL^[17].

Creatinine

Serum creatinine is primarily a metabolite of creatine, almost all of which is located in skeletal muscle. The normal level of creatinine is 0.8 to 1.4 mg/dL. Females usually have a lower creatinine (0.6 to 1.2 mg/dL) than males, because they usually have less muscle mass^[17].

The amount of creatine per unit of skeletal muscle mass is consistent and the breakdown rate of creatine is also consistent. Thus, plasma creatinine concentration

is very stable and a direct reflection of skeletal muscle mass^[18]. Interestingly, Nobuko Harita *et al*^[19], hypothesized that, lower serum creatinine is associated with an increased risk of type 2 diabetes, which might reflect a lower volume of skeletal muscle. Skeletal muscle is a major target tissue of insulin and a lower volume of skeletal muscle would mean fewer target sites for insulin which causes increase in insulin resistance. This leads to the development of type 2 diabetes^[20]. This may explain in part the pathogenesis of type 2 diabetes associated with lower serum creatinine.

Creatinine based GFR

GFR is the best measure of kidney function since it accounts for age, BMI and sex. GFR measures the rate at which the kidneys' two million glomeruli filter plasma in order to process it and remove waste products from it. If the kidneys are injured by chronic kidney disease, the GFR gradually declines, and the amount of remaining kidney function can be estimated by measuring or calculating the GFR. The normal value for GFR in a normal-sized person is 100-150 mL/min.

Currently the two most common methods for determining GFR are creatinine clearance and estimated GFR (eGFR).

Creatinine clearance: Creatinine clearance requires a 24 h urine collection. A blood sample is drawn at some point during the 24 h period, and creatinine clearance, can then be calculated. However, because a small amount of creatinine is released by the filtering tubes in the kidneys, creatinine clearance is not exactly the same as the GFR. In fact, creatinine clearance usually overestimates the GFR, particularly in patients with advanced kidney failure. Normal clearance values are: Male: 97 to 137 mL/min; Female: 88 to 128 mL/min^[21].

There are several factors that may interfere with the accuracy of the test. These include: (1) Incomplete urine collection; (2) Pregnancy; and (3) Vigorous exercise. Creatinine clearance measurements can also be affected by drugs, such as: cimetidine, trimethoprim, and drugs that can damage the kidneys (cephalosporins).

The creatinine clearance test should only be done for patients who are medically stable. Other patients may have a rapidly changing creatinine clearance, and therefore any result may be inaccurate.

eGFR: Formula-derived eGFR results have become widely used in clinical practice. The National Service Framework for Renal Services in the U.K. recommends the adoption of formula-derived eGFR in the annual evaluation of all patients with diabetes^[22]. It is anticipated that this process will aid early identification and therefore improve longterm outcomes for those with diabetic nephropathy.

The American Diabetes Association recommends estimation of glomerular filtration rate by eGFR (in millilitres per min per 1.73 m²), which is calculated by

the Cockcroft-Gault (CG) formula^[23], corrected for Body Surface Area (BSA), and the Modification of Diet in Renal Disease (MDRD)^[24] equation in all patients with diabetes. (1) CG derived eGFR: A simpler method for estimating creatinine clearance is based upon a formula (the Cockcroft-Gault formula) that includes a person's age, gender, weight, and serum creatinine level, but does not require the collection of a 24 h urine sample. The CG formula is^[23] as follows: $eGFR = [140 - \text{age (years)}] \times \text{weight (kg)} \times k \times c / \text{serum creatinine } (\mu\text{mol/L})$, (k is 1.23 for men and 1.04 for women and c adjusts for BSA^[25]. $c = 1.73/\text{BSA}$, with BSA calculated using the following DuBois^[26] formula), $\{\text{BSA (m}^2) = [\text{weight (kg)}]^{0.425} \times [\text{height (cm)}]^{0.725} \times 0.007184\}$; (2) MDRD derived eGFR: Renal function can be assessed by serum creatinine and eGFR and calculated using the abbreviated MDRD formula as follows^[24]: $eGFR = 186 \times (\text{SCR} \times 0.011)^{-1.154} \times (\text{age})^{-0.203} \times (0.742, \text{ if female}) \times (1.210 \text{ if African American})$ (SCR was serum creatinine expressed as $\mu\text{mol/L}$). Renal function has been graded according to the Kidney Disease Outcomes Quality Initiative guidelines: stage 1, ≥ 90 mL/min per 1.73 m²; stage 2, 60-89 mL/min per 1.73 m²; stage 3, 30-59 mL/min per 1.73 m²; stage 4, 15-29 mL/min per 1.73 m²; and stage 5, < 15 mL/min per 1.73 m² (gf4-13); (3) Reexpressed MDRD equation: As significant error is introduced in the MDRD equation by use of different creatinine assays or calibration methods, the simplified MDRD was recently recalculated with serum creatinine measurements calibrated to an enzymatic assay^[27]: $eGFR = 175 \times [\text{serum creatinine (mg/dL)}]^{-1.154} \times (\text{years})^{-0.203} \times 0.742 \text{ (if female)} \times 1.212 \text{ (if African American)}$; (4) MCQ equation: A new equation was developed by Rule *et al*^[28] for GFR estimation in chronic kidney disease patients and in healthy persons for the diagnosis of chronic kidney disease. This is expressed as: $(1.911 + 5.249/\text{SCR} - 2.114/\text{SCR}^2) - [0.00686 \times \text{age (years)}] - 0.205$ if female, where SCR is serum creatinine [in milligrams per deciliter]; and (5) Considerations: eGFR is used for assessment of kidney function in patients with diabetes. However, despite validation in chronic kidney disease, eGFR has limitations in patients with preserved kidney function. These equations do have recognized limitations, including a tendency to significantly underestimate higher levels of GFR^[29]. Additionally, Parving and colleagues^[30] demonstrated that in type 2 diabetic subjects with macroalbuminuria, eGFR had a poor sensitivity for GFR values < 60 mL/min per 1.73 m². In obese patients with established kidney disease, the Cockcroft-Gault equation overestimates GFR while underestimating GFR in lean subjects, possibly due to increasing weight; while performance of the MDRD equation in such patients is consistent regardless of weight. Bias of the Cockcroft-Gault formula was most pronounced in lean subjects, diminishing with increasing body weight. Conversely, bias of the MDRD equation increased with increasing body weight^[31]. In obese patients, excess body weight is mainly adipose

tissue, whereas creatinine is primarily generated by muscle. In the Cockcroft-Gault equation, body weight is proportional to GFR; therefore, increasing body weight without a proportional increase in creatinine generation will tend to increase the estimation of GFR. However, weight is not included in the MDRD equation and therefore cannot influence performance.

There are reports^[32,33] that variation in calibration of the creatinine assay has an adverse impact on the performance of eGFR to estimate GFR, particularly at low levels of serum creatinine.

Cystatin-C based eGFR

A large percentage of individuals with type 2 diabetes pass through a period of pre-diabetes and may experience early renal dysfunction, e.g. a GFR > 60 mL/min per 1.73 m². Serum creatinine has been found to be deficient to detect mild renal impairment, even when used with prediction equations^[34,35]. So, interest has developed in Cystatin-C, a non-glycosylated basic protein, as a potential endogenous filtration marker of GFR. Cystatin-C is a cysteine protease inhibitor that is produced by virtually all nucleated cells and released into the bloodstream. It is entirely filtered by the kidney glomerulus and metabolized by the proximal tubule^[36].

Various formulae have been used to measure serum cystatin levels by different methodologies. Recent estimations were done using a particle-enhanced immunonephelometric^[37] assay or immunoturbidimetric assays. In all formulae, Cys C is serum cystatin-C (in milligrams per liter).

Arnal *et al*^[38] estimated eGFR in 208 patients aged 1-80 years with various etiologies as follows: Cys-eGFR (Arnal-Dade) = 74.835/(Cys C1.333). Rule *et al*^[39] studied native kidney disease (gf7-15) patients (*n* = 204) having hypertension as suspected etiology: Cys-eGFR (Rule) = 66.8 - (Cys C) - 1.30. Isotopic GFR (iGFR) was measured by iothalamate clearance. MacIsaac *et al*^[40] studied 126 diabetic patients (mainly type 2 diabetes). The iGFR was measured by clearance of 99mTc-diethylene-triamine-penta-acetic acid. The equation is as follows: Cys-eGFR (MacIsaac) = (84.6/Cys C) - 3.2. Tan *et al*^[41] used an unbiased conversion algorithm between plasma cystatin-C and iGFR measured by iothalamate clearance in type 1 diabetes, including a subgroup of healthy subjects as follows: Cys-eGFR (Tan) = (87.1/plasma Cys C) - 6.87. Eroshe *et al*^[37] measured GFR using the equation Cys-GFR (Eroshe) = (86.7/Cys C) - 4.2. The intra- and interassay coefficient of variation for Cystatin-C were 2.58 and 3.95%, respectively, at a concentration of 1.54 mg/L.

Considerations: It has been shown that Cystatin-C is a more sensitive indicator of mild renal impairment and may better estimate the GFR than serum creatinine^[42]. Moreover, concentrations of Cystatin-C are not affected by sex, age, or muscle mass^[43]. There is supportive evidence that the reciprocal of Cystatin-C correlates more closely with isotopic GFR than the CG or MDRD

equations in subjects with mild renal impairment^[44]. As the identification of those with pre-diabetes is assuming greater importance, Cystatin-C may play a role in detection of the association between renal and heart disease in etiology of pre-diabetics. Recent clinical trials^[45,46] among people with pre-diabetes have provided convincing evidence that early intervention can significantly delay or prevent the progression to type 2 diabetes. However, concerns remain regarding inpatient variation and the effect of certain drugs and hormonal levels on Cystatin-C concentration^[47].

Microalbumin (urine)

Albuminuria is a well-known predictor of poor renal outcomes in patients with type 2 diabetes and in essential hypertension^[48,49]. Albuminuria has also been shown to be a predictor of cardiovascular outcomes in these populations. There is emerging data that reduction of albuminuria leads to reduced risk of adverse renal and cardiovascular events^[50,51]. It has become increasingly clear that albuminuria should not only be measured in all patients with type 2 diabetes and hypertension, but also that steps should be taken to suppress albuminuria in order to prevent future renal and cardiovascular adverse events. Albuminuria may reflect underlying renal expression of vascular damage, hypertension, endothelial dysfunction^[12], and low-grade inflammation^[52].

Expected results: Microalbuminuria is defined as levels of albumin ranging from 30 to 300 mg in a 24 h urine collection^[53]. Overt albuminuria, macroalbuminuria, or proteinuria is defined as a urinary albumin excretion of > 300 mg/24 h. Urinary albuminuria comprises 20%-70% or urinary total protein excretion. Albuminuria can be measured in several ways (Table 2): (1) measurement of albumin-to creatinine ratio in a random or first morning spot collection; (2) 24 h urine collection with measurement of creatinine to verify adequacy of the collection; and (3) timed (4 h or overnight) urine collections.

Considerations: South Asians are very prone to obesity and type 2 diabetes. This explains their susceptibility for central obesity and insulin resistance. It also indicates the higher rates of end-stage diabetic nephropathy in migrant South Asians^[54]. They have a three times higher risk of developing diabetic nephropathy and an almost 40-fold increased risk for end-stage diabetic nephropathy when compared with Caucasians^[55]. Prataap K *et al*^[56] shows that central obesity is an early and independent risk factor for increased albuminuria in normoglycemic South Asian subjects.

Recently, Michiaki Fukui *et al*^[57] showed the association of serum bilirubin level with microalbuminuria and subclinical atherosclerosis in patients with type 2 diabetes. Serum bilirubin concentrations were significantly lower in patients with cardiovascular disease (CVD). They were an independent determinant of CVD and had a significant inverse correlation to the log urinary albumin excretion.

Table 2 Expected results for microalbuminuria

Tests	Normal	Microalbuminuria	Macroalbuminuria
24 hr protein (mg)	< 150	< 500	≥ 500
24 hr albumin (mg)	< 30	30-300	> 300
Timed collection for albumin (μg/min)	< 20	20-200	> 200
Spot sample collection for albumin (μg albumin/mg creatinine)	< 30	30-300	> 300

PROSPECTIVE FUTURE MARKERS

Several biochemical markers have the potential to be markers of CKD progression. These parameters might reflect diminished glomerular filtration, disturbances in tubular function or unknown contributors to kidney function that are unrelated to glomerular or tubular function. The evidence is still too sparse for most of these markers to be recommended for broad clinical use in the diagnosis of CKD progression. The emerging parameters associated with CKD progression must be studied further to determine whether they are causally related to progression of CKD or whether they simply predict the probability of progression. Few of these are as follows.

Retinol-binding protein 4

Retinol-binding protein 4 (RBP4) is a small visceral protein (approximately 21 kDa), mainly synthesized in the liver and catabolized in the kidneys after glomerular filtration^[58]. RBP4 is complexed by transthyretin before delivering its ligand retinol to the target tissues^[59]. RBP 4 was initially reported as an adipokine that impairs insulin sensitivity. The concentrations of this adipokine were found to increased in human subjects with impaired glucose tolerance (IGT) and type 2 diabetes compared with normal glucose tolerance subjects^[60].

In prior studies, urinary RBP 4 excretion is found to be increased in early diabetic nephropathy and might even be a marker of early renal damage preceding microalbuminuria^[61]. Andrea Henze *et al*^[62] evaluated the influence of eGFR on RBP4 level and found that gradual elevation of RBP4 serum levels was accompanied by decline in eGFR in both, type 2 diabetic and non-diabetic subjects. No influence of type 2 diabetes mellitus or other parameters of diabetes (HbA1c, fasting serum glucose, BMI) on RBP4 serum concentration was seen. The association of RBP4 with several other metabolic parameters has been studied but limited studies are available on the relationship between this adipokine and mild to moderate decrease in GFR.

Adiponectin

Adiponectin is a recently discovered 30 kDa protein exclusively secreted by adipocytes and is present at concentrations of 5-30 μg/mL in healthy humans. It is consid

ered to be an important modulator of insulin sensitivity, dyslipidemia with anti-inflammatory properties^[63,64].

Julie Lin *et al*^[65] found the inverse correlation of serum adiponectin with the presence of renal dysfunction in men with type 2 diabetes, the majority of whom had well-preserved eGFR (87% had eGFR > 60 mL/min per 1.73 m²). Adiponectin was 2.5 times higher in hemodialysis patients (15.0 vs 6.3 μg/mL, $P < 0.0001$)^[66] and three times higher in pediatric peritoneal dialysis patients when compared with healthy control subjects.

Connective tissue growth factor

Connective tissue growth factor (CTGF) is a 36 to 38 kDa polypeptide with functions in extracellular matrix production and other profibrotic activity mediated by transforming growth factor-β1. Other biological functions of CTGF include angiogenesis, chondrogenesis, osteogenesis, and cell adhesion, migration, proliferation, and differentiation^[67]. The upregulation of CTGF has been observed in human and experimental diabetic nephropathy^[68].

Nguyen *et al*^[69] revealed that urinary CTGF excretion is associated with urinary albumin excretion and associated inversely with glomerular filtration rate, both important clinical markers for severity of renal disease. Further, they have shown that^[70] the plasma CTGF level correlates with rate of decline in GFR and that it is an independent predictor of both ESRD and mortality in patients with type 1 diabetic nephropathy. Baseline plasma CTGF was higher in patients with diabetic nephropathy than in patients with normoalbuminuria.

α1-microglobulin

α1-microglobulin is a 26 000-31 000 Da glycoprotein which exists in blood as a free form and or complexed with IgA and albumin. Because of its low molecular weight, the free form is filtered freely through the renal glomerular basement membrane and reabsorbed by the proximal tubular cells^[71]. Hence, any proximal tubular cell dysfunction results in increased quantities of α1-microglobulin in the urine.

Urinary α1- microglobulin levels were found to be elevated in both type 1 and type 2 diabetic subjects. In type 2 diabetic subjects, α1-microglobulin excretion was directly correlated with albuminuria and HbA1c levels, and was decreased with improved glycemic control in caucasians^[72,73]. Similar findings have been shown in Asian population^[74].

Transforming growth factor-β

Transforming growth factor (TGF)-β1 has a central role in fibrotic kidney disease and interstitial fibrosis (5). In type 2 diabetic patients, urinary TGF-β1 is elevated^[75] and associated with histologically-proven severe mesangial expansion^[76]. Although urinary TGF-β1 measurement has been suggested as a marker for diabetic nephropathy, not all studies have shown the association of urinary TGF-β1 with diabetic nephropathy. Eijja *et al*^[77] did not

find a difference in urinary TGF- β 1 excretion between microalbuminuric and normoalbuminuric patients and only weak correlation was found with urinary glucose and β 1-microglobulin. The association between urinary TGF- β 1 and diabetic nephropathy may not be a direct one.

Liver-type fatty acid binding protein (L-FABP)

This protein is expressed in proximal tubular cells^[78]. It has been shown that urinary L-FABP (U-LFABP) excretion is strongly associated with structural and functional tubular kidney damage in diabetic nephropathy^[79]. Suzuki *et al*^[80] performed a cross-sectional study in 356 adult type 2 diabetic patients and found a significant association between the stage of diabetic nephropathy and U-LFABP, although no significant difference between the normoalbuminuric and microalbuminuric groups was seen. Stine *et al*^[81] have shown that U-LFABP is elevated in type 1 diabetic patients compared with nondiabetic healthy control subjects and that the level further increases with micro and macroalbuminuria, reflecting increased tubular damage. There were no significant correlations between U-LFABP and sex, age, or A1C. Large studies with long-term follow-up are required to confirm these findings.

CONCLUSION

Diabetic nephropathy, especially related to type 2 diabetes, has become the single most important cause of ESRD worldwide. Management of traditional risk factors such as hypertension, hyperlipidemia, and smoking to improve cardiovascular and renal outcomes continues to be important in patients with chronic kidney disease. There is, however, growing recognition that nontraditional risk factors such as increased urinary albumin excretion, hypoalbuminemia, elevated serum creatinine levels, and/or decreased haemoglobin levels may also be important in individuals with chronic kidney disease. The RENAAL risk score for ESRD emphasizes the importance of the identification of levels of albuminuria and hypoalbuminemia as well as increased serum creatinine, and decreased haemoglobin levels to predict the development of ESRD in patients with type 2 diabetes and nephropathy. Albuminuria is a known strong predictor for ESRD, but the contribution of serum albumin, serum creatinine, and hemoglobin level further enhances the prediction of ESRD^[82].

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Neurodegeneration: An early event of diabetic retinopathy

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Abstract

Diabetic retinopathy (DR) has been classically considered to be a microcirculatory disease of the retina caused by the deleterious metabolic effects of hyperglycemia *per se* and the metabolic pathways triggered by hyperglycemia. However, retinal neurodegeneration is already present before any microcirculatory abnormalities can be detected in ophthalmoscopic examination. In other words, retinal neurodegeneration is an early event in the pathogenesis of DR which predates and participates in the microcirculatory abnormalities that occur in DR. Therefore, the study of the mechanisms that lead to neurodegeneration will be essential to identify new therapeutic targets in the early stages of DR. Elevated levels of glutamate and the overexpression of the renin-angiotensin-system play an essential role in the neurodegenerative process that occurs in diabetic retina. Among neuroprotective factors, pigment epithelial derived factor, somatostatin

and erythropoietin seem to be the most relevant and these will be considered in this review. Nevertheless, it should be noted that the balance between neurotoxic and neuroprotective factors rather than levels of neurotoxic factors alone will determine the presence or absence of retinal neurodegeneration in the diabetic eye. New strategies, based on either the delivery of neuroprotective agents or the blockade of neurotoxic factors, are currently being tested in experimental models and in clinical pilot studies. Whether these novel therapies will eventually supplement or prevent the need for laser photocoagulation or vitrectomy awaits the results of additional clinical research.

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Key words: Diabetic retinopathy; Angiotensin II; Erythropoietin; Glutamate; Retinal neurodegeneration; Neuropeptides; Pigment epithelial derived factor; Somatostatin

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INTRODUCTION

Diabetic retinopathy (DR) has been classically considered to be a microcirculatory disease of the retina due to the deleterious metabolic effects of hyperglycemia *per se* and the metabolic pathways triggered by hyperglycemia (polyol pathway, hexosamine pathway, DAG-PKC pathway, advanced glycation end-products and oxidative stress). However, retinal neurodegeneration is already

present before any microcirculatory abnormalities can be detected in ophthalmoscopic examination. In other words, retinal neurodegeneration is an early event in the pathogenesis of DR which predates and participates in the microcirculatory abnormalities that occur in DR^[1,2]. This concept was first introduced by Barber *et al.*^[3]. These authors observed that one month after inducing diabetes in rats by using streptozotocin there was a high rate of apoptosis (TUNEL positive cells) in the neuroretina without a significant apoptosis in endothelial cells. In the same paper, the authors found a higher rate of apoptosis in the neuroretina from diabetic donors compared to non-diabetic donors, even in the case of a diabetic donor without microvascular abnormalities. These findings have been further confirmed in experimental models. In addition, it has been demonstrated in experimental models that, apart from apoptosis, another feature of retinal neurodegeneration is glial activation^[1-5]. Our research group has been able to demonstrate that both apoptosis and glial activation occur in the retina of diabetic patients and precede microvascular abnormalities^[6,7] (Figure 1).

Retinal ganglion cells are the earliest cells affected and have the highest rate of apoptosis^[8]. However, an elevated rate of apoptosis has been also observed in the outer nuclear layer (photoreceptors)^[9] and in the retinal pigment epithelium (RPE)^[10].

Neuroretinal damage produces functional abnormalities such as the loss of chromatic discrimination, contrast sensitivity and dark adaptation. These alterations can be detected by means of electrophysiological studies in diabetic patients with diabetes duration of less than two years, i.e. before microvascular lesions can be detected in ophthalmologic examination. In addition, neuroretinal degeneration will initiate and/or activate several metabolic and signalling pathways which will participate in the microangiopathic process as well as in the disruption of the blood-retinal barrier (a crucial element in the pathogenesis of DR)^[11].

The underlying mechanisms that lead to neuronal deficits are likely to be broad. In addition, it is unknown which of the two primordial pathological elements (apoptosis or glial activation) is the first to appear and is consequently the primary event. Nevertheless, it seems that retinal glial cells play an essential role in maintaining the normal function of the retina. When Müller cells (the principal glial cells in the retina) become gliotic, display altered potassium siphoning, glutamate and GABA uptake are also known to express several modulators of angiogenesis^[12].

IN VIVO EXPERIMENTAL MODELS TO STUDY RETINAL NEURODEGENERATION IN THE SETTING OF DR

Since neurodegeneration is an early event in the pathogenesis of DR, it is not necessary to use animal models

with microangiopathic lesions in the eye such as Torii or Goto-Kakizaki rats. The experimental model currently used to study retinal neurodegeneration in DR is the rat with streptozotocin-induced diabetes (STZ-DM). In this model, electroretinographic abnormalities are present two weeks after inducing diabetes^[13] and the presence of neural apoptosis and glial reaction can be clearly detected one month after starting diabetes^[3,5]. However, it should be noted that the interpretation of the results of retinal neurodegeneration in STZ-DM rats might be hampered by the neurotoxic effect of STZ. Streptozotocin is a potent neurotoxic agent and is able to produce neural degeneration. Therefore, neurodegeneration (apoptosis + glial activation) observed in rats with STZ-DM could be due to STZ itself rather than the metabolic pathways related to diabetes. It is worthy of mention that pathological changes to the brain after an intraventricular injection of STZ are very similar to the neurodegeneration reported in DR^[14]. Therefore, it may be advisable to use murine models with a spontaneous development of diabetes or at least experimental models in which diabetes has not been induced by a neurotoxic drug.

Mice have been used much less than rats as experimental models for the study of DR and retinal neurodegeneration. This is because they are more resistant to the STZ effect (mice need 3-5 doses of STZ to induce diabetes whereas in rats one dose is sufficient), have lower eye cups and present a lower degree of lesions compared to rats. This relative protection in developing pathological lesions related to diabetes can be partly attributed to a lower activity of aldose reductase (polyol pathway) compared to rats^[5]. Nevertheless, because of its great potential for genetic manipulation, the mouse offers a unique opportunity to study the molecular pathways involved in disease development. Among mice, C57BL/KsJ-*db/db* is the model that best reproduces the neurodegenerative features observed in patients with DR. C57BL/KsJ-*db/db* mice carry a mutation in the leptin receptor gene and are a model for obesity-induced type 2 diabetes. They develop hyperglycemia starting at ~8 wk of age as a result of excessive food consumption. It is noteworthy that they present an abundant expression of aldose-reductase in the retina (an important differential trait from other mouse models)^[15]. Therefore, C57BL/KsJ-*db/db* seems appropriate for investigating the underlying mechanisms of retinal neurodegeneration associated with diabetes and for testing new drugs.

NEUROTOXIC AND NEUROPROTECTIVE FACTORS

The main neurotoxic metabolite involved in diabetic retinal neurodegeneration is glutamate. In addition, there is emerging information about the neurotoxicity due to angiotensin II in the setting of the RAS overexpression that exists in DR. The role of other neurotoxic factors has yet to be elucidated.

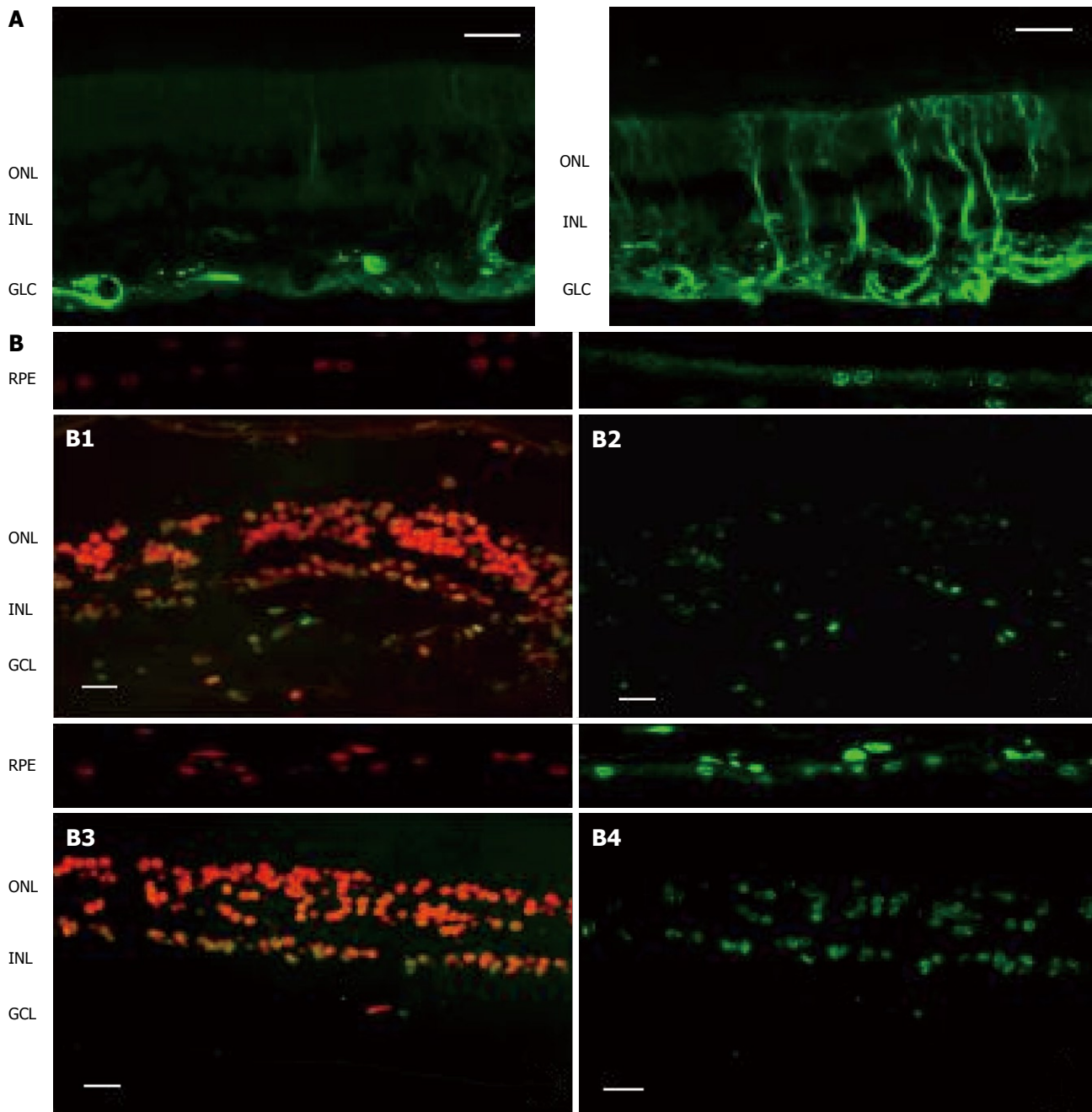


Figure 1 Comparison of the two key elements of neurodegeneration (glial activation and apoptosis) between a representative case of diabetic patient without DR and a non-diabetic subject. As can be seen, neurodegeneration is higher in the retina from the diabetic donor. A: Glial activation in the human retina. Glial fibrillar acidic protein (GFAP) immunofluorescence (green) from a non-diabetic donor (left panel) and a diabetic donor (right panel); B: Apoptosis in the human retina. Upper panel: Non-diabetic donor (B1: Propidium iodide, B2: TUNEL immunofluorescence). Low panel: Diabetic donor (B3: Propidium iodide, B4: TUNEL immunofluorescence). RPE: Retinal pigment epithelium; ONL: Outer nuclear layer; INL: Inner nuclear layer; GCL: Ganglion cell layer. The bar represents 20 μm.

Several types of insult cause the upregulation of neurotrophic factors and their receptors in the retina resulting in decreased photoreceptor cell death from subsequent injury. This phenomenon is more prominent in rats than in mice and neurotrophic factors are more efficacious in rats than mice^[16]. Among the neuroprotective factors, pigment epithelial derived factor (PEDF), somatostatin (SST) and erythropoietin (Epo) seem to be the most relevant and will be reviewed in this paper. However, there are other neuroprotective factors such as neuroprotectin D1 (NPD1), brain-derived neurotrophic factor (BDNF),

glial cell-line-derived neurotrophic factor (GDNF), ciliary neurotrophic factor (CNTF) and adrenomedullin (AM). It is worthy of mention that the balance between the neurotoxic and neuroprotective factors will determine the fate of the retinal neurons.

Glutamate

Glutamate is the major excitatory neurotransmitter in the retina and is involved in neurotransmission from photoreceptors to bipolar cells and from bipolar cells to ganglion cells. However, an elevated glutamate level (which

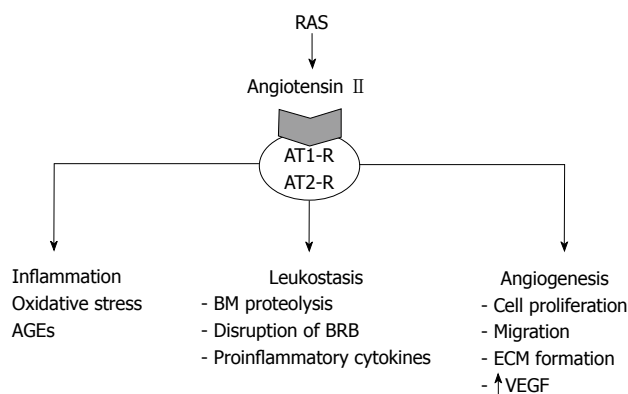


Figure 2 AT1-R activation by angiotensin II produced by the retina stimulates several pathways involved in the pathogenesis of DR such as inflammation, oxidative stress, leukostasis and angiogenesis. AT1-R: Angiotensin II type 1 receptor; AT2-R: Angiotensin II type 2 receptor; AGEs: Advanced glycosylated end products; BM: Basal membrane; BRB: Blood retinal barrier; ECM: Extracellular matrix; VEGF: Vascular endothelial growth factor.

results in excessive stimulation) is implicated in the so called “excitotoxicity” which leads to neurodegeneration. The excitotoxicity of glutamate is the result of over-activation of N-methyl-D-aspartate receptors which have been overexpressed in DM-STZ rat receptors^[17]. There are at least two mechanisms involved in glutamate-induced apoptosis: a caspase-3-dependent pathway and a caspase-independent pathway involving calpain and mitochondrial apoptosis inducing factor^[18].

Elevated levels of glutamate in the retina have been found in experimental models of diabetes as well as in the vitreous fluid of diabetic patients with PDR^[19,20]. However, there is no information about this issue in the earlier stages of DR.

The cause of the high levels of glutamate in DR has been related to a dysfunction of macroglia in metabolising glutamate^[21]. The reason for this dysfunction seems to be related to impairment in the glutamate transporter of Müller cells due to diabetes-induced oxidative stress^[22]. In addition, two enzymatic abnormalities in glutamate metabolism have been found in the diabetic retina: transamination to alpha-ketoglutarate and amination to glutamine. The reduced flux through these pathways may be associated with the accumulation of glutamate^[23].

Angiotensin II

The blockade of the RAS with a converting enzyme inhibitor or by using angiotensin II type 1 (AT1) receptor blockers (ARBs) is one of the most used strategies for hypertension treatment in diabetic patients. Apart from the kidney, the RAS system is expressed in the eye. In the retina, RAS components are largely found and synthesized in two sites: neurons and glia cells in the inner retina and in blood vessels^[24]. The finding of renin and angiotensin in glia and neurons suggests a role for these molecules in neuromodulation.

There is growing evidence that RAS activation in the eye plays an important role in the pathogenesis of DR^[24]. Therefore, apart from lowering BP, the blockade

of the RAS could also be beneficial “per se” in reducing the development and progression of DR. In fact, recent evidence supports the concept that RAS blockade in normotensive patients has beneficial effects in the incidence and progression of DR^[25-27].

The major components of RAS have been identified in ocular tissues and are overexpressed in the diabetic retina. Angiotensin II binds and activates two primary receptors, AT1-R and AT2-R. In adult humans activation of the AT1-R dominates the pathological states. AT1-R activation by angiotensin II produced by the retina stimulates several pathways involved in the pathogenesis of DR such as inflammation, oxidative stress, cell proliferation, pericyte migration, remodelling of extracellular matrix by increasing matrix metalloproteinases, angiogenesis and fibrosis (Figure 2)^[24]. In addition, AT1-R activation by angiotensin II promotes leukostasis (the inappropriate adherence of leukocytes to the retinal capillaries) and neurodegeneration^[24,28]. Apart from reducing microvascular disease, there is growing evidence pointing to neuroprotection as a relevant mechanism involved in the beneficial effects of ARBs in DR. In this regard, it has recently been reported that candesartan (the ARB with the best diffusion across the blood-brain barrier) has a neuroprotective effect after brain focal ischemia^[29]. In addition, telmisartan and valsartan inhibit the synaptophysin degradation that exists in the retina of a murine model of DR^[30]. Moreover, valsartan is able to prolong the survival of astrocytes and reduce glial activation in the retina of rats with hypoxia-induced retinopathy^[31]. Furthermore, mitochondrial oxidative stress associated with retinal neurodegeneration has been improved by using losartan in a model of spontaneously hypertensive rats^[32]. Taken together, it seems that neuroprotection is a relevant mechanism involved in the beneficial effects of ARBs in DR.

PEDF

PEDF is a 50 kDa protein encoded by a single gene that is preserved across phyla from fish to mammals. It shares homology with the serine proteinase inhibitor (Serpin) family but lacks proteinase activity. PEDF was first purified from human RPE cells and was described as a neurotrophic factor with neuroprotective properties^[33]. In this regard, it should be noted that intraocular gene transfer of PEDF significantly increases neuroretinal cell survival after ischemia-reperfusion injury^[34] and excessive light exposure^[35]. In addition, PEDF protects neurons from glutamate-mediated neurodegeneration^[36].

Apart from its neurotrophic factor and neuroprotective properties, there is growing evidence that PEDF is among the most important natural inhibitors of angiogenesis and that it is the main factor accounting for the antiangiogenic activity of vitreous fluid where it is found in abundant quantities^[37]. PEDF is responsible for the avascularity of the cornea and vitreous fluid and under hypoxic conditions its secretion is decreased. In addition, elevated glucose down-regulates PEDF expression in

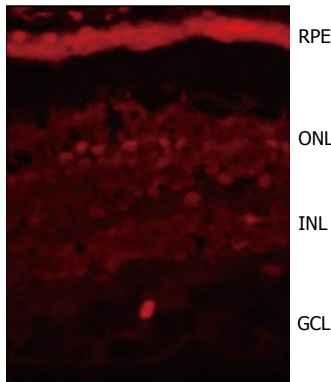


Figure 3 SST immuno-fluorescence (red) in the human retina showing a higher expression in RPE than in the neuroretina from a human eye donor. RPE: Retinal pigment epithelium; ONL: Outer nuclear layer; INL: Inner nuclear layer; GCL: Ganglion cell layer.

RPE cells. The receptors for PEDF are not known but experimental studies suggest that there may be receptors in the retina^[38-40]. In addition, it has been suggested that antiangiogenic and neurotrophic activities reside in separate regions of the molecule, thus suggesting that more than one receptor exists^[40,41].

Therefore, there are enough arguments to propose PEDF as a serious new candidate for DR treatment. PEDF can successfully be delivered to the eye by viral vectors. As an alternative to viral-mediated gene transfer, transplantation of autologous cells transfected with plasmids encoding for PEDF delivers therapeutic doses of PEDF to the eye. Another mechanism for delivering PEDF to the eye is to exploit its endogenous availability or production. It seems likely that much of the endogenous PEDF in the eye is bound to extracellular matrix molecules and thus may not be active. Drugs that release PEDF from these matrix molecules could increase free PEDF to therapeutic levels. In addition, levels of PEDF mRNA and secreted protein could be increased by either dexamethasone or retinoic acid^[42]. Therefore, new strategies for diabetic retinopathy treatment based on PEDF activation are warranted.

SST

SST is a peptide that was originally identified as the hypothalamic factor responsible for the inhibition of the release of the growth hormone from the anterior pituitary. Subsequent studies have shown that SST has a much broader spectrum of inhibitory actions and is much more widely distributed in the body, occurring not only in many regions of the central nervous system but also in many tissues of the digestive tract and in the retina^[43]. SST mediates its multiple biological effects via specific plasma membrane receptors that belong to the family of G-protein coupled receptors with seven transmembrane domains. So far, five SST receptor subtypes (SSTRs) have been identified (SSTRs 1-5).

Neuroretina and, in particular, the amacrine cells have been classically described as the main source of SST in the retina. However, we have found that SST expression and content is higher in RPE than in the neuroretina from human eye donors^[6] (Figure 3). Therefore, RPE rather than neuroretina is the main source of SST, at least in humans. The amount of SST produced by the

human retina is significant as deduced by the strikingly high levels found in the vitreous fluid^[44,45]. Apart from SST, SSTRs are also expressed in the retina, with SSTR1 and SSTR2 being the most widely expressed^[43,46,47]. The production of both SST and its receptors simultaneously suggests an autocrine action in the human retina.

The main functions of SST for retinal homeostasis are the following: (1) SST acts as a neuromodulator through multiple pathways, including intracellular Ca^{2+} signaling, nitric oxide function and glutamate release from the photoreceptors. In addition, a loss of SST immunoreactivity occurs after degeneration of the ganglion cells. Therefore, the neuroretinal damage that occurs in DR might be the reason for the decreased SST levels detected in the vitreous fluid of these patients. In fact, we have recently found that low SST expression and production is an early event in DR and is associated with retinal neurodegeneration (apoptosis and glial activation)^[6]; (2) SST is a potent angiostatic factor. SST may reduce endothelial cell proliferation and neovascularisation by multiple mechanisms including the inhibition of postreceptor signalling events of peptide growth factors such as IGF-I, VEGF, epidermal growth factor and PDGF^[48]; and (3) SST has been involved in the transport of water and ions. Various ion/water transport systems are located on the apical side of the RPE adjacent to the subretinal space and a high expression of SST-2 has been shown in this apical membrane of the RPE^[46].

In DR there is a downregulation of SST associated with retinal neurodegeneration^[6]. The lower expression of SST in RPE and neuroretina is associated with a dramatic decrease of intravitreal SST levels in both PDR^[39,40] and DME^[49]. As a result, the physiological role of SST in preventing both neovascularisation and fluid accumulation within the retina could be reduced and consequently the development of PDR and DME is favoured. In addition, the loss of neuromodulator activity could also contribute to neuroretinal damage. For all these reasons, intravitreal injection of SST analogues or gene therapy has been proposed as a new therapeutic approach in DR^[50].

Epo

Erythropoietin (Epo) was first described as a glycoprotein produced exclusively in fetal liver and adult kidney that acts as a major regulator of erythropoiesis. However, Epo expression has also been found in the human brain and in the human retina^[51,52]. In recent years, we have demonstrated that both Epo and its receptor are expressed in the adult human retina^[53]. Epo and EpoR mRNAs are significantly higher in RPE than in the neuroretina^[53]. In addition, intravitreal levels of Epo are ~3.5 fold higher than those found in plasma^[52]. The role of Epo in the retina remains to be elucidated but it seems that it has a potent neuroprotective effect^[54,55].

Epo is upregulated in DR^[52,53,56,57]. Epo overexpression has been found in both the RPE and neuroretina of diabetic eyes (Figure 4)^[52,53]. This is in agreement with the elevated concentrations of Epo found in the vitreous

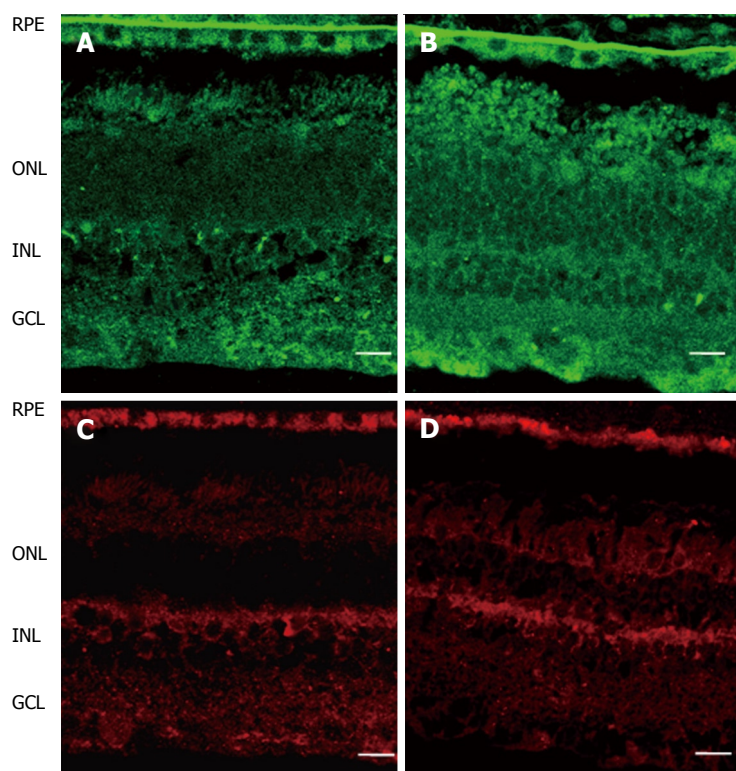


Figure 4 Comparison of Epo (upper panel, green) and EpoR (lower panel, red) immunofluorescence in the human retina between representative samples. A, C: Non-diabetic donor; B, D: Diabetic donor. RPE: Retinal pigment epithelium; ONL: Outer nuclear layer; INL: Inner nuclear layer; GCL: Ganglion cell layer. The bar represents 20 μ m.

fluid of diabetic patients (~30 fold higher than plasma and ~10 fold higher than in non-diabetic subjects)^[52]. Hypoxia is a major stimulus for both systemic and intraocular Epo production. In fact, high intravitreal levels of Epo have recently been reported in ischemic retinal diseases such as PDR^[52,56-58]. In addition, it has been reported that Epo has an angiogenic potential equivalent to VEGF^[57,59]. Therefore, Epo could be an important factor involved in stimulating retinal angiogenesis in PDR. However, intravitreal levels of Epo have been found at a similar range in PDR to that in DME (a condition in which hypoxia is not a predominant event)^[52]. In addition, intravitreal Epo levels are not elevated in non-diabetic patients with macular edema secondary to retinal vein occlusion^[60]. Finally, a higher expression of Epo has been detected in the retinas of diabetic donors at early stages of DR compared to non-diabetic donors and this overexpression is unrelated to mRNA expression of hypoxic inducible factors (HIF-1 α and HIF-1 β)^[53]. Therefore, stimulating agents other than hypoxia/ischemia are involved in the upregulation of Epo that exists in the diabetic eye.

The reason why Epo is increased in DR remains to be elucidated but the bulk of the available information points to a protective effect rather than a pathogenic effect at least in the early stages of DR. In addition, Epo is a potent physiological stimulus for the mobilization of endothelial progenitor cells (EPCs) and therefore could play a relevant role in regulating the traffic of circulating EPCs towards injured retinal sites^[61]. In this regard, the increase of intraocular synthesis of Epo that occurs in DR can be contemplated as a compensatory mechanism to restore the damage induced by the diabetic milieu.

In fact, exogenous Epo administration by intravitreal injection in early diabetes may prevent retinal cell death and protect the blood retinal barrier function in STZ-DM rats^[62]. Nevertheless, in advanced stages, the elevated levels of Epo could potentiate the effects of VEGF thus contributing to neovascularisation and consequently worsening PDR^[61,63].

The potential advantages of Epo or EpoR agonists in the treatment of DR include neuroprotection, vessel stability and enhanced recruitment of EPCs to the pathological area. However, as mentioned above, timing is critical since if Epo is given at later hypoxic stages the severity of DR could increase. However, in the case of the eye, disease progression is easy to follow without invasive investigation and allows timing of the administration of drugs to be carefully monitored hopefully resulting in better clinical outcomes.

CONCLUSION

Neurodegeneration is an early event in the pathogenesis of DR. Elevated levels of glutamate and the overexpression of the RAS system play an essential role in the neurodegenerative process that occurs in the diabetic retina. Among the neuroprotective factors, PEDF, SST and Epo seem to be the most important contributing factors but the role of NPD1, BDNF, GDNF, CNTF and AM should also be taken into account. In fact, the balance between neurotoxic and neuroprotective factors rather than the levels of neurotoxic factors alone will determine the presence or not of retinal neurodegeneration in the diabetic eye.

Finally, it should be stressed that the study of the

mechanisms that lead to neurodegeneration will be essential for identifying new therapeutic targets in the early stages of DR. At present this is a growing and increasingly important field in medicine which involves several areas of knowledge such as diabetology, ophthalmology and the neurosciences and consequently clinical trials with a multidisciplinary approach are needed.

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Events Calendar 2010

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Brussels, Belgium
30th International Symposium on
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Medicine

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Cairo, Egypt
14th Pan Arab Conference on
Diabetes PACD14

May 01-05
New Orleans, LA, United States
Digestive Disease Week Annual
Meeting

June 09-12
Singapore, Singapore
13th International Conference on
Emergency Medicine

June 25-29
Orlando, FL, United States
70th ADA Diabetes Scientific
Sessions

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Boston, MA, United States
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Instructions to authors

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Format

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- 1 Jung EM, Clevert DA, Schreyer AG, Schmitt S, Rennert J, Kubale R, Feuerbach S, Jung F. Evaluation of quantitative contrast harmonic imaging to assess malignancy of liver tumors: A prospective controlled two-center study. *World J Gastroenterol* 2007; **13**: 6356-6364 [PMID: 18081224 DOI: 10.3748/wjg.13.6356]

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- 2 **Lin GZ**, Wang XZ, Wang P, Lin J, Yang FD. Immunologic effect of Jianpi Yishen decoction in treatment of Pixu-diarrhoea. *Shijie Huaren Xiaobua Zazhi* 1999; **7**: 285-287

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- 3 **Tian D**, Araki H, Stahl E, Bergelson J, Kreitman M. Signature of balancing selection in Arabidopsis. *Proc Natl Acad Sci USA* 2006; In press

Organization as author

- 4 **Diabetes Prevention Program Research Group**. Hypertension, insulin, and proinsulin in participants with impaired glucose tolerance. *Hypertension* 2002; **40**: 679-686 [PMID: 12411462 PMID:2516377 DOI:10.1161/01.HYP.0000035706.28494.09]

Both personal authors and an organization as author

- 5 **Vallancien G**, Emberton M, Harving N, van Moorselaar RJ; Alf-One Study Group. Sexual dysfunction in 1, 274 European men suffering from lower urinary tract symptoms. *J Urol* 2003; **169**: 2257-2261 [PMID: 12771764 DOI:10.1097/01.ju.0000067940.76090.73]

No author given

- 6 21st century heart solution may have a sting in the tail. *BMJ* 2002; **325**: 184 [PMID: 12142303 DOI:10.1136/bmj.325.7357.184]

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- 7 **Geraud G**, Spierings EL, Keywood C. Tolerability and safety of frovatriptan with short- and long-term use for treatment of migraine and in comparison with sumatriptan. *Headache* 2002; **42** Suppl 2: S93-99 [PMID: 12028325 DOI:10.1046/j.1526-4610.42.s2.7.x]

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- 8 **Banit DM**, Kaufer H, Hartford JM. Intraoperative frozen section analysis in revision total joint arthroplasty. *Clin Orthop Relat Res* 2002; **(401)**: 230-238 [PMID: 12151900 DOI:10.1097/00003086-200208000-00026]

No volume or issue

- 9 Outreach: Bringing HIV-positive individuals into care. *HRSA Careaction* 2002; 1-6 [PMID: 12154804]

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- 10 **Sherlock S**, Dooley J. Diseases of the liver and biliary system. 9th ed. Oxford: Blackwell Sci Pub, 1993: 258-296

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- 11 **Lam SK**. Academic investigator's perspectives of medical treatment for peptic ulcer. In: Swabb EA, Azabo S. Ulcer disease: investigation and basis for therapy. New York: Marcel Dekker, 1991: 431-450

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- 12 **Breedlove GK**, Schorfheide AM. Adolescent pregnancy. 2nd ed. Wiczorek RR, editor. White Plains (NY): March of Dimes Education Services, 2001: 20-34

Conference proceedings

- 13 **Harnden P**, Joffe JK, Jones WG, editors. Germ cell tumours V. Proceedings of the 5th Germ cell tumours Conference; 2001 Sep 13-15; Leeds, UK. New York: Springer, 2002: 30-56

Conference paper

- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic

Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

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- 15 Morse SS. Factors in the emergence of infectious diseases. Emerg Infect Dis serial online, 1995-01-03, cited 1996-06-05; 1(1): 24 screens. Available from: URL: <http://www.cdc.gov/ncidod/EID/eid.htm>

Patent (list all authors)

- 16 **Pagedas AC**, inventor; Ancel Surgical R&D Inc., assignee. Flexible endoscopic grasping and cutting device and positioning tool assembly. United States patent US 20020103498. 2002 Aug 1

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Write as mean \pm SD or mean \pm SE.

Statistical expression

Express *t* test as *t* (in italics), *F* test as *F* (in italics), chi square test as χ^2 (in Greek), related coefficient as *r* (in italics), degree of freedom as *v* (in Greek), sample number as *n* (in italics), and probability as *P* (in italics).

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Use SI units. For example: body mass, *m* (B) = 78 kg; blood pressure, *p* (B) = 16.2/12.3 kPa; incubation time, *t* (incubation) = 96 h, blood glucose concentration, *c* (glucose) 6.4 ± 2.1 mmol/L; blood CEA mass concentration, *p* (CEA) = 8.6 24.5 μ g/L; CO₂ volume fraction, 50 mL/L CO₂, not 5% CO₂; likewise for 40 g/L formaldehyde, not 10% formalin; and mass fraction, 8 ng/g, etc. Arabic numerals such as 23, 243, 641 should be read 23 243 641.

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Italics

Quantities: *t* time or temperature, *c* concentration, *A* area, *l* length, *m* mass, *V* volume.

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