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Stress granules in colorectal cancer: Current knowledge and potential therapeutic applications

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Abstract

Stress granules (SGs) represent important non-membrane cytoplasmic compartments, involved in cellular adaptation to various stressful conditions (e.g., hypoxia, nutrient deprivation, oxidative stress). These granules contain several scaffold proteins and RNA-binding proteins, which bind to mRNAs and keep them translationally silent while protecting them from harmful conditions. Although the role of SGs in cancer development is still poorly known and vary between cancer types, increasing evidence indicate that the expression and/or the activity of several key SGs components are deregulated in colorectal tumors but also in pre-neoplastic conditions (e.g., inflammatory bowel disease), thus suggesting a potential role in the onset of colorectal cancer (CRC). It is therefore believed that SGs formation importantly contributes to various steps of colorectal tumorigenesis but also in chemoresistance. As CRC is the third most frequent cancer and one of the leading causes of cancer mortality worldwide, development of new therapeutic targets is needed to offset the development of chemoresistance and formation of metastasis. Abolishing SGs assembly may therefore represent an appealing therapeutic strategy to re-sensitize colon cancer cells to anti-cancer chemotherapies. In this review, we summarize the current knowledge on SGs in colorectal cancer and the potential therapeutic strategies that could be employed to target them.

Key Words: Stress-Granules; Colorectal cancer; Adenylate-Uridylate-rich element-binding proteins; Post-transcriptional regulation; Oncogenes; Tumor suppressors

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Core Tip: Colorectal cancer (CRC) represent the second cause of cancer mortality worldwide. Although changes in genetic landscape associated with CRC development have been identified, most frequent mutations are currently undruggable. The development of chemoresistance represent a major cause of CRC-associated mortality and identifying mechanisms allowing cancer cells to avoid these treatments may considerably improve clinical outcomes. Current findings indicate that cancers cells can preserve their expressed mRNAs in harmful conditions by storing them in small cytoplasmic granules, called Stress granules (SGs), where they are kept translationally silent. Targeting these SGs proteins may therefore represent a novel and efficient therapeutic approach.

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INTRODUCTION

Colorectal cancer (CRC) represents the second cause of cancer mortality worldwide and the third most frequent cancer, with 1.8 million new cases and 881000 death in 2018^[1]. CRC development results from a long term-deregulated process starting with the development of small adenomas, which evolve toward large adenomas and CRC. In most of the cases CRC develops sporadically (70%) and occurs in an aging population (> 50 years), whereas inherited genetic disorders such as Familial Adenomatous Polyposis or Lynch Syndrome are relatively rare and occurs at a younger age (before 50). Although the causes of sporadic CRC remain unclear, several risk factors have been identified, including inflammatory bowel disease (IBD) (*e.g.*, Crohn's disease and ulcerative colitis), obesity, diabetes, sedentary lifestyle, alcohol consumption, high fat-containing diet, and aging. Therefore, with the prevalence of obesity and diabetes worldwide, CRC incidence is expected to dramatically increase in the future, making this cancer a major public health concern and a growing economic burden. CRC is mostly treated by surgery, chemotherapy (*e.g.*, FOLFOX: Folinic acid, 5-fluorouracil, oxaliplatin) and targeted therapy. However, despite these therapeutic options, the average survival rate of colon cancer between 2009 and 2015 was 63% (all SEER stages combined) and only 14% for distant CRC (American Cancer Society: <https://www.cancer.org/cancer/colon-rectal-cancer/detection-diagnosis-staging/survival-rates.html>). This high mortality rate is predominantly due to metastasis and the development of chemoresistance^[2]. Therefore, greater efforts are needed in identifying and targeting the mechanisms involved in both these processes in order to improve patient outcomes.

The development of chemoresistance is a major feature of CRC-associated mortality. Several chemoresistance mechanisms have been identified, including the induction of pro-survival factors and downregulation of pro-apoptotic proteins, along with the induction of transporters or detoxifications enzymes (*e.g.*, P-glycoprotein), which reduce the efficiency of chemotherapy. More recently, it has been proposed that cancer cells can adapt to stress conditions (*e.g.*, oxidative stress, hypoxia, chemotherapy) by generating small cytoplasmic ribonucleoprotein (RNP) foci called stress granules (SGs), which protect expressed mRNAs from degradation. SGs represent membrane-less cytoplasmic compartments containing mRNAs stalled at translation initiation. The mechanism underlying their formation is complex and tightly regulated by several proteins, which interact with mRNAs. SGs formation is also reversible, but in cases of prolonged stress, mRNAs are degraded into other cytoplasmic foci called processing bodies (P-Bodies). In cancer cells, SGs importantly contribute to cancer cell survival but also to resistance to various anti-cancerous agents. Several SGs components are upregulated in cancer cells as compared to their normal cellular counterparts. Moreover, several anti-cancerous agents elicit SGs assembly in cancer cells. Recent efforts aiming at identifying the mRNA/protein content of SGs have uncovered key players in carcinogenesis (*e.g.*, oncogenes or tumor suppressors). Finally, impairment of SGs formation can re-sensitize several cancer types to chemotherapy or other anti-cancer agents (*e.g.*, sorafenib) and thus may represent an appealing approach in combination with current treatments (*e.g.*, FOLFOX, FOLFIRI)^[3]. In this review, we

discuss the role of SGs in colon cancer but also in pre-cancerous conditions favoring its development (*e.g.*, inflammatory bowel disease). Because this cellular process has not been extensively studied in the context of CRC, we also discuss the current gaps in knowledge of SGs biology in CRC cells. Finally, we discuss potential therapeutic approaches that could be used to impact SGs assembly in cancer cells.

COMPLEXITY OF STRESS GRANULES FORMATION AND CARCINOGENESIS

Basics of SGs assembly

SGs are non-membrane cytoplasmic compartments, composed of untranslated RNPs formed in stressful conditions. SGs exhibit liquid-like behavior allowing rapid exchanges of components (*e.g.*, mRNAs and proteins) with the cytosol^[4,5]. The formation of SGs is a dynamic and conserved process, triggered by various stress conditions (*e.g.*, nutrients deprivation, osmotic shock, hypoxia, heat shock, ultraviolet irradiation, oxidative stress), but also various molecules (*e.g.*, chemotherapy, endoplasmic reticulum stressors, translation/proteasome inhibitors). Proteomic-based approaches have identified many of proteins located within mammalian SGs (<https://msgp.pt/>; <http://rnagranuledb.lunenfeld.ca/>). To date, more than 400 proteins have been identified in stress granules, but their composition may vary between cell types and/or stimuli. Among them, about 50% are RNA-Binding Proteins, while the remaining proteins are presumably recruited through protein-protein interaction and are involved in various cellular processes (*e.g.*, cell cycle progression, apoptosis) or SGs assembly regulation.

The mechanisms involved in SGs formation are still unclear and several models have been proposed. SGs assembly is a multi-step process starting with the phosphorylation of eIF2 α , which prevents the formation of the eIF2/GTP/tRNAi initiation complex^[6] and leads to the dissociation of mRNAs from polysomes. However, this step is not mandatory for SGs assembly, as other non-canonical eIF2-independent models of SGs formation have been described (*e.g.*, change in the activity of the eIF4F complex, which is also involved in translation initiation)^[7,8]. Currently two models of SGs formation have been proposed^[9]. In the “*core first*” model, untranslated mRNAs are nucleated into oligomers through the binding of proteins (*e.g.*, T Cell-Restricted Intracellular Antigen-1, TIA1, G3BP1) having a Prion-Like Domain or Intrinsically Disordered Domains, which provide scaffolds necessary for the recruitment of other proteins (primary aggregation). These domains consist of polar residues, which favor liquid-liquid phase separation (LLPS) through electrostatic interactions. Due to these biophysical properties, SGs have been qualified as “*liquid droplets*”^[10]. Then, the growth of these oligomers, through the addition of other untranslated RNPs give rise to the SGs “*cores*”. This step is supported by the microtubule’s cytoskeleton and motor proteins (*e.g.*, dyneins, kinesins), which bring additional RNPs to the SGs^[11]. Finally, the heterotypic associations of SGs components (*e.g.*, G3BP1/TIA1; Polyadenylate-binding protein 1, PABP1) promote the growth and fusion of the granules (coalescence) and the recruitment of a dynamic shell, leading to the formation of large macroscopically visible SGs. However, this model has been challenged by the “*LLPS First*” model, where the nucleation of RNP generate phase separated droplets connected by weak interactions in which core granules are formed.

The formation of SGs is a tightly regulated process with participation of several signaling pathways and post-translational modifications (*e.g.*, phosphorylation, acetylation)^[12] of SGs components that regulate SGs assembly. For instance, phosphorylation of G3BP1 on ser¹⁴⁹ by casein kinase 2 (CK2)^[13] impairs SGs assembly, while arginine methylation, or deacetylation of G3BP1 by PRMT1/5 (protein arginine methyltransferase) and HDAC6^[12], respectively^[14,15], promotes their formation. Several signaling pathways regulate SGs assembly, including the PI3K or the Stress-Activated Kinase (p38/MAPK) signaling, which enhance SGs formation by activating mTORC1 kinase in stress conditions^[16]. These pathways are usually overactivated in many cancers, following mutations of their key regulators (*e.g.*, AKT, PTEN), thus providing a favorable landscape for SGs formation. However, it is still unclear the role of mTORC1 in SGs assembly, as other studies have suggested an opposite mechanism where AMPK inhibits mTORC1 and induces SGs assembly^[17]. These differences may originate from the different models and stimuli used to trigger SGs. Finally, SGs formation is a reversible process and the clearance of SGs can be mediated by: (1) Translation re-initiation (after stress dissipates); (2) Chaperone proteins; (3) Autophagy (also referred as “*granulophagy*”); (4) mRNA degradation in processing

bodies (P-Bodies); and (5) Proteasome-dependent degradation of SGs proteins.

While SGs formation is an adaptive response to physiological conditions where transient mRNA storage can occur, the role of SGs in human diseases has been recently recognized^[6,18]. Dysregulation of SGs in various pathologies including neurodegenerative, viral infections, vascular diseases, and cancers indicate that SGs to be linked to disease progression. The mechanisms underlying SGs dysregulation in disease are not fully understood, yet aberrant expression of SGs components and altered pathway activity regulating their assembly and clearance appear to be contributing factors to the development of disease-associated SGs formation.

SGs and carcinogenesis

Overexpression of SGs assembly-related proteins, along with impairment of proteins/processes involved in their clearance are the main causes of SGs formation in cancers cells. Overexpression of nucleating proteins (*e.g.*, G3BP1, TIA1, TIA-1-related, TIAR) is sufficient to trigger SGs formation in absence of stress^[19]. Moreover, the stressful conditions present within the tumor microenvironment (*e.g.*, hypoxia, oxidative stress, nutrient deprivation, chronic inflammation)^[20], as well as specific molecules present (prostaglandin J2 and A1), promote SGs assembly in cancer cells^[19]. Other factors including oxidized-low density lipoprotein or high-fat diet are also contributing factors to SGs formation^[21]. These data suggest that lifestyle and chronic inflammatory/metabolic diseases (*e.g.*, diabetes, fatty liver diseases, ulcerative colitis), which represent major risk factors for cancer development (*e.g.*, hepatocellular carcinoma, CRC), may considerably influence SGs formation. Several anti-cancer treatments such as sorafenib, bortezomib, 5-FU, Oxaliplatin^[19], FCCP [Carbonyl cyanide p-(trifluoromethoxy) phenylhydrazone]^[22] and radiotherapy^[19] increase SGs assembly in cancer cells, which in turn renders them more resistant to these treatments. SGs are also implicated in controlling cancer-related processes including apoptosis and migration/invasion of cancer cells. Although the precise mechanisms are still unclear, the sequestration and inhibition of pro-apoptotic factors (*e.g.*, TRAF2, RACK1) has been suggested^[23]. Furthermore, several RNA-binding proteins (*e.g.*, tristetraprolin, HuR) located in SGs regulate the stability and translation of cancer-related mRNA transcripts involved in various cancerous hallmarks, including cell proliferation (*e.g.*, MYC)^[24], angiogenesis (*e.g.*, VEGFA)^[25], inflammation (*e.g.*, cyclooxygenase-2, COX-2)^[26] and cell death (antiapoptotic protein: BCL2, MCL1)^[27,28]. SGs also inhibits cellular senescence by sequestering plasminogen activator inhibitor-1 in fibroblasts^[29]. As senescence represents an important barrier against carcinogenesis^[30], these findings further support the oncogenic function of SGs. Finally, defective P-body formation is observed in several cancers (*e.g.*, CRC)^[6], and this together with the increased SGs assembly may act in concert to promote tumor progression.

The current methodologies to study SGs functions are mostly based on gain and loss of function analyses of SGs components, microscopy, and cell fractionation methods to isolate SGs. This latest methodology, coupled with transcriptomic and proteomic-based approaches, have identified both proteins and mRNA transcripts associated with these granules. This information is publicly available in several databases (*e.g.*, <https://msgp.pt/>; <http://rnagranuledb.lunenfeld.ca/>) and interestingly several transcripts and proteins have been associated to various cancer-related processes, suggesting that the role of SGs in carcinogenesis is largely underestimated. While the majority of studies utilize cell-based *in vitro* approaches, *in vivo* mouse models with constitutive deletion of specific SGs factors (*e.g.*, TIA1KO or G3BP1KO mice) have been generated^[31,32]. Further efforts utilizing tissue-specific and inducible knockout approaches will further aid in understanding the role of SGs play in development and progression of specific tumor types.

ROLE OF STRESS GRANULES IN COLORECTAL CANCER

Although the role of SGs has been studied in various cancers, their functions in the development of CRC and inflammatory bowel disease remain to be characterized. While more than 400 proteins have been identified in mammalian SGs (*e.g.*, <https://msgp.pt/>), only few of them have been involved in SGs assembly and disassembly are abundantly expressed in epithelial and goblet cells of the colon (single cell sequencing of large intestine: <https://tabula-muris.ds.czbiohub.org/>) and also in the other cell types (*e.g.*, enteroendocrine cells). In addition, several proteins (*e.g.*, RNA-binding proteins, pro-apoptotic factors, cell cycle-related proteins) involved in

cancer-related processes in CRC are localized in SGs.

SG nucleators and CRC

SGs nucleators refer to the proteins that are directly involved in the early aggregation phase of SGs formation and their sole overexpression is sufficient for spontaneous SGs assembly, even in absence of stress. Conversely, knockdown of these proteins severely impairs SGs assembly. Moreover, alteration of their expression occurs in preneoplastic conditions, such as ulcerative colitis, thus suggesting that defects in their expression are early alterations fostering CRC development.

UBAP2L: A component of the ubiquitin-proteasome pathway containing a ubiquitin-associated (UBA) domain which binds to ubiquitin and multi-ubiquitin chains^[33]. UBAP2L plays a key role in stress granules assembly even in stress-null conditions^[34,35]. The Arg-Gly-Gly (RGG) motif of UBAP2L plays a key role in SGs assembly^[35] by mediating the recruitment of other components (*e.g.*, RNPs)^[35]. Importantly, this domain can be methylated by the protein arginine methyltransferase PRMT1, which impairs SGs formation^[35]. The Domain of Unknown Function motif of UBAP2L is also necessary to bind to G3BP1/2^[35]. Recent findings have suggested that UBAP2L acts upstream of G3BP1/2 and can form SGs core independently of G3BP1/2^[36]. The function of UBAP2L in cancers is poorly known but increasing evidence indicates that UBAP2L promotes progression of hepatocellular carcinoma^[37], prostate cancer^[38] and glioblastoma^[39]. The expression of UBAP2L in CRC is currently unknown (**Table 1**) but its knockdown in colon cancer cells (*i.e.*, HCT116 and RKO cells)^[40] hinders cell cycle progression^[40] and induces apoptosis through activation of BAD, BAX, and the cleavage of Caspase-3 and Poly(ADP-ribose) Polymerase^[40]. Although these results indicate an oncogenic function of UBAP2L in CRC, they are currently no studies documenting its function in SGs in CRC.

Ras GTPase-activating protein-binding protein (G3BP): A family of RNA-binding proteins composed of three different members, G3BP1, GBP2a and G3BP2b. Through their interaction with the SH3 domain of RasGAP (Ras GTPase activating protein), these proteins promote Ras signaling^[41]. G3BP proteins contain a RNA recognition motif (RRM), which allows for interaction with the 40S subunit of ribosomes and RGG domains involved in mRNA binding^[42]. Among them, G3BP1 is strongly overexpressed in a variety of cancers especially colon cancer^[43] and exert oncogenic functions by promoting cancer cell proliferation, and inhibiting apoptosis^[44]. Accordingly, downregulation of G3BP1 in colon cancer cells leads to a decrease of Ras signaling and cell growth arrest^[43]. Despite the lack of a PLD, G3BP1 is an important SGs nucleator, as its sole overexpression is sufficient to trigger SGs assembly^[45]. Although the mechanism involved is still unclear, recent studies have indicated that protein partners including CAPRIN1 or USP10, which promote and inhibit SGs assembly, respectively^[46]. In CRC, the role of CAPRIN1 is currently unknown but a loss of USP10 expression was reported in 18.6% of CRC tumors^[47]. Importantly, this loss was associated to distal metastasis and lymphovascular invasion.

The mechanism involved in G3BP1 overexpression is currently unknown but the RNA-binding protein Y-box binding protein (YB-1), which is overexpressed in CRC and ulcerative-associated lesions^[48], may be involved in the increase of G3BP1 translation as suggested in other cancers^[49]. G3BP1 is also regulated by post-translational modifications. G3BP1 phosphorylation on Ser¹⁴⁹ by CK2 was reported to inhibits SGs formation^[13]. However, the role of this phosphorylation is still controversial, as an *erratum* reporting that ser¹⁴⁹ phosphorylation was unchanged during stress, has been published^[50]. Arginine methylation in the RGG domain by protein arginine methyltransferase inhibits SGs formation^[14]. Interestingly, this methylation is promoted by the Wnt/ β -catenin pathway in mouse embryonic F9 cells^[15], suggesting that overactivation of this oncogenic pathway in CRC may account for the increased SGs assembly in colon cancer cells. Finally, acetylation of Lysine-376 (K376) in the RRM domain, impairs the RNA binding function of G3BP1 as well as its interaction with PABP1, USP10 or Caprin1^[12]. Accordingly, an increased acetylation of K376 was observed during SGs disassembly. HDAC6 and the CBP/p300 acetylase directly control the acetylation status of G3BP1^[12] and thus HDAC6 inhibition impairs SGs formation^[51]. While these findings indicate that the role of G3BP1 in SGs assembly, its role in CRC remains to be better characterized. Moreover, the other members of the G3BP family are potentially important for SGs assembly in colon cancer cells. For instance, G3BP2 overexpression can also trigger SGs formation in absence of stress^[41,44]. The role of G3BP2 in CRC is currently unknown but *in silico* analysis of its mRNA level in CRC patients indicates an upregulation of G3BP2 in tumors as

Table 1 Expression and prognostic value of stress granule-associated proteins in colorectal cancer

Components	Role in SG	mRNA expression in tumors (GEPIA)	Expression in CRC patients (literature)	Overall survival (GEPIA)	Overall survival (Human Protein Atlas)
<i>G3BP1</i>	Promotes SG assembly	Up	Unknown	No significant difference	Better prognosis with high expression
<i>G3BP2</i>	Promotes SG assembly	Up	Unknown	No significant difference	Better prognosis with high expression
<i>USP10</i>	Promotes SG assembly	Up (trend)	Down in 18.6% of patients ^[47]	No significant difference	Better prognosis with high expression
<i>CAPRIN1</i>	Promotes SG assembly	Up	Unknown	No significant difference	Better prognosis with high expression
<i>UBAP2L</i>	Promotes SG assembly	No significant difference	Unknown	No significant difference	No significant difference
<i>TIA1</i>	Promotes SG assembly	Down (trend)	sTIA1 (spliced variant) is Up ^[171]	Poor prognosis with high expression	Better prognosis with high expression
<i>TIAL1</i>	Promotes SG assembly	Down (trend)	Unknown	Poor prognosis with high expression	No significant difference
<i>DDX3</i>	Promotes SG assembly	No significant difference	Poor prognosis with high expression ^[57]	No significant difference	Better prognosis with high expression
<i>PABP1</i>	Promotes SG assembly	Up	Unknown	NA	No significant difference
<i>FMR1</i>	Promotes SG assembly	No significant difference	Unknown	No significant difference	Better prognosis with high expression
<i>PDCD4</i>	Promotes SG assembly	Down (trend)	Down ^[172]	No significant difference	No significant difference
<i>ATXN2</i>	Promotes SG assembly	No significant difference	Unknown	No significant difference	No significant difference
<i>ANG</i>	Promotes SG assembly	No significant difference	Up	No significant difference	No significant difference
<i>ZFP36</i>	Promotes SG clearance and SG-P-Bodies fusion	Down	Down ^[26]	Poor prognosis with low expression ($P = 0.16$; trend)	No significant difference
<i>ZFP36L1</i>	Promotes SG-P-Bodies fusion	Down	Unknown	No significant difference	No significant difference
<i>ELAVL1</i>	mRNA stabilization	Up (trend)	Up ^[26]	No significant difference	Better prognosis with high expression
<i>CUGBP2</i>	mRNA stabilisation	No significant difference	Down ^[173]	No significant difference	Better prognosis with high expression
<i>MSI-1</i>	Promotes SG assembly	No significant difference	Up ^[54]	No significant difference	No significant difference
<i>KHSRP</i>	Unknown	No significant difference	Unknown	No significant difference	No significant difference
<i>BAG3</i>	Promotes SG clearance	No significant difference	Up ^[174]	No significant difference	Poor prognosis with high expression
<i>PRMT1</i>	Inhibition of SG formation	Up (trend)	(Poor prognosis with high expression ^[119])	Better prognosis with high expression (not significant; marked trend)	Better prognosis with high expression
<i>PRMT5</i>	Inhibition of SG formation	Up (trend)	Up ^[175]	Better prognosis with high expression (not significant; marked trend)	Better prognosis with high expression
<i>HDAC6</i>	Promotes SG assembly	Down	Up ^[176]	Poor prognosis with high expression (not significant; marked trend)	Poor prognosis with high expression
<i>SIRT6</i>	Promotes SG assembly	No significant difference	Down ^[113]	No significant difference	No significant difference
<i>EP300</i>	Inhibition of SG	No significant	Up ^[105]	No significant difference	No significant

	formation	difference		difference	difference
JMJD6	Promotes SG assembly	No significant difference	Up ^[121]	No significant difference but marked trend for a poor prognosis with high expression	No significant difference
CK2	Inhibition of SG formation	Up (trend)	Up ^[177]	No significant difference	Poor prognosis with high expression
PRKAA1 (AMPK)	Promotes SG assembly	No significant difference	Up ^[126,127]	No significant difference	Better prognosis with high expression
MTOR	Unclear	No significant difference	mTORC1 Up ^[122]	No significant difference	No significant difference
TARDBP	Promotes SG assembly	No significant difference	Unknown	No significant difference	No significant difference
RBFOX2	Regulation of cell cycle	Down	Up ^[101]	No significant difference	No significant difference
RACK1	Regulation of apoptosis	Up		No significant difference	No significant difference
ULK1	Promotes SG disassembly	Down	Up ^[178] (Poor Prognosis)	No significant difference	Poor prognosis with high expression
ULK2	Promotes SG disassembly	Down	Down ^[179]	No significant difference	No significant difference
VCP	Promotes SG disassembly	No significant difference	Up (poor prognosis with high expression) ^[180]	No significant difference	No significant difference

The differential mRNA expression of stress granule proteins in colorectal cancer as compared to matched non-tumoral tissues were retrieved from the GEPIA database (<http://gepia.cancer-pku.cn/detail>; normal tissues: *n* = 349; tumors: *n* = 275) and compared with published studies. Survival analyses were retrieved from the GEPIA (cutoff-High: 80%; cutoff-Low: 20%) and the Human Protein Atlas Database (<https://www.proteinatlas.org>) using the best separation method between low and high expression of protein candidates. SG: Stress granule; NA: Not available.

compared to surrounding non-tumoral tissue (Table 1).

TIA1 and TIAR: TIA1 is an RNA-binding protein comprised of three RRM necessary for the binding to AU-Rich Elements (AREs) within the 3'UTR of target mRNAs and a PLD in C-terminal, which promotes self-aggregation of the protein. In stress conditions (*i.e.*, hypoxia, oxidative stress), TIA1 interacts with co-factors (*e.g.*, TIAR) to promotes the sequestration of target transcripts into SGs and inhibits their translation. In CRC, TIA1 expression is reduced. The mechanisms involved in TIA1 silencing haven't been fully depicted but current findings indicate that the overexpression of miR-19a in CRC tissues and cell lines directly reduces TIA1 expression^[52]. In CRC, TIA1 acts as a tumor suppressor by binding to the 3'UTR of COX-2 mRNA, thereby inhibiting its translation^[53]. This tumor suppressive function is further supported with better prognosis observed in patients expressing a high level of TIA1 (Table 1). Intriguingly, TIA1 also contributes to chemoresistance to 5-FU in CRC cells^[54]. These data suggest that although TIA1 exerts a tumor suppressive function in CRC, its role in SGs assembly may paradoxically favor cancer cell survival.

DEAD-Box RNA helicase 3 (DDX3 also called CAP-Rf): A ubiquitously expressed protein having an ATPase and helicase activity involved in RNA metabolism (*e.g.*, mRNA splicing, transcription). DDX3 inhibits translation by directly interacting with eIF4E and with the SGs component PABP1, as evidenced in HeLa cells^[55], indicating that this protein is important for SGs assembly. The role of DDX3 in SGs assembly is independent of its ATPase and helicase activity and downregulation of DDX3 in HeLa cells leads to a reduction of SGs formation, a re-localization of PABP1 to the nucleus, and an increased susceptibility to death stimuli (*i.e.*, osmotic stress induced by sorbitol)^[55]. However, the role of DDX3 in CRC is unclear with studies reporting both oncogenic^[56,57] and tumor suppressive functions^[58]. High tumor DDX3 expression correlates with a reduced survival in CRC patients^[57]. Moreover, DDX3 expression is upregulated in colon biopsies from patients with inflammatory bowel disease^[59], which may provide a favorable landscape for SGs formation. Interestingly, the DDX3 inhibitor RK-33 decreases expression of MMP-1, -2, -3 and -10 in HCEC1CT and HCEC2CT human colonic epithelial cells^[59]. Interestingly, differentiation of HT-29 colon cancer cells is associated to decreased of DDX3 levels, suggesting that SGs

formation is also influenced by the differentiation status of cancer cells^[59].

G-quadruplex DNA structures (G4DNA): Current models of SGs formation have primarily focused on protein components triggering SGs assembly (*e.g.*, G3BP, UBAP2L). However, recent studies have also highlighted the role of G-quadruplex DNA structures in liquid-liquid phase separation upon oxidative-stress-induced DNA damage. G4DNAs represent quartets of guanine linked by hydrogen bonds and organized as a planar ring^[60]. Treatment of melanoma cells with hydrogen peroxide induces DNA damage and the production of ssDNA (single strand DNA), which forms G4DNA structures. Once exported into the cytosol, G4DNA interacts with various RNA-binding proteins involved in SG assembly, including YB-1, TIA1, TIAR, DHX36, and those involved in the control of the mRNA stability and translation (*e.g.*, HuR)^[60]. Accordingly, transfection of G4DNA is sufficient to trigger SG assembly in melanoma cells even in absence of stress, establishing G4DNA structures as potent SG nucleators^[60]. The role of G4DNA in SG assembly in CRC cells has not been studied yet. However, increasing evidence indicate that G4DNA promotes CRC development and their inhibition with specific ligands (*e.g.*, Emicoron) can promote antitumor activities^[61].

tiRNA-Derived stress-induced RNAs (tiRNA): Several non-coding RNAs, including microRNAs, long-non-coding RNAs and transfer RNAs have been involved in the adaptation of cells to stress stimuli^[62]. Among them, tiRNA represent a novel class of non-coding RNAs generated in stress conditions by cleavage of mature tRNAs in the anticodon loop by angiogenin^[62]. tiRNAs contribute to SGs formation by interacting with YB-1^[62]. Moreover, tiRNAs can form G-quadruplex structures, which impair translation initiation by sequestering eIF4F complex^[62]. Although the role of tiRNA in carcinogenesis is an emerging field, angiogenin is strongly upregulated in CRC as compared to non-tumoral tissues and promotes cancer progression by generating tiRNAs (*e.g.*, 5'-tiRNA-val)^[63]. Therefore, the accumulation of tiRNA together with the overexpression of nucleating proteins (*e.g.*, G3BP) in colon cancer cells, provides a notable mechanism for SG assembly in absence of stress.

RNA-binding proteins controlling the expression of key oncogenes/tumor suppressors

During SGs formation, the binding of several RNA-binding proteins to their mRNA targets importantly regulate their stability and/or translation. Among them, Adenylate-Uridylate-rich elements binding proteins (AUBPs) represent critical post-transcriptional regulators of gene expression, through their ability to bind to AREs within the 3'UTR of mRNA transcripts and promote their recruitment toward P-bodies or SGs. Aberrant ARE-dependent post-transcriptional regulation has been associated to a variety of cancers, including CRC, by favoring the overexpression of oncogenes (*e.g.*, c-myc) and pro-inflammatory mediators (*e.g.*, COX-2), and the silencing of tumor suppressors (*e.g.*, p53).

Tristetraprolin (TTP): TTP (*ZFP36*) belongs to a family of Cys-Cys-Cys-His zinc finger proteins and is an immediate-early response gene, whose expression can be induced by diverse stimuli such as insulin^[64,65], TGF- β ^[66,67], LPS^[68] and TNF α ^[69]. TTP is the best-characterized AU-Rich Element binding protein (AUBP) involved in promoting ARE-mediated mRNA decay. This process occurs through TTP-dependent delivery of ARE-mRNAs to P-bodies and recruit mRNA decay enzymes involved in deadenylation, decapping, and exonucleolytic decay^[66,70-72]. TTP is also localized in SGs under conditions of energy deprivation^[22]. However, the presence of TTP in SGs appears to be context-dependent as in models of oxidative stress, TTP is excluded from SGs due to phosphorylation of TTP by MK2^[22]. Current findings suggest that TTP is involved in the shuttling between SGs and P-bodies^[22] and SG-P-bodies fusion^[73], and thus can contribute to SG clearance. TTP is considered as a tumor suppressor due to its capacity to reduce the expression of key inflammatory cytokines and also control expression of several factors involved in CRC carcinogenesis (*e.g.*, COX-2, VEGF α)^[74-76]. Accordingly, TTP expression is strongly reduced in colorectal tumors^[26,77] as well as in early adenomas and adenocarcinomas, suggesting that early reduction of TTP may promote the establishment of a neoplastic phenotype. However, the link between TTP loss and SG dynamics in colon cancer cells remains unexplored.

Butyrate response factor 1 (TIS11b, ERF-1, cMGI, Berg36, ZFP36L1): An RNA-binding protein encoded by the *ZFP36L1* gene, which belongs to the *ZFP36* family^[78,79]. Similar to TTP, BRF1 contains a tandem zinc finger domain bearing a double zinc

finger motif (Cys-Cys-Cys-His) and promotes the decay of various cancer-promoting transcripts (*e.g.*, VEGFA, cIAP2) by targeting them to P-bodies^[79]. BRF1 is also a SG component and its overexpression promotes SG and P-body fusion^[73]. However, the role of BRF1 in CRC is limited with only one study showing that 17-beta-oestradiol induces BRF1 in COLO205 colon cancer cells^[80]. Nevertheless, *in silico* analyses of its mRNA level in CRC patients (Table 1) indicate a significant reduction of its expression similar to TTP, which may account for the deregulated expression pattern of various oncogenic transcripts. This downregulation may also reduce SG-P-body fusion in cancer cells, warranting further investigation.

HuR: A ubiquitously expressed RNA-binding protein encoded by the *ELAVL1* gene, which belongs to the “Embryonic-Lethal Abnormal Vision in *Drosophila*” (ELAV) family^[81]. HuR possess two tandem RRM, followed by a hinge region and a third RRM. The HuR nucleocytoplasmic shuttling domain within the hinge region is subjected to phosphorylation by various kinases, which regulate the nucleocytoplasmic shuttling of the protein^[82]. In the cytoplasm, HuR binds and stabilizes mRNA transcripts bearing an AU-rich sequences within their 3’UTR, by competing or displacing destabilizing factors (*e.g.*, microRNAs, TTP)^[26]. Moreover, HuR can directly bind and sequester miRNAs (*e.g.*, miR-16, miR-21), thereby preventing the downregulation of their mRNA targets^[83,84]. In stress conditions, HuR accumulates in SGs and promotes stabilization of various oncogenic transcripts^[85]. However, other studies have suggested that the formation of SGs is dispensable for mRNA stabilization^[86]. HuR is overexpressed in CRC as compared to normal tissues and exerts an oncogenic function by stabilizing the mRNAs of cancer and inflammatory-promoting factors involved in cancer cells proliferation, survival, and migration^[26]. Moreover, HuR expression is also increased in colonic epithelial cells from patients with inflammatory bowel disease^[87], thus adding another early event potentially fostering CRC development.

CUGBP2 (CUG-Binding Protein ELAV-like family member 2): CUGBP2 is a member of the CUGBP-ETR-3-like factors family that is ubiquitously expressed. This protein contains two N-terminal RRM and one C-terminal RRM. CUGBP2 is a SG-associated RNA-binding protein involved in stabilizing and impairing the translation of bound target mRNAs^[88]. Its expression is strongly reduced in various cancers and in CRC, CUGBP2 downregulation is mediated by Prostaglandin-E2 and its overexpression promotes apoptosis and mitotic catastrophe induced by radiation in colon cancer cells^[89]. Furthermore, CUGBP2 overexpression in HCT-116 cells triggers cell cycle arrest in G2/M and an induction of apoptosis due to a direct binding to the 3’UTR of Mcl-1 mRNA and an impairment of its translation^[90].

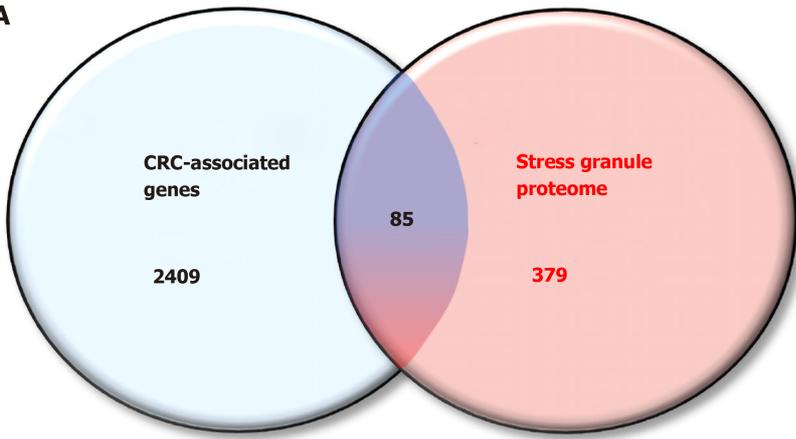
Musashi-1 (Msi-1): An RNA-binding protein, which promotes mRNA stability and translation inhibition^[91]. Msi-1 is overexpressed in a variety of cancers and contributes to the overexpression of oncogenes (*e.g.*, oncotachykinin 1 in breast cancer)^[92] or cancer-promoting factors^[91]. Msi-1 is also overexpressed in CRC and its knockdown severely impairs tumor growth *in vitro* and *in vivo*^[93,94]. Moreover, Msi-1 overexpression enhances the development of CD44 positive-colon cancer stem cells and promotes chemoresistance in cells treated with 5-FU, by enhancing SGs assembly^[54].

K-homology splicing regulator protein (KSRP): An RNA-binding protein involved in mRNA stability, splicing, transcription, as well as microRNA biogenesis^[95,96]. In CRC, KSRP acts as a tumor suppressor by promoting the mRNA decay of β -catenin and iNOS transcripts^[97,98]. In stress conditions (*e.g.*, oxidative stress), KSRP localizes in SG^[99,100]. However, it is unclear the role of KSRP in SGs and whether this event occurs in colorectal cancer cells.

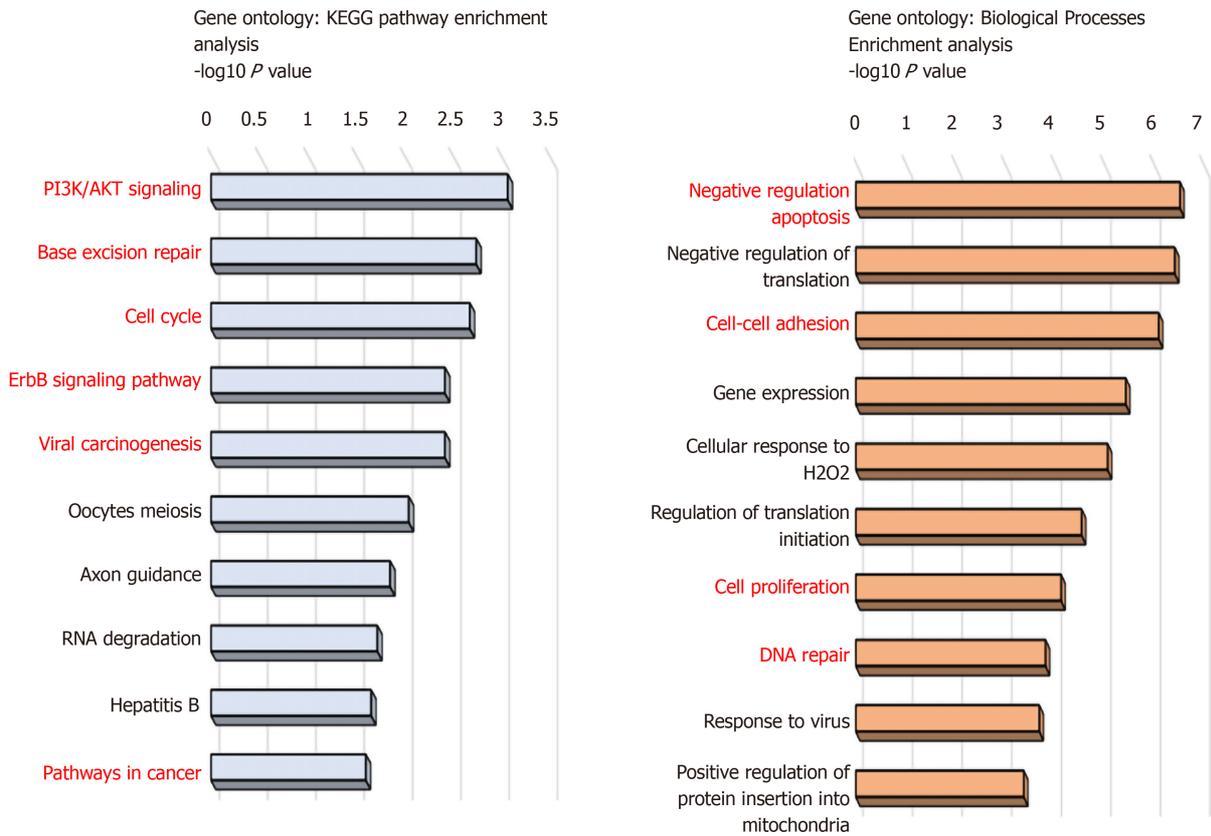
Other proteins involved in CRC development

Proteome-based analysis has revealed more than 400 different proteins to be associated with SGs, and cross comparison with CRC-associated genes reveals 89 proteins (Figure 1A). Based on gene ontology analyses these proteins are involved in biological processes (negative regulation of apoptosis, cell adhesion, DNA repair) and pathways (*e.g.*, PI3K, cell cycle) promoting colon carcinogenesis (Figure 1B and C). Moreover, gene set enrichment analysis indicates a significant enrichment of SG-associated genes in tumors as compared to non-tumor tissues (Figure 1B), with several oncogenes (*e.g.*, CDK1, SND1, HSPD1) upregulated in CRC. Together, these data suggest that the SGs proteome represents an important “reservoir” of cancer-related

A



B



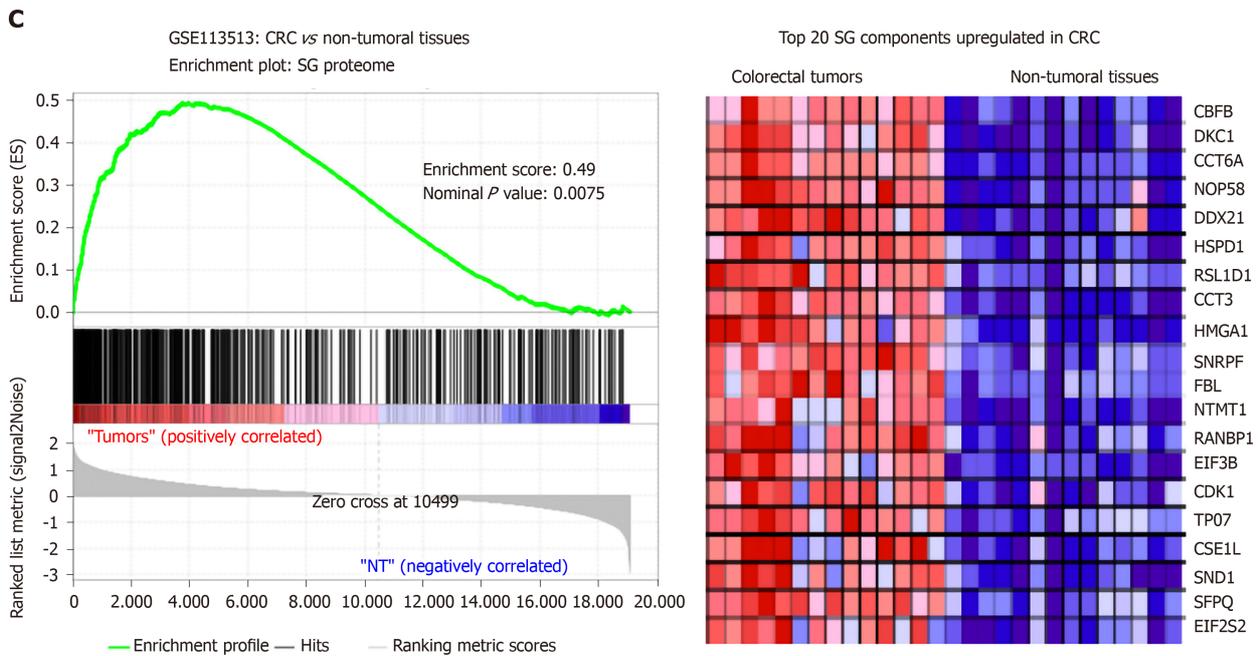


Figure 1 The stress granule proteome contains several colorectal cancer-associated proteins. A: Venn diagram merging a list of colorectal cancer (CRC)-associated genes (retrieved from Metacore software) and the mammalian stress granule (SG) proteome from <https://msgp.pt>; B: Gene ontology analysis of SG proteome using KEGG pathway and biological processes analysis. Enrichment is represented with a $-\log_{10} P$ value. Processes and pathways in red are those involved in cancer development; C: Gene-Set Enrichment Analysis (version 3.0, Broad Institute, Cambridge, MA, United States) of the SG proteome on CRC patients (GSE113513). The top 20 genes upregulated in CRC patients as compared to non-tumoral tissues are presented in a heatmap. The enrichment score was calculated using the number of genes ranking at the top or the bottom of the gene list (permutation type: Phenotype; with 1000 permutations). The Signal2Noise was used for ranking genes. A nominal P value < 0.05 and an FDR < 0.2 were considered significant.

factors, suggesting that the role of SGs in CRC is largely underestimated. Moreover, how various factors such as the genetic landscape (mutations), tumor etiology, lifestyle factors, and the gut microbiota influence the composition of the SGs proteome and tumor transcriptome is currently unknown. Therefore, it is likely that a different composition of SGs may differentially affect cancer-related processes based on intrinsic and external factors.

Several SG-associated proteins affect cancer hallmarks and pathways. For instance, under stress conditions the RBFOX2 (RBP fox-1 homolog 2) localizes in SGs and promotes cell cycle progression by decreasing RB1 protein expression in colon cancer cells^[101]. Accordingly, RBFOX2 was found strongly upregulated in colon tumors, while RB1 was downregulated as compared to normal tissues. The pro-apoptotic factor RACK1 (Receptor for Activated C Kinase), which binds to and activates the stress responsive MTK1 MAPKKK^[23], is sequestered into SGs in stress conditions and impairs its pro-apoptotic function. This effect has been also observed with chemotherapeutic agents such as 5-FU in HeLa cells, thus suggesting that RACK1 overexpression in CRC may also contribute to CRC chemoresistance^[102]. In CRC, RACK1 is overexpressed and acts as a tumor promoter correlated with clinical outcomes^[103]. Finally, PDCD4, another pro-apoptotic factor^[104] is also localized in SGs^[21] but it is currently unclear whether its sequestration in SGs impairs its pro-apoptotic function.

Post-translational modifications and SGs formation in CRC

Although several post-translational modifications of key proteins involved in SGs assembly have been identified, these alterations have yet to be studied in the CRC context. Nevertheless, it has been observed that the expression and activity of the proteins involved in modifying SGs factors can be altered in CRC.

Acetylation and deacetylation of SGs components: Acetylation of SG-associated proteins importantly regulate SGs assembly with several acetylases and deacetylases linked to this regulation. As previously discussed, acetylation of K376 of G3BP1 by the CBP/P300 acetylase is a key modification impeding SGs assembly by impairing its RNA binding function, as well as its interaction with PABP1, USP10 or Caprin1^[12]. However, this link in CRC is unclear considering that the expression of CBP/P300 is

upregulated in CRC^[105,106]. Conversely, the histone deacetylase HDAC6 directly interacts and deacetylates G3BP1 and promotes SGs formation^[12]. In agreement with these findings, SG disassembly is associated with increased acetylation of K376^[12] and inactivation of HDAC6 catalytic domain impairs SGs formation in 293T cells^[51]. The interaction of HDAC6 with G3BP1 is prevented by G3BP1 phosphorylation on Ser¹⁴⁹^[51]. Moreover, microtubules contribute to SG growth by supplying additional RNPs and other SG-associated proteins, are also subjected to acetylation modifications that markedly alter their dynamics. HDAC6 is also a microtubule-associated deacetylase^[107] and its activity reduces tubulin- α acetylation on Lys40 in NIH3T3 cells and increases cell motility^[107]. The activity of HDAC6 on microtubules and other motor proteins (*e.g.*, dyneins) promotes SGs formation^[51]. Taken together, these findings indicate that HDAC6 displays pleiotropic functions to promotes SGs assembly. While the role of HDAC6 in SGs assembly in CRC is currently unknown, its overexpression is observed in colorectal tumors compared to adjacent normal tissue and this may considerably favor SGs assembly^[51]. Moreover, HDAC6 inhibitors can sensitize CRC cells to oxaliplatin^[108].

SIRT6 is a NAD⁺-dependent deacetylase, which directly interacts with G3BP1. SIRT6 deficiency promotes G3BP1 phosphorylation at Ser¹⁴⁹ and reduces SGs assembly^[109]. Similar to HDAC6, the link between SIRT6 and SGs in CRC has not been established and discrepant observations have been reported regarding SIRT6 level in human CRC with studies reporting downregulation^[110,111] or overexpression^[112]. Nevertheless, SIRT6 overexpression correlates with a better prognosis in CRC patients and inhibits tumor progression^[113,111].

Casein Kinase-2 (CK2): Phosphorylation of G3BP1 on Ser¹⁴⁹ by CK2 impairs SGs formation in U2OS osteosarcoma cells^[13]. This link has not been explored in CRC and the role of CK2 in colon cancer is currently unclear, with studies reporting both oncogenic and tumor suppressive functions^[114,115]. CK2 expression and activity is increased in animal models of ulcerative colitis^[116], suggesting that its altered expression represents an early alteration, potentially involved in colorectal carcinogenesis. In colon cancer cells, CK2 overexpression sensitizes cells to 5-FU^[117,118] and promotes the degradation of several cancer-promoting transcripts by enhancing TTP function^[115]. In contrast, CK2 enhances colon cancer cell viability by promoting COX-2 expression and PGE2 production^[114].

Methylation of SG components: Protein Arginine Methyltransferase 1/5 (PRMT1/5) methylates several SGs components including G3BP1, G3BP2, FUS/LTS and UBAP2L. This methylation impairs the interaction of these SGs components (*e.g.*, UBAP2L/G3BP1) and inhibits SGs assembly^[65]. Paradoxically, various studies indicate an increase of SGs formation in colorectal cancer, PRMT1 and 5 are upregulated in tumors^[119] (Table 1), suggesting that colon cancer cells adapt to circumvent this negative regulatory mechanism. A potential mechanism involves the histone arginine demethylase JMJD6 (Jumonji domain-containing 6), which promotes SGs formation by demethylating G3BP1^[120]. In colon cancer JMJD6 is upregulated and exerts oncogenic functions (*e.g.*, negative regulation of p53 signaling)^[121]. Therefore, SG formation in colon cancer may depend on a fine-tuned equilibrium between PRMTs and JMJD6 activities.

AMPK/mTORC1 signaling: The role of AMPK and mTORC1 signaling in SGs formation is intriguing because in many models, SGs formation has been associated to a reduction of mTORC1 activity and/or activation of AMPK. However, in CRC mTORC1 activity is increased^[122] and the link between mTORC1 inhibition and SGs assembly is likely to be cell type and context dependent^[123]. In agreement with this, increased activity of mTORC1 by PI3K or p38 MAPK kinases has been associated to SGs formation in breast cancer cells^[16]. These pathways are commonly overactive in CRC^[124,125], and the downstream activation of mTORC1 may represent an important event triggering SGs assembly in colon cancer cells. The complexity mTORC1 signaling is further enhanced by AMPK α , which is a negative upstream regulator of mTORC1 signaling, in promoting SGs assembly^[17] and is frequently upregulated in CRC^[126,127]. Besides its regulatory function on SGs assembly, mTORC1 is also localized to SGs in stress conditions, thus impairing protein synthesis^[128]. Once the stress signals dissipate, DYRK3 (Dual Specificity Tyrosine Phosphorylation Regulated Kinase 3) promotes the re-localization of mTORC1 to the cytosol to facilitate protein synthesis^[128]. However, this regulatory mechanism remains to be demonstrated in the context of CRC.

SGs clearance in CRC

In addition of overexpression of nucleating proteins, alteration of SGs clearance contribute also to increased SGs in cancer cells. In this section, we discuss the various mechanisms involved in SGs dissolution and deregulated in colon cancer cells.

HspB8-HSP70-Bag3 complex: Several chaperones proteins are required for SGs clearance. In particular, the HspB8-HSP70 complex and co-chaperone protein Bag3 is involved in the “quality control” of SGs composition by preventing accumulation of misfolded ubiquitinated proteins in SGs^[129]. Through an interaction with p62, an autophagy receptor accumulating in SGs^[130], the complex targets misfolded proteins for degradation by autophagy^[131]. Although they are currently no studies pertaining to HSPB8 in CRC, HSP70 and Bag3 are frequently overexpressed in CRC and contribute to cancer progression^[132,133]. Although the HspB8-HSP70-Bag3 complex favors the maintenance of a normal SGs proteome function^[129], this complex can also promote SGs disassembly in cases where stress persists. While this function remains to be better defined, some studies suggest that SGs clearance is mediated by autophagy^[129].

Autophagy-dependent SGs clearance: Autophagy plays an important role in SGs clearance (also called “granulophagy”)^[134]. Interestingly, autophagy and SGs are concomitantly increased in cancer cells^[134] and have been recognized as important survival mechanisms in cancer cells, thus suggesting that these two processes act in concert to favor cancer cells survival. The role of autophagy in CRC development has been well characterized and like for many cancers, autophagic flux is strongly increased in CRC^[135]. However, the link between autophagy and SGs clearance in CRC is currently unknown.

Valosin-containing protein (VCP/p97): An ATPase, which belongs to the AAA family (ATPases-associated with diverse cellular activities)^[136]. Together with several cofactors, VCP interacts with ubiquitinated proteins and promotes their extraction from protein complexes for degradation^[136]. This function is required during SGs disassembly^[137]. In addition, VCP is essential for autophagosome maturation^[138]. Accordingly, in several diseases (*e.g.*, Inclusion body myopathy, Paget Disease), VCP mutations leads to a reduction of autophagy and an accumulation of SGs. VCP is also subjected to post-translational modifications, in particular phosphorylation by Unc-51-like kinases 1 and 2 (ULK1 and 2), which activates Vcp/p97 and causes SGs disassembly^[137]. In CRC, ULK1 is overexpressed, while ULK2 is downregulated in tumors and the respective impact of these alterations on SG dynamics is unknown.

P-Bodies: Similar to SGs, P-bodies are also non-membrane RNA-protein complexes and their assembly is triggered by various stimuli including stress or inflammation^[73]. In contrast to SGs, P-Bodies are mostly involved in mRNA decay and do not contain any translation initiation and elongation factors, but contain enzymes required for deadenylation (CAF-1, CCR4), decapping (DCP1/2), 5' to 3' degradation (XRN1) of mRNA transcripts^[139,140]. mRNA degradation by P-bodies importantly contributes to SGs dissolution and disruption of P-body formation is likely to foster SGs accumulation^[77]. Our full current understanding of the crosstalk between SGs and P-bodies is limited but appears to be a determinant of the fate of cancer-related transcripts. Some proteins like tristetraprolin (TTP) or BRF1, are localized in both compartments and can mediate the shuttling of mRNAs and promotes SG-P-body fusion^[73,141]. Thus, the loss of TTP and BRF1 expression and activity in colon cancer cells may considerably alter SGs clearance. Moreover, the loss of TTP expression has been associated with a reduction of P-bodies in CRC cells^[66,77].

SGS AS POTENTIAL BIOMARKERS AND THERAPEUTIC TARGETS

SGs as potential biomarkers

SGs importantly contribute to cancer cell survival to harmful conditions and represent an important barrier to chemotherapy. Assessing the expression of SGs nucleators in CRC biopsies may therefore represent a predictive approach to evaluate patient response to chemotherapy. However, the expression levels of several SGs components as well as their links with the clinical outcome are limited or unclear. Only one study has suggested that the presence of TIA-1 in tumor infiltrating lymphocytes represents a favorable survival predictive marker in colorectal cancer patients^[142]. The use of public available database combining transcriptomic and survival analyses of CRC patients (GEPIA database: <http://gepia.cancer-pku.cn/>) can be useful to correlate the

expression level of SGs components with clinical outcomes (Table 1). However, these correlations only consider respective mRNA levels in the analyses and these alterations do not necessarily translate at the protein level. As shown in Table 1, several discrepant findings between published observations and the transcriptomic data (*e.g.*, USP10, PRMT1) can be observed. These discrepancies may also originate from heterogeneity between the patients and clinical samples evaluated. Finally, assessing the expression of individual SGs components may be insufficient considering that these proteins act in concert to promote SGs assembly. While using bioinformatic approaches to identify potential novel SG-based correlations are a notable starting point, validation efforts are still required to conclude the relevance of SGs as potential biomarkers for CRC.

SGs as therapeutic target

Inhibiting SGs formation may re-sensitize cancers cells to physiological death stimuli and anti-cancer agents (chemotherapy), as evidenced in various pre-clinical models^[143]. Several strategies impairing SG assembly or SG-oncogenic activities have been developed and tested in various cancer cell types, which are discussed in the following section (Table 2).

Reducing the expression of SGs nucleators: As previously discussed, the inhibition or silencing of several proteins can efficiently prevent SGs assembly in cancer cells (*e.g.*, G3BP1, UBAP2L). Therefore, developing therapeutic strategies to limit these SGs components specifically in cancer cells may represent a novel approach to reducing tumor growth and to re-sensitizing cells to chemotherapy. Although there are currently no studies assessing the therapeutic potential of inhibiting SGs in CRC, one approach using delivery of specific siRNAs (*e.g.*, Aptamers) as a means to reduce expression of specific oncogenic targets has shown anti-tumor efficacy in CRC^[144]. Such approaches could be also applied for microRNA delivery as a means to control the expression of SGs nucleators. Moreover, various small molecules have been shown to reduce the expression of SGs components in CRC cells, such as resveratrol or EGCG (Epigallocatechin-Gallate) for G3BP1^[145,146]. Similarly, the peptide GAP161 can efficiently reduce G3BP1 activity and may represent a valuable tool to prevent SGs formation. This peptide markedly inhibits colon cancer cell proliferation by inducing apoptosis and sensitizing cells to cisplatin-induced apoptosis^[143]. Furthermore, GAP161 reduces tumor growth *in vivo*, as evidenced in xenograft models. However, these antitumoral properties have been associated to an impairment of its interaction with RasGAP, so it is unclear whether SGs assembly is prevented in this model.

Targeting G4DNA/RNA structures: The importance of G4DNA/RNA structures in SGs assembly suggest them as novel therapeutic targets in various cancers. In agreement, the G-quadruplex ligand RHPS4 (3,11-difluoro-6,8,13-trimethyl-8Hquino) displays anti-tumor properties. However, this molecule also induces side effects such as cardiovascular alterations, suggesting caution regarding its clinical use. EMICORON, another G-quadruplex ligand displays also anti-tumor properties^[147]. In colon cancer, EMICORON markedly reduces cancer progression^[147] and potentiates chemotherapy in colon cancer cell lines^[147].

A number of angiogenin inhibitors have been also developed and may reduce tiRNA accumulation in cancer cells. Among them, chANG, an antiangiogenin peptide, has been studied in colon cancer and shows antiangiogenic activity^[148]. Moreover, a neutralizing monoclonal antibody to angiogenin prevents HT-29 colon cancer tumor progression in a xenograft model^[149].

Targeting the AMPK/mTORC1 axis: SGs assembly is frequently associated to mTORC1 inhibition. Therefore, restoring normal mTORC1 activity has the potential to inhibit SGs assembly. However, increased activity of mTORC1 by PI3K or p38/MAPK kinases has been associated with SGs formation in MCF-7 breast cancer cells^[150] and use of mTORC1 inhibitors may represent a potential therapeutic approach. Targeting upstream regulators of mTORC1, such as AMPK, which is a potent inhibitor of mTORC1 may also potentially impair SGs formation in cancer cells. The AMPK inhibitor Compound-C, efficiently prevents SGs assembly induced by a cold shock in yeast^[151] and displays anti-cancer properties in colon cancer cells^[152].

Targeting microtubules: The integrity of microtubules and motor proteins is required for RNP transport during SGs formation. Accordingly, microtubule destabilizing agents such as vinblastine or nocodazole can prevent SGs assembly, while drugs stabilizing them (*e.g.*, paclitaxel) promote SGs formation^[153]. However, vinblastine is currently not used clinically for CRC treatment due to its gastrointestinal toxicity^[154].

Table 2 Potential therapeutic approaches to impair stress granule function in cancer cells

Strategies	Target	Models	Known impact on SGs	Anticancer effect on CRC	Clinical trials for CRC (ID)
Targeting proteins involved in SG assembly					
EGCG	G3BP1	Lung cancer ^[146]	Reduction of SG assembly	Yes ^[181]	NCT02891538; NCT02321969; NCT01239095
Resveratrol	G3BP1	CRC ^[145]	Unknown	Yes ^[145]	NCT00433576; NCT00920803
GAP161 peptide	G3BP1	CRC ^[43]	Unknown	Yes ^[43]	None
RK-33	DDX3	CRC ^[182]	Unknown	Yes ^[182]	None
Targeting G4DNA/RNA structures					
EMICORON	G4DNA	CRC ^[147]	Unknown	Yes ^[147]	None
chANG	angiogenin	CRC ^[148]	Unknown	Yes ^[148]	None
(mAb), 26-2F	angiogenin	CRC ^[149]	Unknown	Yes ^[149]	None
Targeting AMPK/mTORC1 axis					
Compound C	AMPK	Yeast ^[151] CRC ^[152]	Impairs SG assembly in yeast ^[151]	Yes ^[152]	None
Rapamycin	mTORC1	CRC ^[183]	Unknown	Yes ^[183]	NCT00409994; NCT03439462
Everolimus	mTORC1	Breast ^[16]	SG inhibition	Yes ^[184]	NCT01154335; NCT00419159; NCT01387880
Temsirolimus	mTORC1	CRC ^[185]	Unknown	Yes ^[185]	NCT00593060; NCT00827684; NCT01183663
Targeting HDACS/SIRT6					
OSS_128167	SIRT6	Pancreas cancer ^[161]	Unknown	Unknown	No
A-452	HDAC6	CRC ^[158]	Unknown	Yes ^[158]	None
C1A	HDAC6	CRC ^[157]	Unknown	Yes ^[157]	None
ACY-1215	HDAC6	CRC ^[108]	Unknown	Yes ^[108]	None
MPT0G612	HDAC6	CRC ^[159]	Unknown	Yes ^[159]	None
Targeting SGs-associated RNA-binding proteins controlling cancer-related factors					
MS-444	HuR	CRC ^[166]	Unknown	Yes ^[166]	None
DHTS	HuR	CRC ^[186]	Unknown	Yes ^[186]	None
Resveratrol	RBFOX2	CRC ^[101]	Unknown	Yes ^[101]	NCT00433576; NCT00920803
Targeting microtubules					
Paclitaxel	Microtubules	Green monkey kidney fibroblasts (CV-1 cells) ^[153]	Promotes SG formation	Yes ^[187]	NCT00598247; NCT00024401; NCT00667641
Vinblastine	Microtubules	Green monkey kidney fibroblasts (CV-1 cells) ^[153]	Prevents SG assembly	Yes ^[188]	None

Several approaches can be used to efficiently reduce stress granule assembly and their oncogenic activities. This table provides some examples for each strategy. Some of them have been tested in colorectal cancers models and others have reached clinical trials (<https://clinicaltrials.gov/>). SG: Stress granule; CRC: Colorectal cancer.

Identifying new microtubule destabilizing agents with less side effects may potentially provide beneficial outcome to CRC patients. Several microtubule destabilizing agents have been developed and are currently used for the treatment of other cancers, such as eribulin for breast cancer^[155,156].

HDAC and SIRT inhibitors: HDAC6 and SIRT6 activity promote SGs formation in cancer cells^[51,109]. Several HDAC6 inhibitors have been developed such as A452, C1A, ACY-1215, MPT0G612, and have been shown to reduce CRC tumor growth and sensitize to cells to chemotherapeutic agents^[108,157-159]. Targeting SIRT6 with specific inhibitors may also represent a potential approach to impair SGs assembly. However,

only few SIRT6 inhibitors have been developed (*e.g.*, OSS_128167)^[160-162] and their effects on SGs assembly and CRC is currently unknown.

Targeting autophagy: The clearance of SGs is mediated by autophagy^[163] and increasing autophagic flux in cancer cells may potentially lower the amount of SGs and re-sensitize cancer cells to chemotherapy. Alternatively, autophagy has been considered as an important survival mechanism of CRC cells and several molecules impairing autophagy have been implicated as novel therapeutics^[135]. However, it remains to determine whether autophagy impairment can lead to an impairment of SGs clearance, which may potentially favor cancer cell survival and tumor recurrence.

Targeting SGs-associated RNA-binding proteins controlling cancer-related factors: Several RBPs are localized in SGs and control the translation/stability of various cancer-related transcripts (*i.e.*, oncogenes, tumor suppressors). Targeting these proteins may represent an appealing approach to reduce the oncogenic properties of SGs in CRC. In that sense, several strategies aiming at inhibiting HuR expression and activity have been proposed^[164]. Among them, the HuR inhibitor MS-444, a polyketides purified from microbial extracts, represents an interesting candidate due to its potent anti-cancerous properties in various cancers (*e.g.*, colorectal cancer, pancreatic cancer, malignant glioma)^[165,166]. MS-444 prevents HuR cytoplasmic export by inhibiting its homodimerization, thereby reducing the stability of its mRNA targets. Moreover, the anti-tumor properties of MS-444 was further observed in a mouse model of Familial Adenomatous Polyposis (*i.e.*, APC^{Min} mice)^[87], thus showing the effectiveness of this molecule *in vivo*.

Finally, molecules preventing the sequestration of pro-apoptotic factors within SGs may also represent a potential approach to reduce cancer cell survival. For instance, resveratrol can prevent RBFOX2 localization in stress granules, thus inhibiting cancer cell proliferation^[101].

CONCLUSION

Due to the aging population and increased incidence of chronic bowel diseases, coupled with less than optimal lifestyle habits, an increased incidence in CRC cases is expected in the near future^[167]. Further investigation into the molecular mechanisms associated with colon carcinogenesis is therefore needed in order to identify new targets for novel therapeutic approaches. Increasing evidence indicate that SGs are key players involved in CRC tumorigenesis and chemoresistance. Based on current findings, the assembly of SGs and their role in CRC development relies on multiple changes in the factors involved in SG nucleation and clearance (Figure 2). Early alterations of SGs components in preneoplastic conditions (*e.g.*, IBD) may also allow altered cells to survive and accumulate further defects contributing to tumorigenesis. Moreover, the link between other chronic diseases such as diabetes and obesity, which are important risk factors for CRC development, represent new areas where SGs assembly needs to be clarified. Other potential contributing factors, such as gut microbiota dysbiosis should also be considered as a potential driver of SGs formation in cancer cells. Beside the proteins discussed in this review, several other SG components have been identified and have been recognized as regulators of SGs assembly in other cancer types, such as FMRP, ATX-2, the RNA helicase DDX3X^[168], TDP-43^[169], DYRK3^[128], PDCD4^[21] or FUS^[170], and continued work will determine the function of these proteins in CRC. Other proteins, which are associated with SGs are also important regulators of cancerous processes (*e.g.*, cell cycle progression, cancer cell migration and invasion). Although the role of these factors in SG biology is currently unclear, their storage in these granules may represent an important “reservoir”, favoring cancer cell survival in stress-related conditions. As CRC remains one of the deadliest cancers worldwide, employing strategies aimed at impairing SG assembly may re-sensitize cancer cells to chemotherapy and improve clinical outcomes. Such approaches may provide beneficial effects to CRC patients, along with other cancers where clinical options are limited and only a few therapeutic options exist. In this review, we discussed several strategies that could be employed to reduce SG formation in cancer cells. However, the efficiency of such approaches in colorectal cancer and SG assembly needs to be firmly established. Moreover, the potential side effects that could be associated with these strategies (*e.g.*, the G-quadruplex ligand RHPS4 which induces cardiovascular side effects) need to be carefully evaluated using *in vivo* models. Moreover, the role of some regulators of SGs formation in CRC is still

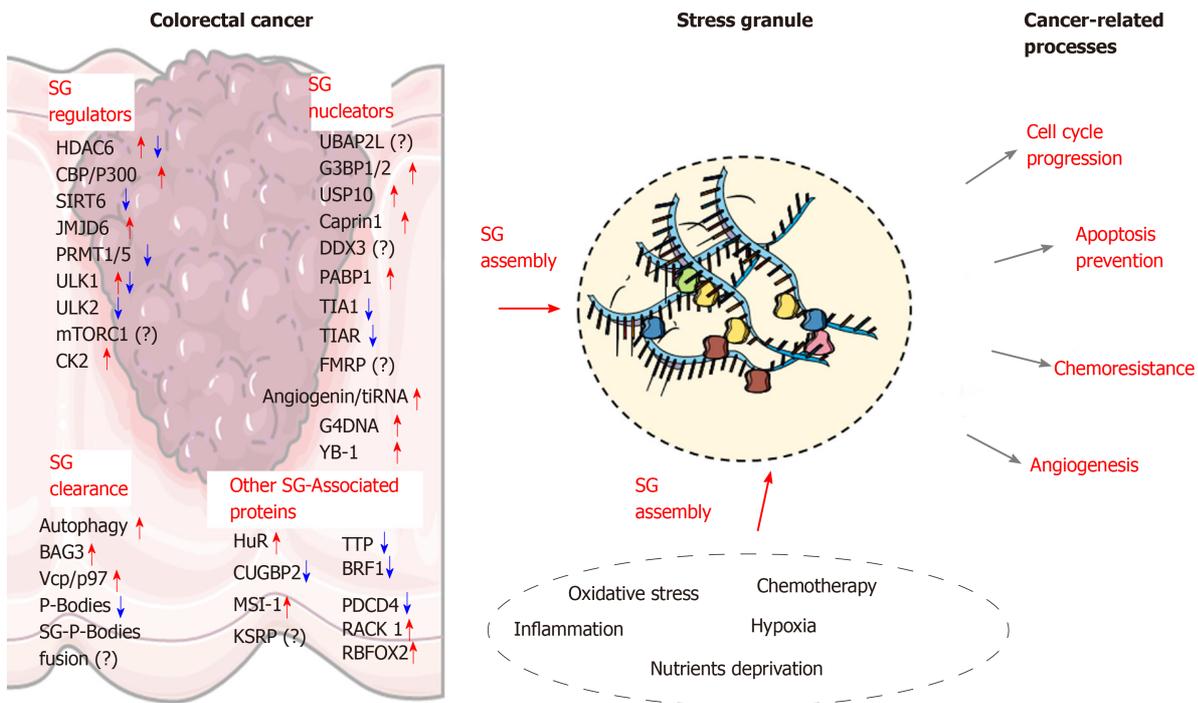


Figure 2 The molecular landscape underlying stress granules formation in colorectal cancer. Stress granules (SGs) assembly in colorectal cancer cells is associated with several alterations in the expression of proteins involved in SG nucleation or clearance. The stress-related conditions within the tumor microenvironment and various antitumor agents can further promote SGs assembly. Several SG-associated proteins (RNA-binding proteins or others) contribute to various cancer-related processes such as cell cycle progression, apoptosis inhibition, angiogenesis, and chemoresistance. Illustrations were retrieved from Servier Medical art (<https://smart.servier.com/>). SG: Stress granules.

unclear (*e.g.*, mTORC1, AMPK) and thus a better understanding of their function in SG formation in CRC is required prior to any therapeutic interventions.

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Is artificial intelligence the final answer to missed polyps in colonoscopy?

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Abstract

Lesions missed by colonoscopy are one of the main reasons for post-colonoscopy colorectal cancer, which is usually associated with a worse prognosis. Because the adenoma miss rate could be as high as 26%, it has been noted that endoscopists with higher adenoma detection rates are usually associated with lower adenoma miss rates. Artificial intelligence (AI), particularly the deep learning model, is a promising innovation in colonoscopy. Recent studies have shown that AI is not only accurate in colorectal polyp detection but can also reduce the miss rate. Nevertheless, the application of AI in real-time detection has been hindered by heterogeneity of the AI models and study design as well as a lack of long-term outcomes. Herein, we discussed the principle of various AI models and systematically reviewed the current data on the use of AI on colorectal polyp detection and miss rates. The limitations and future prospects of AI on colorectal polyp detection are also discussed.

Key Words: Artificial intelligence; Adenoma; Colonoscopy; Colorectal cancer; Polyps

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Core Tip: This review highlights the results of recent studies on the use of artificial intelligence for the detection of colorectal polyps and its role in reducing missed lesions during colonoscopy.

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INTRODUCTION

Colorectal cancer (CRC) is the third most common cancer worldwide. In 2015, there were 1.7 million new cases, resulting in more than 800000 deaths worldwide^[1]. Screening colonoscopy and polypectomy have been shown to be effective in reducing the incidence of colorectal cancer as well as the associated cancer mortalities^[2,3]. However, colonoscopy is not risk proof, and CRC can still develop within a short interval after a negative colonoscopy for cancer. In particular, post-colonoscopy colorectal cancer (PCCRC) is the preferred term used to define cancers appearing after a colonoscopy in which no cancer is diagnosed. Specifically, PCCRC can be further subdivided into “interval cancer,” where cancer is identified before the next recommended screening or surveillance examination. PCCRC, or interval cancer, could account for up to 9% of all colorectal cancers and is usually associated with an adverse outcome^[4]. Recent studies showed that missed polyps and adenoma by colonoscopy accounted for at least 50% of all PCCRCs^[5-7]. Therefore, ways to minimize missed lesions during colonoscopy are of utmost importance to maintain the quality and effectiveness of colonoscopy in preventing CRC.

STRATEGY TO MINIMIZE MISSED POLYPS

It was shown in a recent meta-analysis that up to 26% of colonoscopies could have missed adenomas^[8]. While many factors could affect the adenoma miss rate (AMR), the endoscopist factor was recognized to be one of the main determinants of AMR. High adenoma detection rate (ADR), high adenomas per index colonoscopy and high adenomas per positive index colonoscopy of the endoscopist were all shown to be negatively associated with AMR^[8]. In particular, higher adenomas per positive index colonoscopy was independently associated with a lower advanced adenoma miss rate, which was an important predictor for PCCRC. Intuitively, ways to improve the ADR could also help to minimize AMR^[9].

While “to err is human,” the mitigation of human factors, such as distraction, fatigue, impaired level of alertness, visual perception and recognition errors, may be the key to improving adenoma detection and hence reducing miss rates^[10-14]. Additionally, patient factors, mainly poor bowel preparation, were also associated with lower ADR^[15] and higher AMR^[8]. However, there was minimal difference between fair- and good-quality bowel preparation in ADR and AMR^[8], implying that at least fair bowel preparation should be achieved. Adequate withdrawal time, a minimum of 6 min, is another important quality measure to optimize ADR and AMR^[16-18]. Another factor that would improve the ADR and reduce the AMR was the use of auxiliary techniques. There are a large number of auxiliary techniques, including second-pass colonoscopy^[19], retroflexion in right-sided colon^[20], water-aided colonoscopy^[21], team detection approach (endoscopist and experienced nurse)^[13,22], wide-angle endoscopy^[23], high-definition endoscopy with or without a special imaging technique^[24-26] and add-on devices^[27], that have been reported to increase the ADR.

ARTIFICIAL INTELLIGENCE SYSTEMS USED IN THE DETECTION OF COLORECTAL POLYPS

Artificial intelligence (AI) has been applied in the medical field since the early 1950s. AI is defined as any machine that has cognitive functions mimicking humans, *e.g.*, problem solving or learning^[28]. The machine learning model, which is a subtype of AI, is characterized by a set of methods that can automatically detect patterns in data and then use the uncovered patterns to predict outcomes^[29]. Conventional AI systems utilize a supervised type of machine learning model that extracts the covariates of training data to achieve pattern recognition or classification. It is important to note that each piece of information included in the representation of the patient is known as a covariate, and the traditional type of machine learning, *e.g.*, logistic regression, only examines the relationships of “predefined covariates” with the outcome^[30]. Nevertheless, the machine learning model cannot change the way in which covariates are defined. The deep learning model actually solves this problem by defining covariates and builds up complex concepts from simple covariates, which is particularly useful in image classification and object location because features of a group of similar subjects can be complex and difficult to be defined by humans^[30].

(Figure 1).

In recent years, the deep learning model was increasingly used in the detection and localization of colorectal polyps. Once training data were provided with proper labels, the deep learning model could automatically extract the important features in the training data for differentiation and classification. Without the need of human intervention or indication, the internal parameters of each “neuron” in a single layer would be tuned towards a model with the least degree of error^[31]. The most common architecture used in the deep learning model of early colonoscopy studies was convolutional neural networks, which mimics the structure of the human brain and contains multiple layers with “artificial neurons” under each layer. The convoluted layers actually act as a filter for extraction of the important features from the original image or data. The pooling layers can downsize the parameters of the layers to streamline the underlying computation. Finally, with the fully connected layers, these features are combined together to create a model to classify different outputs^[32,33].

ROLE OF AI IN THE DETECTION OF COLORECTAL POLYPS DURING COLONOSCOPY

Our meta-analysis of recently published AI studies on colorectal polyp detection suggested that a well-designed AI system could achieve more than 90% accuracy^[34-36]. Compared to a traditional machine learning based algorithm, studies using the deep learning model were found to have high accuracy (up to 91%) with a pooled sensitivity of 94% and a specificity of 92% on the detection of colorectal polyps^[36].

As yet, most of the previously published studies have been retrospective in nature, and there have been limited high-quality prospective real-time studies on the use of AI in actual patients until recently. The first randomized controlled trial was reported in 2019 by Wang *et al*^[37]. They showed that the use of real-time automatic polyp detection system (CADe) based on a deep learning architecture can increase the ADR in patients with a low prevalence of adenoma (20%-30%). Among the 1130 patients randomized, the ADR of the CADe group was significantly higher than that of the conventional colonoscopy group (0.29 *vs* 0.20, $P < 0.001$). The mean numbers of polyp and adenoma detected in the CADe group also increased from 0.50 to 0.95 ($P < 0.001$) and from 0.31 to 0.53 ($P < 0.001$), respectively, when compared with conventional colonoscopy.

Five recently published randomized controlled trials (RCTs) in 2020 again confirmed that AI-assisted colonoscopy significantly increased the adenoma detection rate when compared to conventional colonoscopy. Wang *et al*^[38] further reported another RCT to compare a CADe system with a sham system. Again, the CADe system had a significantly higher ADR than the sham system (34% *vs* 28%, $P = 0.03$). In the same trial, adenoma or sessile serrated adenoma missed by endoscopists were characterized by isochromatic color, flat shape and located at the edge of the visual field or even partly behind colonic folds. Another randomized controlled trial by Repici *et al*^[39] involving three centers in Italy also found that the CADe system was associated with a higher ADR with an odds ratio (OR) of 1.30 (95%CI: 1.14-1.45). Subgroup analysis showed that the performance of the CADe system was not affected by the size, shape and location of the polyps.

In addition to polyp location systems, Gong *et al*^[40] reported a CADe system that aimed to monitor real-time withdrawal speed and to minimize blind spots during withdrawal. Their study showed that the ADR also improved from 8% to 16% ($P = 0.001$) with the CADe system. Similarly, Su *et al*^[41] reported an automatic quality control system on colorectal polyp and adenoma detection that would also remind the endoscopist of the withdrawal time and speed and the need to re-examine unclear colonic segments on top of a polyp localization system. The system was found to have a significantly higher ADR than conventional colonoscopy (28.9% *vs* 16.5%, $P < 0.001$).

In view of these newly available RCTs after the publication of our meta-analysis^[36], we have summarized the results of the latest prospective RCTs here in a new meta-analysis. In this meta-analysis of six RCTs, the pooled OR for the improvement of ADR was 1.91 (95%CI: 1.51-2.41) under a random effects model with a heterogeneity of $I^2 = 63\%$ (Figure 2). Hence, there is convincing data from RCTs to show that the existing AI models could already help to boost the ADR by 90%.

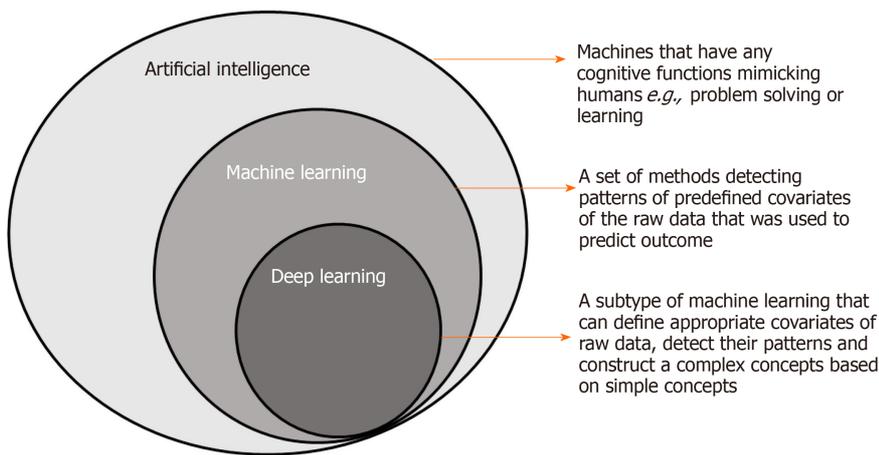


Figure 1 Diagrammatic presentation of artificial intelligence, machine learning and deep learning.

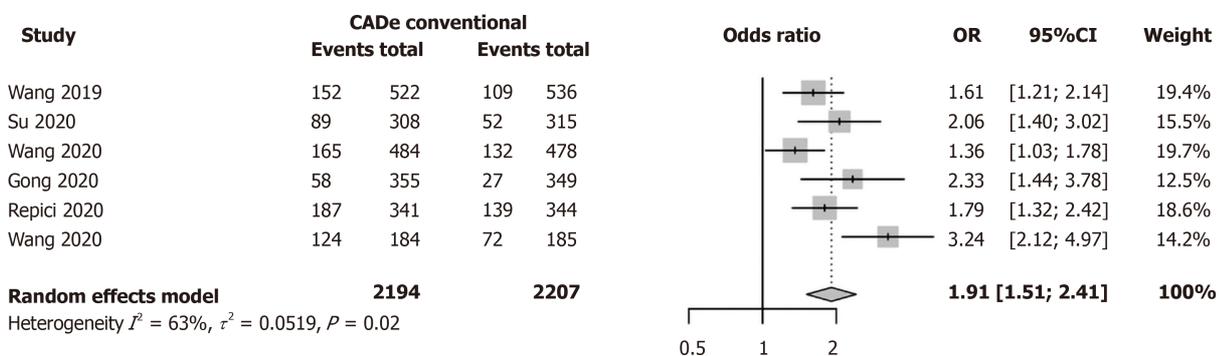


Figure 2 Pooled analysis for improvement of adenoma detection rate of all the randomized controlled trials. Events: number of patients with adenoma detected. CADe: Real-time automatic polyp detection system; CI: Confidence interval; OR: Odds ratio.

ROLE OF AI IN MISSED POLYPS

In addition to its role in enhanced colorectal polyp detection, there are emerging data to suggest that AI could also help to reduce missed lesions during colonoscopy. In our recent study^[42], we showed that the validated real-time deep learning AI model could help endoscopists to prevent missed colorectal lesions. We first applied the validated AI system to review 65 videos of tandem examinations of the proximal colon (from cecum to splenic flexure) and found that the AI system could detect up to 79.1% of adenomas that were missed by the endoscopist during the first-pass examination. In the second part of the prospective study, the same deep learning AI model was able to detect missed adenomas in 26.9% of patients during real-time examination. In multivariable analysis, missed adenomas were associated with findings of multiple polyps during colonoscopy (adjusted OR, 1.05) or colonoscopy performed by less-experienced endoscopists (adjusted OR, 1.30).

A recent single-center RCT by Wang *et al*^[43] also showed that the use of CADe-assisted colonoscopy can reduce AMR from 40.0% to 14.0%. In particular, there were significant improvements in the ascending, transverse and descending colon. However, the AMR in this RCT (up to 40%) was much higher than previously reported. Therefore, a multicenter trial would still be required to validate this finding.

STATE OF THE ART: ROLE OF AI IN MISSED COLORECTAL POLYPS

While supporting the role of AI in reducing missed lesions, these results suggested that the main reason for missed adenoma could still be due to human factors, as nearly 80% of these missed lesions were actually shown on screen and were not picked up by endoscopists for various reasons, such as inexperience, fatigue or distraction. Therefore, the AI could serve as an additional "eye" for the endoscopist with which

distraction and fatigue would never occur.

However, our study also showed that approximately 20% of missed adenomas were still not detected even by AI. These missed lesions were usually not shown “on screen.” They were located behind a fold or at a difficult flexure position or hidden under the fecal contents in patients with poor bowel preparation. In a recent meta-analysis by Zhao *et al*^[8] including 43 studies and 15000 tandem colonoscopies, the use of auxiliary techniques and good bowel preparation were associated with fewer missed adenomas. Intuitively, the combination of AI and auxiliary devices in the presence of satisfactory bowel preparation may be necessary to completely eliminate the risk of missed colonic lesions during colonoscopy.

USE OF AI IN THE CHARACTERIZATION OF POLYPS

In addition to detection of colorectal polyps, AI has also been shown to be accurate in histology prediction and polyp characterization in a number of studies^[36]. Although there was a high degree of heterogeneity in the algorithms and design, along with potential selection biases, studies using a deep learning model as a backbone generally performed better than those using other types of algorithms. A study by Byrne *et al*^[44] showed that the use of a deep learning model can achieve a 94% accuracy in the real-time classification of polyps. A similar result was reproduced by a study^[45] using magnifying colonoscopy, and both studies used narrow-band imaging as the imaging technique. Our recent meta-analysis further showed that the pooled accuracy from studies using narrow-band imaging was generally better than that of non-narrow-band imaging studies in histology characterization^[36].

LIMITATIONS AND FUTURE DIRECTIONS

Although there have been promising prospective trials supporting the use of AI in real-time polyp detection during colonoscopy, there are a number of issues to be addressed before AI can be implemented in routine clinical practice. Because the algorithms of AI and deep learning models are still evolving and there is substantial heterogeneity among different models and training data^[36], an independent prospective validation would be required for each AI system. The latest guideline issued by the European Society of Gastrointestinal Endoscopy suggested that the possible incorporation of computer-aided diagnosis (detection and characterization of lesions) into colonoscopy should be supported by an acceptable and reproducible accuracy for colorectal neoplasia, as demonstrated in high-quality multicenter clinical studies^[14]. Another important question regarding the use of AI in colonoscopy is the actual impact on long-term clinical outcomes. It is still unknown whether the use of AI-assisted colonoscopy can decrease the PCCRC rate or lengthen the current recommended surveillance interval after colonoscopy, which would require long-term prospective cohort studies to address.

The current role of AI in colonoscopy is possibly to act as a virtual assistant to the endoscopist during real-time colonoscopy, particularly in withdrawal time monitoring and polyp detection. The prospect of a fully automated independent colonoscopy system is still too premature at this stage. Moreover, the “black box” nature of the AI algorithm, especially the deep learning model, may require considerable effort to convince the regulatory authority to approve for its routine use. The liability and indemnity issues related to the manufacturers of the AI system also need to be resolved. Hence, there are still considerable obstacles to overcome before the application of AI-assisted colonoscopy becomes widespread in daily practice.

CONCLUSION

An externally validated AI system could be one of the promising solutions to increase adenoma detection and to minimize missed lesions during real-time colonoscopy. As of yet, means to ensure adequate mucosal exposure, such as add-on devices and optimal bowel preparation, are also critical in reducing the polyp miss rate in daily colonoscopy practice. Long-term data are also needed to determine the actual clinical benefits of this emerging technology in the reduction of PCCRC.

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Artificial intelligence-assisted esophageal cancer management: Now and future

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Abstract

Esophageal cancer poses diagnostic, therapeutic and economic burdens in high-risk regions. Artificial intelligence (AI) has been developed for diagnosis and outcome prediction using various features, including clinicopathologic, radiologic, and genetic variables, which can achieve inspiring results. One of the most recent tasks of AI is to use state-of-the-art deep learning technique to detect both early esophageal squamous cell carcinoma and esophageal adenocarcinoma in Barrett's esophagus. In this review, we aim to provide a comprehensive overview of the ways in which AI may help physicians diagnose advanced cancer and make clinical decisions based on predicted outcomes, and combine the endoscopic images to detect precancerous lesions or early cancer. Pertinent studies conducted in recent two years have surged in numbers, with large datasets and external validation from multi-centers, and have partly achieved intriguing results of expert's performance of AI in real time. Improved pre-trained computer-aided diagnosis algorithms in the future studies with larger training and external validation datasets, aiming at real-time video processing, are imperative to produce a diagnostic efficacy similar to or even superior to experienced endoscopists. Meanwhile, supervised randomized controlled trials in real clinical practice are highly essential for a solid conclusion, which meets patient-centered satisfaction. Notably, ethical and legal issues regarding the black-box nature of computer algorithms should be addressed, for both clinicians and regulators.

Key Words: Artificial intelligence; Computer-aided diagnosis; Deep learning; Esophageal squamous cell cancer; Barrett's esophagus; Endoscopy

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Core Tip: Deep-learning-based artificial intelligence (AI) is a breakthrough technology that has been widely explored in diagnosis, treatment and prediction of esophageal cancer. Recent studies have dealt with limitations of previous researches, including small sample size, selection bias, lack of external validation and algorithm efficiency. Favorable outcomes that are comparable to experienced endoscopists have been achieved with satisfactory robustness, indicating a real-time potential. Future randomized controlled trials are needed to further address these issues concerning AI to provide an ultimate patient-centered satisfaction, in an interpretable, ethical and legal manner.

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INTRODUCTION

Esophageal cancer (EC) is one of the top ten leading prevalent malignancies worldwide, ranking the seventh in incidence and the sixth in mortality in 2018^[1]. The major histological types are squamous cell carcinoma (SCC), which is predominant worldwide, and adenocarcinoma (AC) which is more prevalent in Caucasian people^[2-4]. Data collected from 12 countries have indicated that AC will possibly experience a dramatic increase in incidence up to 2030, while the incidence of SCC will continuously decrease^[5]. It is estimated that EC causes absolute years of life lost reduction of 7.8 (95%CI: 2.3-12.7)^[6]. Although EC is not the most common cause of admission or readmission to hospital^[7], it certainly imposes economic burdens. A cohort study conducted in the United Kingdom showed that the mean net costs of care per 30 patient-days of AC were \$1016, \$669, and \$8678 for the initial phase, continuing care phase and terminal phase, respectively^[8]. The cost grows with an increase of tumor node metastasis (TNM) staging at first diagnosis^[8].

Apparently, EC is a serious health threat, imposing economic burden on both high-income and low-income countries. Therefore, early diagnosis and evidence-based expert opinions on selecting the optimal treatment modality are crucial for reducing such burden. Although various diagnostic methodologies [including endoscopic ultrasonography (EUS), chromoendoscopy, optical coherence tomography (OCT), high-resolution microendoscopy (HRM), confocal laser endomicroscopy (CLE), volumetric laser endomicroscopy (VLE), and positron emission tomography (PET)], serous and genetic predictors have been developed to improve diagnostic accuracy and predict outcomes, inter-observer variabilities in interpreting images and heavy workloads limit their clinical efficiency^[9-11]. A practical tool that can improve accuracy and reduce workload is in urgent need for clinical practice.

Artificial intelligence (AI), which mimics human mind's cognitive behavior, has been an emerging hot spot globally in various disciplines. Numerous models have been attempted for machine learning (ML), and the terminologies can be referred in the previous studies^[12,13]. ML models are trained by datasets to extract and transform features, thereby achieving the goal of classification and prediction by self-learning^[13-15]. In gastroenterology, AI-based technologies, which are characterized by deep learning (DL) as state-of-the-art machine learning algorithms, have been mainly developed to identify dysplasia in Barrett's esophagus (BE), SCC, gastric cancers, and *Helicobacter pylori* in upper gastrointestinal (UGI) tract^[16], and to diagnose polyps, inflammatory bowel diseases, celiac disease, and gastrointestinal (GI) bleeding in lower GI tract^[17]. Various models have been developed and studied to detect anatomical structure, discriminate dysplasia, and predict therapeutic and survival outcomes of EC. The ultimate goal of AI is to assist physicians and patients to make a superior data-based diagnosis or decision. In the following sections, we will (1) provide an overview of AI applications in diagnosis and prediction of advanced cancer; (2) specify computer-aided diagnosis (CAD) for early detection of esophageal SCC (ESCC) and esophageal adenocarcinoma (EAC) based on optical imaging; and (3) outline limitations of the existing studies and future perspectives. We searched PubMed database using terms "esophageal cancer" and "artificial intelligence" for papers published up to March 1, 2020, and initially obtained 172 studies. After exclusion of 128 items, 44 research articles that provided detailed data were included

in the review and discussion (Figure 1).

IMPLICATIONS FOR DIAGNOSIS AND THERAPEUTIC DECISIONS

EC is highly malignant, and the 5-year survival rate of late-stage EC is less than 25%^[18]. Radical therapies, including surgery, chemotherapy, radiotherapy or their combination are highly essential to improve survival outcome. Accurate diagnosis, precise staging, optimal modality selection, as well as responsiveness and survival outcome prediction are necessary in making true clinical decisions. However, these decisions are made mainly based on the current guidelines and expertise in clinical practice. AI technologies have been therefore developed to enhance the reliability of those decisions in an individualized manner.

Diagnosis

One of the important roles of AI is to detect malignant lesions. In 1996, Liu *et al*^[19] proposed a tree-based algorithm called PREDICTOR, to classify patients with dyspeptic symptoms into EC, which achieved a discriminating accuracy of 61.3%, with sensitivity (SEN) and specificity (SPE) of 94.9% and 39.8%, respectively. In 2002, a probabilistic network-based decision-support system was developed, which could correctly predict the cancer stage of 85% of tested data in reasonable time^[20]. In the same year, a robust classifier, artificial neural network (ANN), imitating neural network of the human brain, was adopted to distinguish BE from EC^[21]. The ANN was trained using 160 genes selected by significance analysis of microarrays (SAM) from cDNA microarray data of esophageal lesions. This ANN outperformed cluster analysis by correctly diagnosing all the tested samples. Kan *et al*^[22] also combined ANN with SAM-extracted 60 gene clones to accurately predict lymph node metastasis in 86% of all SCC cases, with SEN and SPE of 88% and 82%, respectively, better than clustering or predictive scoring. Kan *et al*^[22] suggested that AI was a potential tool to detect lymph node metastasis when the SEN of coherence tomography (CT), EUS, and PET is insufficient^[23,24]. Since tumor risk factors have complex nonlinear correlations, a fuzzy neural network, trained on hybridization of chaotic optimization algorithm and error back propagation (EBP), was able to correctly diagnose 87.36% of ESCC and 70.53% of dysplasia^[25]. This fuzzy-logic based model outperformed traditional statistics, such as multivariate logistic regression model that was previously described by Etemadi *et al*^[26].

While symptoms are not quite reliable and gene analysis or PET scans are expensive, a simpler noninvasive detection method may be more practical. Li *et al*^[27] combined support vector machine (SVM), a traditional classifier, with surface-enhanced Raman spectroscopy in order to distinguish serum spectra of EC patients from healthy controls. Eventually, a combination of SVM with principle component analysis (PCA) on the basis of radial basis function (RBF), namely RBF PCA-SVM algorithm, exhibited the greatest efficacy among others with accuracy, SEN, and SPE of 85.2%, 83.3% and 86.7%, respectively.

Outcome prediction

Another significant role of AI is to predict prognosis of EC based on various demographic, clinicopathologic, hematologic, radiologic, and genetic variables. Surgery and neoadjuvant chemotherapy, radiotherapy or chemoradiotherapy are important definitive modalities for advanced EC. Selecting the optimal strategy with superior predictive outcome is of vital importance.

Traditionally, TNM staging system is used as a predictor. However, a previous study showed that it was not very accurate^[28]. Hence, multiple computational algorithms were developed to assist more reliable predictions. In 2005, Sato *et al*^[29] trained an ANN to predict survival outcome. They found that the best predictive accuracy was obtained, with 65 clinicopathologic, genetic and biologic variables for 1-year survival and 60 variables for 5-year survival. The area under ROC curve (AUC), SEN, and SPE were 0.883, 78.1%, 84.7% and 0.884, 80.7%, 86.5%, respectively. Similar results with high SEN and SPE could be achieved in another ANN model to predict the 1- and 3-year post-operative survival of EC and esophagogastric junction cancer^[30]. These two ANNs both outperformed TNM staging system^[29,30].

In addition to ANN, other models were also proposed to solve certain problems. A prognostic scoring system, using serum C-reactive protein and albumin concentrations, was fused with expertise by fuzzy logic^[31]. The proposed model could perform 1-year survival prediction with an AUC of 0.773. Another hierarchical

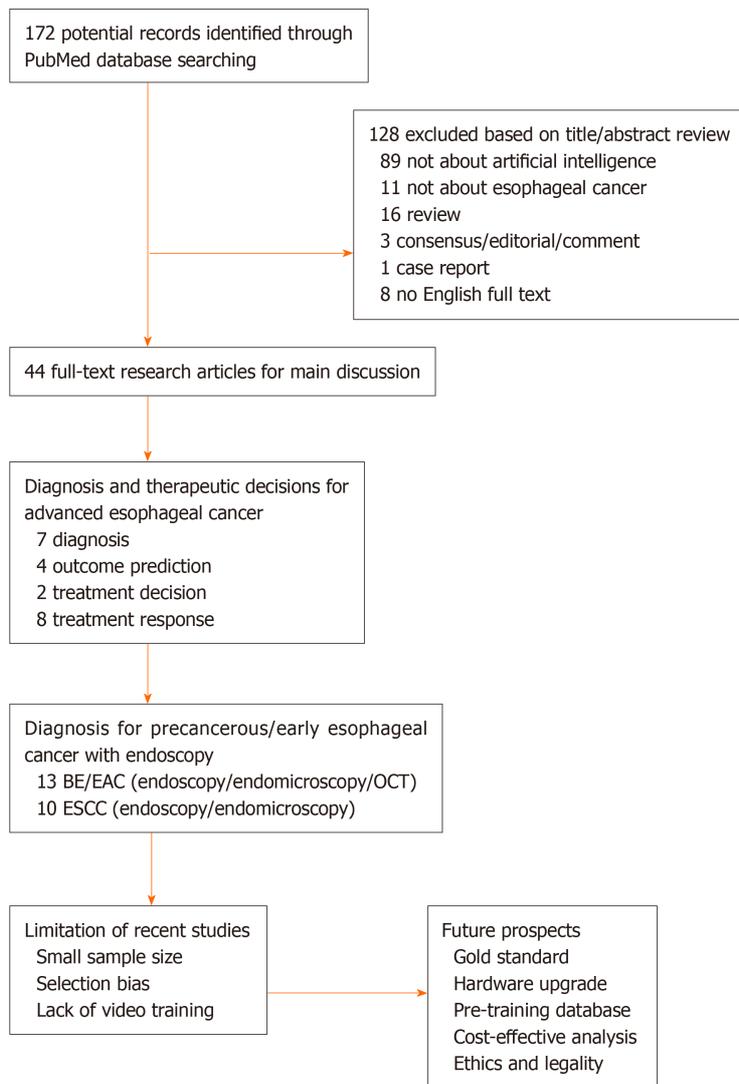


Figure 1 Flow chart of study selection and logic arrangement of review. BE: Barrett's esophagus; EAC: Esophageal adenocarcinoma; OCT: Optical coherence tomography; ESCC: Esophageal squamous cell carcinoma.

forward selection (HFS), a wrapper feature selection method, was developed to solve the problem of small sample size^[32]. In this SVM-validated model, clinical and PET features were learned to predict disease-free survival. The results unveiled that HFS achieved the highest accuracy of 94%, with robustness of 96%. Robustness could be further increased to 98%, if HFS was incorporated prior knowledge (pHFS).

Treatment decision

Based on the condition and prognosis of patient, an individualized treatment strategy is needed. For instance, when chemotherapy is prescribed for a patient, what is the optimal medication with appropriate dosage and period? Generally, clinicians make decisions according to their own experience, guidelines or consensus. However, those recommendations are often fixed and human errors are sometimes inevitable. A group of Iranian experts attempted to train a multilayer neural network with particle swarm optimization and EBP algorithms, in order to determine the dosage of chemotherapy^[33]. Encouraging results showed that accuracy of particle swarm optimization and EBP was both 77.3%. Zahedi *et al.*^[33] were positive about its future application as a supplementary decision-making system.

While the majority of decisions are made before treatment, is it possible to make real-time treatment decisions? The answer is YES. Maktabi *et al.*^[34] tested a relatively new hyperspectral imaging system. They found that SVM was able to detect cancerous tissue with 63% SEN and 69% SPE within 1s. It is promising that hyperspectral imaging may assist surgeons in identifying tumor borders intra-operatively in real

time.

Treatment response

A good treatment response is crucial for consequential therapeutic decision and predicting outcome^[35]. Endeavors have been made to select candidate factors that correlate with responsiveness to treatment. However, it is often extremely laborious to testify these numerous variables in clinical trials. AI technologies are potential powerful tools for this selection.

One indicator is the genetic biomarker. In 2010, Warnecke-Eberz *et al*^[36] reported their usage of ANN to predict histopathologic responsiveness of treatment-naïve patients to neoadjuvant chemoradiotherapy by analyzing 17 genes using the TaqMan low-density arrays. Their results were promising, with 85.4% accuracy, 80% SEN, and 90.5% SPE. Radiology is another important indicator to assess tumor regression after treatment. One rationale for this exploration is that tumor heterogeneity exists within radiologic images^[37]. The standardized uptake values of ¹⁸F-fluorodeoxyglucose in PET imaging were reported to have predictive potential^[38]. However, this predictive power is limited^[39] due to some confounding factors, such as intra-observer variations. Ypsilantis *et al*^[40] adopted a three-slice convolutional neural network that could extract features from pre-treatment PET scans automatically to predict response to chemotherapy. It achieved a moderate accuracy of 73.4%, with SEN and SPE of 80.7% and 81.6%, respectively, which outperformed other ML algorithms trained on handcrafted PET scan features. Recently, CT radiomics three months after chemoradiotherapy were combined with dosimetric features of gross tumor volume and organs at risk to identify non-responders. Jin *et al*^[41] found that these combinative features trained by the model of extreme gradient boosting plus PCA achieved an accuracy of 70.8%, with AUC of 0.541.

While tumor regression is an important indicator to assess responsiveness, post-treatment distant metastasis is also vital to evaluate responsiveness, which is correlated with survival outcome. In order to predict post-operative distant metastasis of ESCC, further SVM models incorporated with clinicopathological and immunohistological variables were established^[42]. Finally, the SVM model with four clinicopathological features and nine immunomarkers had better performance, with accuracy, SEN, SPE, positive predictive value, and negative predictive value of 78.7%, 56.6%, 97.7%, 95.6%, and 72.3%, respectively. Another least squares SVM model was also proposed to predict post-operative lymph node metastasis in patients who received chemotherapy preoperatively, by exploiting preoperative CT radiomics^[43]. Tumor length, thickness, CT value, long axis and short axis size of the largest regional lymph node were analyzed. The model reached an AUC of 0.887.

In addition to its diagnostic and predictive value, AI has learned to identify meaningful alterations in molecular and genetic level. In 2017, Lin *et al*^[44] compared the serum chemical elements concentrations between ESCC patient and healthy controls, and found that nearly half of the elements were different between the two groups. They then trained several classifiers to perform the discrimination, with Random Forest being the best (98.38% accuracy) and SVM the second (96.56% accuracy). Later, Mourikis *et al*^[45] developed a robust sysSVM algorithm to identify 952 genes that promoted EAC development, using 34 biological features of known cancer genes. They called these rare and highly individualized genes "helper" genes, which function alongside known drivers.

AI may be a feasible option to help determine an optimal treatment strategy. This was previously evidenced by a study of 13 365 EACs from 33 cancer centers worldwide, which incorporated random forest algorithm, and found that the predicted survival of AI-generated therapy was superior to actual human decisions^[46]. However, most of the above-mentioned ML algorithms described were developed for the sake of advanced cancer. Diagnosing EC in an early stage contributes to a far better outcome when treatment is undertaken appropriately. This is highly dependent on the development of optical imaging technologies that can directly visualize the morphology of esophageal lesions.

MORPHOLOGY-BASED CAD

In recent decades, endoscopic optical imaging techniques have been rapidly advanced, which provide endoscopists a fine inspection of the morphology of esophageal mucosa, micro-vessels, and even cells. In lieu of white light imaging (WLI) and magnifying endoscopy (ME), emerging OCT, CLE, VLE, and HRM techniques have

been developed to diagnose BE^[47-49]. Meanwhile, the diagnosis of SCC more relies on chromoendoscopy and intra-epithelial papillary capillary loop (IPCL) observed under narrow band imaging (NBI) plus ME^[50]. Although these modalities have yielded preferable diagnostic value, the interpretation of these images need expert's experience (inter- and intra-observer variability^[51]), and processing large dataset is laborious and time consuming. Researchers in medicine and information engineering have collaborated to develop different AI models for this purpose.

BE versus dysplasia or EAC

The current screening and surveillance recommendation for BE is endoscopic examination plus random biopsy^[52], which is limited by sampling error. AI models trained with various endoscopic modalities and pathologies aimed to overcome these shortcomings (Table 1).

Endoscopy: In 2009, German experts developed a content-based image retrieval framework^[53]. In this frame, novel color-texture features were combined with an interactive feedback loop. The algorithm could correctly recognize 95% of normal mucosa and 70% of BE from 390 training images, with a moderate inter-rater reliability of 0.71. The authors thought that the CAD system might be incorporated to the endoscopic system to help lesser experienced clinicians. In 2013, van der Sommen *et al*^[54] tried an SVM algorithm, which could automatically identify and locate irregularities of esophagus on high-definition endoscopy with an accuracy of 95.9% and AUC of 0.99, taking a first step towards CAD. Later, these authors used a CAD system to automatically recognize region of interest (ROI) in dysplastic BE^[55]. The SVM-based classification yielded a SEN and SPE of 83% for per-image level, and 86% and 87%, for the patient level, respectively. However, the *f*-score of the system, which indicates the similarity with the gold standard, was lower than experts.

In order to improve the outcome, Horie *et al*^[56] were the first who adopted a deep CNN (Single Shot MultiBox Detector, SSD) model to detect EC from WLI and NBI images in 2018. Only 8 EACs were used in that study. The diagnostic accuracy for EAC was 90%, and SEN for WLI and NBI at patient level was both equal to 88%. The system processed one image in only 0.02 s, which is promising for a real-time job. This ability of SSD to detect EAC was assessed in another study, which outperformed their proposed regional-based CNN (R-CNN), Fast R-CNN and Faster R-CNN in both precision and speed, which achieved F-measure, SEN, and SPE of 0.94, 96% and 92%, respectively^[57]. The authors stated that SSD worked faster due to its single forward pass network nature. CNN was then validated in a more recent study to detect early dysplastic BE^[58]. The system was pretrained on ImageNet, and was then trained with 1853 images and tested with 458 images. The CNN accurately detected 95.4% of the dysplasia, with 96.4% SEN and 94.2% SPE. One highlight for this study is that it studied WLI and NBI images, as well as images with standard focus and near focus. Another highlight is its ability to deal with real-time videos.

Except for the above-mentioned CNNs, another CNN built upon residual net (ResNet) was introduced. Ebigbo *et al*^[59] tested this system in two databases, Augsburg and Medical Image Computing and Computer-Assisted Intervention, with SEN both being over 90%. Later, de Groof *et al*^[60] used a custom-made hybrid ResNet/U-Net which was pretrained on GastroNet to distinguish non-dysplastic BE from dysplasia. The system was trained using state-of-the-art ML techniques (transfer learning and ensemble learning) and validated in a sequential five datasets, with accuracy of 89% and 88% for two external validation datasets, which were slightly superior to the model pre-trained with ImageNet in its supplementary ablation experiment.

Endomicroscopy: In 2017, Hong *et al*^[61] reported their experience in adopting CNN as a classifier to distinguish intestinal metaplasia (IM), gastric metaplasia (GM) and neoplasia (NPL) of BE using endomicroscopic images. The total accuracy was 80.77%. It performed well for IM and NPL. However, it could not identify GM in the tested samples. VLE is an advanced imaging technique that can provide a 3-mm deep scan of the esophagus in full circumference, which is commercially available (Nvision VLE™ Imaging System). In the same year, Swager *et al*^[62] reported the first attempt of using CAD to detect NPL by adopting histology-correlated *ex-vivo* VLE. The authors used eight separate ML algorithms that were trained with clinically inspired features. They found that "layering and signal decay statistics" feature performed the best, with AUC, SEN, and SPE of 0.95, 90%, and 93%, respectively. Similar results were obtained by van der Sommen *et al*^[63], with a maximum AUC of 0.93 in identifying early EAC in BE. Notably, the authors discovered that scanning depth of 0.5-1 mm was the most appropriate range for classifying tissue categories.

Table 1 Computer-aided endoscopic diagnosis for dysplastic Barrett's esophagus

Ref.	Year	Study design	Lesions	Diagnostic method	AI technology	Dataset capacity	Validation	Outcomes	Compared to expert	Processing speed
Münzenmayer <i>et al</i> ^[53]	2009	Retrospective	BE	WLI	Color-texture analysis in a CBIR framework	390 images with 482 ROIs	LOO (N-fold cross-validation)	Accuracy: BE/CC/EP 70%/74%/95%	NA	NA
van der Sommen <i>et al</i> ^[55]	2016	Retrospective	HGD, early EAC	WLI	SVM	100 images	LOO	Per-image SEN/SPE: 83%/83%; Per-patient SEN/SPE: 86%/87%	Inferior	NA
Horie <i>et al</i> ^[56]	2019	Retrospective	EAC	WLI; NBI	CNN-SSD	8 patients	Caffe DL framework	Accuracy: 90%; Per-image SEN: WLI/NBI: 69%/71%; Per-case SEN: WLI/NBI: 88%/88%	NA	0.02 s/image
Ghatwary <i>et al</i> ^[57]	2019	Retrospective	EAC	WLI	VGG'16-based; R-CNN; Fast R-CNN; Faster R-CNN; SSD	100 images (train 50, test 50)	5-fold cross-validation and LOO	F-measure: 0.94 (SSD); SEN/SPE: 96%/92% (SSD)	NA	0.1-0.2 s/image
Hashimoto <i>et al</i> ^[58]	2020	Retrospective	HGD, early EAC	WLI and NBI with both standard and near focus	CNN	1835 images	NA	Per-image accuracy: 95.4%; Per-image SEN/SPE: 96.4%/94.2%; 98.6%/88.8% (WLI); 92.4%/99.2% (NBI)	NA	GPU gtx 1070: 0.014 s/frame; YOLO v2: 0.022 s/frame
Ebigbo <i>et al</i> ^[59]	2019	Retrospective	Early EAC	WLI; NBI	CNN-ResNet	248 images	LOO	SEN/SPE of Augsburg database: 97%/88% (WLI); 94%/80% (NBI); SEN/SPE of MICCAI database: 92%/100%	Superior	NA
de Groof <i>et al</i> ^[60]	2019	Retrospective	Early dysplastic BE	WLI	ResNet-UNet hybrid	1704 images (train 1544, validation 160)	4-fold cross-validation (external validation)	Accuracy/SEN/SPE: 89%/90%/88% (dataset 4); 88%/93%/83% (dataset 5)	NA (superior to non-expert)	Classification: 0.111 s/image; Segmentation: 0.124 s/image
Swager <i>et al</i> ^[62]	2017	Retrospective	HGD, early EAC	VLE	SVM, DA, Adaboost, RF, kNN, NB, LR, LogReg	60 images	LOO	AUC: 0.95; SEN/SPE: 90%/93%	Superior	NA
van der Sommen <i>et al</i> ^[63]	2018	Retrospective	HGD, early EAC	VLE	SVM, RF; AdaBoost; CNN, kNN; DA, LogReg	60 frames	LOO	AUC: 0.90-0.93	Superior	24 ms/full dataset for clinically-inspired features
Struyvenberg <i>et al</i> ^[65]	2020	Prospective	HGD, early EAC	VLE	PCA-CAD	3060 frames	NA	AUC of Multi-frame: 0.91; AUC of Single-frame: 0.83	NA	0.001 s/frame; 1.5s/full VLE scan
van der Putten <i>et al</i> ^[66]	2020	Prospective	HGD, early EAC	VLE	Multi-step PDE-CNN on an A-line basis	In-vivo: 140 images (train 111, test 29)	4-fold cross-validation	AUC: 0.93; F1 score: 87.4%	NA	50000 A-lines/s
Shin <i>et al</i> ^[67]	2016	Retrospective	HGD, EAC	HRM	Two-class LDA-based automated sequential classification algorithm	230 sites (train 77, validation 153)	NA	Accuracy: 84.9%; SEN/SPE: 88%/85%	NA	52 s/image

Qi <i>et al</i> ^[68]	2006	Retrospective	Dysplastic BE	OCT	PCA	106 images	LOO	Accuracy: 83%; SEN/SPE: 82%/74%	NA	NA
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AdaBoost: Adaptive boost; AUC: Area under ROC curve; BE: Barrett's esophagus; CAD: Computer-aided diagnosis; CBIR: Content-based image retrieval; CC: Mucosa of cardia; CNN: Convolutional neural network; DA: Discriminant analysis; EAC: Esophageal adenocarcinoma; EP: Epithelium; HGD: High-grade dysplasia; HRM: High-resolution microendoscopy; Knn: K-nearest neighbor; LDA: Linear discriminant analysis; LogReg: Logistic regression; LOO: Leave-one-out cross-validation; LR: Linear regression; NA: Not available; NB: Naïve bayes; NBI: Narrow band imaging; OCT: Optical coherence tomography; PCA: Principle component analysis; PDE: Principle dimension encoding; R-CNN: Regional-based CNN; RF: Random forest; SEN: Sensitivity; SPE: Specificity; SSD: Single shot multibox detector; SVM: Support vector machine; VLE: Volumetric laser endomicroscopy; WLI: White light imaging.

Since VLE produces an overwhelming number of images in a short time, a real-time CAD system is more helpful in actual clinical practice. In 2019, Trindade *et al*^[64] reported a video case illustrating an intelligent real-time image segmentation system which employed three established features to dynamically enhance abnormal VLE images with color in endoscopic procedure. They are now undergoing a multicenter RCT (NCT03814824) to further validate this CAD system. While most studies use single frame to include ROI, a recent study tried to add neighboring VLE images to pathology-correlated ROI^[65]. Hopefully, the so-called multi-frame analysis combing PCA improved the performance of single-frame analysis, from an AUC of 0.83 to 0.91. Meanwhile, the novel CAD system needs only 1.3 ms to automatically differentiate non-dysplastic BE from dysplasia in one image, and this is also a promising result for a real-time setting.

While previous studies employed *ex-vivo* scan images, the following study conducted by van der Putten *et al*^[66] used *in-vivo* histology-correlated images. In addition, they used principle dimension encoding (PDE) to encode images into score vector. They combined this PDE with traditional ML algorithms, *e.g.*, random forest and SVM, to classify the degree of dysplasia (high-grade dysplasia *vs* early EAC). They obtained an AUC of 0.93 and F1 score of 87.4%, which outperformed some traditional DL classifiers, such as Squeezenet and Inception.

Another kind of endomicroscopic technique is HRM. Shin *et al*^[67] designed an automated imaging processing algorithm extracting epithelium morphology and BE glandular architecture features, and a classification algorithm, which distinguished NPL from dysplasia in BE with an accuracy, SEN and SPE of 84.9%, 88%, and 85% in validation dataset, respectively. This quantitative CAD is cost-effective and may be applied in clinical settings after improvement of image acquisition quality and processing speed.

OCT: OCT is also a noninvasive imaging technique that can detect BE, dysplasia and early EAC, in compensation to routine endoscopy. In 2006, Qi *et al*^[68] attempted to extract image features using center-symmetric auto-correlation method and a PCA-based CAD algorithm was used for classification. A total of 106 pathology-paired images were included for training, which ended up with an accuracy of 83%, SEN of 82% and SPE of 74% to distinguish non-dysplastic BE from dysplasia. In general, the accuracy of OCT in identifying dysplasia is not satisfactory, which limits its

application^[69].

In addition to endoscopic images, pathologic morphology has also been studied. Sabo *et al*^[70] employed an ANN-validated computerized nuclear morphometry (pseudostratification, pleomorphism, chromatin texture, symmetry and orientation) model to discriminate the degree of dysplasia in BE. The model was able to differentiate non-dysplastic BE from low-grade dysplasia with an accuracy of 89%, and low-grade dysplasia from high-grade dysplasia with an accuracy of 86%.

ESCC

ESCC is the dominant histological type of esophageal cancer worldwide. Diagnosing early cancer mainly depends on endoscopic screening, which also produces a large number of images that needs special training to interpret. AI technologies have also been explored globally to address this issue (Table 2).

Endoscopy: In 2016, Liu *et al*^[71] designed an algorithm called joint diagonalization principle component analysis, which correctly detected 90.75% of EC with an AUC of 0.9471. To improve the performance of CAD system, Horie *et al*^[56] did the first attempt to use DL to diagnose ESCC with a large number of endoscopic images. The CNN had a diagnostic accuracy of 99% for ESCC, 99% for superficial cancer, and 92% for advanced one. The SEN of CNN was 97% for per-patient level and 77% for per-image level. Later in 2019, Cai *et al*^[72] proposed a novel CAD system called deep neural network (DNN). They used only standard WLI images to train the model. The DNN-CAD model could detect 91.4% of early ESCC, higher than senior endoscopists. By using this model, the average diagnostic performance of endoscopists improved satisfactorily, in terms of accuracy, SEN, and SPE. However, these studies excluded magnified images.

Later, Ohmori *et al*^[73] evaluated both ME and non-ME images [including WLI and NBI/blue laser imaging (BLI)] using a CNN based on SSD to recognize SCC. The accuracy for ME, non-ME + WLI, and non-ME + NBI/BLI was 77%, 81%, and 77%, respectively, all with high SEN and moderate SPE. The result was similar to experienced endoscopists tested in this study. Zhao *et al*^[74] conducted another study and evaluated ME + NBI images by employing a double-labeling fully convolutional network. This system used ROI-label and segmentation-label to delineate IPCLs based on the AB classification by the Japan Esophageal Society^[75]. The study showed that senior observers had significant higher diagnostic accuracy than mid-level and junior ones. The model reached a diagnostic accuracy of 89.2% and 93% in lesion and pixel level, respectively, for distinguishing type A, B1 and B2 IPCLs, which was similar to that of senior group. Specifically, the model had a higher sensitivity for type A IPCL than clinicians (71.5% *vs* 28.2%-64.9%), which might avoid unnecessary radical treatment. Instead of identifying IPCL patterns, the study conducted by Nakagawa *et al*^[76] aimed to predict invasion depths. The authors developed two separate SSD-based CNNs for ME and non-ME images. The ability of the system to correctly distinguish EP/submucosal (SM) 1 cancers from SM2/SM3 cancers was 91%, 92.9%, and 89.7% for the ME+ non-ME, non-ME and ME images, respectively. Regrading M and SM cancers, the differentiating accuracy was 89.7%, 90.3%, and 92.3% for the total, non-ME, and ME, respectively. The performance of this CAD model was also comparable to experts, but much faster.

A processing speed over 30 images/s is necessary for dynamic video analysis^[56]. Although Horie *et al*^[56], Ohmori *et al*^[73] and Nakagawa *et al*^[76] reported that their systems could process one image in 0.02, 0.027, and 0.033 s, respectively, they have not tested the systems in real-time videos. After Cai *et al*^[72] had validated the efficacy of their DNN-CAD model, they split the video into images and then assembled them, enabling the model to delineate early cancer in real time. Everson *et al*^[77] validated another CNN investigating IPCLs using sequential still images in real time of 0.026 to 0.037 s per image. The CNN could differentiate type A from type B IPCLs with a mean accuracy of 93.3%. Last year, Luo *et al*^[78] reported a multicenter, comparative study, exploiting 1 036 496 endoscopic images to construct a gastrointestinal artificial intelligence diagnostic system (GRAIDS) based on the concept of DeepLab's V3+. The GRAIDS yielded a diagnostic accuracy of UGI cancer ranging from 91.5% to 97.7% for internal, external, and prospective validation datasets, with favorable sensitivities, which were similar to experts and superior to non-experts. They also incorporated the CAD model to endoscopic videos in real time, with the highest speed of 0.008 s per image and latency less than 0.04 s. However, they did not report their outcome in distinct histology. Recently, Guo *et al*^[79] specially developed a CNN-CAD system built on SegNet architecture, aiming at real-time application in clinical settings. In this

Table 2 Computer-aided endoscopic diagnosis for early esophageal squamous cell cancer

Ref.	Year	Study design	Lesions	Diagnostic method	AI technology	Dataset capacity	Validation	Outcomes	Compared to expert	Processing speed
Liu <i>et al</i> ^[71]	2016	Retrospective	Early ESCC	WLI	JDPCA + CCV	400 images	10-fold cross-validation	Accuracy: 90.75%; AUC: 0.9471; SEN/SPE: 93.33%/89.2%	NA	NA
Horie <i>et al</i> ^[56]	2019	Retrospective	ESCC	WLI; NBI	CNN-SSD	41 pts (train 8428 images; test 1118 images without histology distinction)	Caffe DL framework	Accuracy: 99%; Per-image SEN: 72%/86% (WLI/NBI, respectively); Per-case SEN: 79%/89% (WLI/NBI, respectively)	NA	0.02 s/image
Cai <i>et al</i> ^[72]	2019	Retrospective	Early ESCC	WLI	DNN	2615 images (train 2428, test 187)	NA	Accuracy: 91.4%; SEN/SPE: 97.8%/85.4%	Superior	NA
Zhao <i>et al</i> ^[74]	2019	Retrospective	Early ESCC	ME + NBI	Double labeling FNN	1350 images with 1383 lesions	3-fold cross-validation	Accuracy/SEN/SPE at lesion level: 89.2%/87%/84.1%; Accuracy at pixel level: 93%	Comparable	NA
Ohmori <i>et al</i> ^[73]	2020	Retrospective	Superficial ESCC	ME + NBI/BLI; Non-ME + WLI/NBI/BLI	CNN	23289 images (train 22562, test 727)		Accuracy/SEN/SPE: 77%/100%/63% (Non-ME + NBI/BLI); 81%/90%/76% (Non-ME + WLI); 77%/98%/56% (ME)	Comparable	0.028 s/image
Nakagawa <i>et al</i> ^[76]	2019	Retrospective	ESCC (EP-SM1/SM2+SM3)	ME; Non-ME	CNN-SSD	15252 images (train 14338, test 914)	Caffe DL framework	Accuracy/SEN/SPE: 91%/90.1%/95.8%	Comparable	0.033 s/image
Everson <i>et al</i> ^[77]	2019	Retrospective	ESCC IPCLs (type A/type B)	ME + NBI	CNN	7046 images	5-fold cross-validation+eCAM	Accuracy/SEN/SPE: 93.3%/89.3%/98%	NA	0.026-0.037 s/image
Guo <i>et al</i> ^[79]	2020	Retrospective	Early ESCC	NBI (ME + non-ME)	CNN-SegNet	13144 images (train 6473, validation 6671), 80 videos (47 lesions, 33 normal esophagus)	NA	Per-image SEN/SPE: 98.04%/95.03%; Per-frame SEN/SPE: 91.5%/99.9%	NA	< 0.04 s/frame; Latency <0.1 s
Shin <i>et al</i> ^[82]	2015	Retrospective	HGD, ESCC	HRM	Two-class LDA	375 sites of images (train 104, test 104, validation 167)	NA	AUC: 0.95; SEN/SPE: 84%/95%	NA	3.5 s/image
Quang <i>et al</i> ^[83]	2016	Retrospective	ESCC	HRM	A fully automated algorithm	375 biopsied sites from Shin <i>et al</i> ^[82] (train 104, test 104, validation 167)	NA	AUC: 0.937; SEN/SPE: 95%/91%	NA	Average 5 s for computing

BLI: Blue laser imaging; CCV: Color coherence vector; DL: Deep learning; CNN: Convolutional neural network; DNN: Deep neural network; eCAM: Explicit class activation map; EP: Epithelium; ESCC: Esophageal squamous cell cancer; FNN: Fuzzy neural network; HGD: High-grade dysplasia; HRM: High-resolution microendoscopy; IPCLs: Intra-papillary capillary loops; JDPCA: Joint diagonalisation principal component analysis; LDA: Linear discriminant analysis; ME: Magnifying endoscopy; NA: Not available; NBI: Narrow band imaging; SEN: Sensitivity; SM: Submucosa; SPE: Specificity; SSD: Single shot multibox detector; WLI: White light imaging.

study, 13144 NBI (ME + non-ME) images and 80 video clips were employed. In the image dataset, the SEN, SPE, and AUC were 98.04%, 95.03% and 0.989, respectively. For the video dataset, the SEN of per frame for non-ME and ME was 60.8% and 96.1%,

respectively; the SEN of per lesion for non-ME and ME was both 100%. When they analyzed 33 original videos of full-range normal esophagus, they acquired a SPE of 99.95% and 90.9% for per-frame and per-case analysis, respectively. The ability of this model to process each frame with a maximum time of 0.04 s and latency less than 0.1 s set a good example for future model optimization for real-time applications^[80].

Endomicroscopy: In 2007, Kodashima *et al.*^[81] used ImageJ software to label the border of nuclei under endo-cytologic images from 10 ESCC patients. They found that the computer-labelled nuclei area of ESCC was significantly different from that of normal tissues, which demonstrated the diagnostic possibility of computer. HRM is another low-cost tool that can illustrate the esophageal epithelium in cellular level, which compensates the low specificity of iodine staining and is also more cost-effective compared with CLE. In 2015, Shin *et al.*^[82] developed a 2-class linear classification algorithm using nuclei-related features to identify neoplastic squamous mucosa (HGD + cancer). It resulted in an AUC, SEN, and SPE of 0.95, 87%, 97% and 0.93, 84%, 95% for the test and validation datasets, respectively. However, the application of this system for real-time practice needs acceleration of analyzing speed. To solve this problem and reduce the cost of equipment, a smaller, tablet-interfaced HRM with real-time algorithm was developed by Quang *et al.*^[83]. The algorithm was able to automatically identify SCC with an AUC, SEN, and SPE of 0.937, 95%, and 91%, respectively, which is comparable to the result achieved by the first generation bulky laptop-interfaced HRM^[82] or the combination of Lugol chromoendoscopy and HRM^[84].

STUDY LIMITATIONS AND FUTURE PERSPECTIVES

Limitations

The exciting and promising findings of various CAD models have been summarized in detail above. Researches are ongoing worldwide because none of the studies were perfect. The limitations and problems are driving forces for evolution and innovation. We hereby discuss several major drawbacks that limit the strength of the studies.

Firstly, the most mentioned drawback is insufficient training sample size. The number of endoscopic images that the majority of studies employed ranged from 248 to about 7000 (Tables 1 and 2). The limited number of training data, lack of imaging variability, and single-center nature are likely to cause overfitting^[85], which attenuates the ability of AI models to perform well in unused datasets and leads to unstable results^[12,55]. To overcome this problem, various regularization methods have been developed, such as segmenting the image or using cross validation with 5 folds or even 10 folds to augment the datasets. Recently, the size of datasets has been greatly enlarged in several studies^[56,73,79], the largest of which included over one million UGI images from six centers^[78]. Therefore, further multicenter studies including large dataset with different kinds of images (*i.e.*, WLI, NBI, ME and non-ME) harvested by different endoscopic systems for SCC and AC are likely to produce results with robustness and external generalizability. In addition, different AI algorithms tested in prospective external dataset need to be developed to increase the diversity of AI technology^[13].

Secondly, selection bias is another contributor to limited generalizability. Most of the previous studies were retrospective and used only high-quality images. Suboptimal quality images with mucus, blur, or blood. were excluded. Additionally, unbalanced distribution of lesion types (SCC *vs* AC, type B1 *vs* B2 and B3 IPCLs), different numbers of images for each patient, and non-uniform processing method for different lesions all might cause bias in the result. Further prospective RCTs will be required in the future.

Thirdly, almost all of the studies employed still images to train AI model. Not until recently did the researchers validate the efficacy in dealing with endoscopic videos in a real-time manner. Future video-based researches are needed to narrow the gap between study and clinical practice.

Future perspectives

Gold standard: Consensus-based ground truth for lesions is preferred over a single expert's annotation. The committees of expert endoscopists and pathologists from different countries need to be formed to improve the precision of annotation. In addition, the AI should play a role in helping endoscopists recognize lesions and target biopsies for gold standard pathological examination, rather than replacing our "job".

Hardware upgrade: Computers equipped with powerful GPU are needed to perform more sophisticated algorithms and process large volume of graphical data, in order to achieve the goal of real-time recognition.

Pre-training database: ImageNet and GastroNet have been introduced, which store mass datasets of manually labeled images. These databases should be constantly enriched, since CAD models with prior knowledge are prone to have better discriminative ability^[60].

Cost-effect analysis: When a novel diagnostic method is introduced to clinical practice, whether it is cost-effective is an important issue. A recent multi-center add-on analysis revealed that AI is able to reduce cost of colonoscopic management of polyps^[86]. Since medical cost is one of the major concerns for both patients and government, it is necessary to assess whether AI can improve diagnostic performance of EC while reducing cost of unnecessary examinations and radical therapies. Future studies concerning medical cost and reimbursement should be conducted in different countries with different healthcare and insurance systems to address this issue.

Ethics and legality: Believe it or not to believe it, it is a real question. While we have taken a giant leap of AI technology in medicine which has the potential to improve the performance of clinicians with different experience and reduce error, the black-box^[87] nature of the ML algorithms truly brings doubts^[88]. Can we trust the results of AI, since they lack explainability? What should we do with these computer-generated results? Are they certified to be legal evidence? Challenges for legislation, regulation, insurance and clinical practice are inevitable. Supervised RCTs and AI participation in clinical workflow are needed to provide solid evidence that AI is acceptable within the range of legal and ethical concerns^[89]. Nevertheless, trends of AI are irreversible. The ultimate role of AI in medicine might be a supervised task performer^[90].

CONCLUSION

In this manuscript, we provided a comprehensive review of AI technology in diagnosis, treatment decision and outcome prediction for EC. We searched only PubMed database for clinical researches and applications. Issues regarding computer science and image processing are not our topics. The CAD systems have evolved from traditional ML algorithms to neural network-based DL, and from still image analysis to real-time video processing. AI can improve non-expert's performance while correct erroneous classification by experts^[78]. Researches with larger datasets and more reliable CAD models are being conducted worldwide. It is promising that AI may facilitate early cancer screening, surveillance and treatment in high-risk regions. However, it is noteworthy that patient's consent and satisfaction are of first priority.

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Basic Study

New approach of medicinal herbs and sulfasalazine mixture on ulcerative colitis induced by dextran sodium sulfate

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Abstract

BACKGROUND

Sulfasalazine has been used as a standard-of-care in ulcerative colitis for decades, however, it results in severe adverse symptoms, such as hepatotoxicity, blood disorders, male infertility, and hypospermia. Accordingly, the new treatment strategy has to enhance pharmacological efficacy and simultaneously minimize side effects.

AIM

To compare the anti-inflammatory action of sulfasalazine alone or in combination with herbal medicine for ulcerative colitis in a dextran sodium sulfate (DSS)-induced colitis mouse model.

METHODS

To induce ulcerative colitis, mice received 5% DSS in drinking water for 7 d. Animals were divided into five groups ($n = 9$ each) for use as normal (non-DSS), DSS controls, DSS + sulfasalazine (30 mg/kg)-treatment experimentals, DSS + sulfasalazine (60 mg/kg)-treatment experimentals, DSS + sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and *Bupleuri radix* mixture (30 mg/kg) (SCPB)-treatment experimentals.

RESULTS

The SCPB treatment showed an outstanding effectiveness in counteracting the ulcerative colitis, as evidenced by reduction in body weight, improvement in crypt morphology, increase in antioxidant defenses, down-regulation of proinflammatory proteins and cytokines, and inhibition of proteins related to apoptosis.

ARRIVE guidelines statement: The authors have read the ARRIVE guidelines, and the manuscript was prepared and revised according to the ARRIVE guidelines.

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CONCLUSION

SCPB may represent a promising alternative therapeutic against ulcerative colitis, without inducing adverse effects.

Key Words: Dextran sulfate sodium; Ulcerative colitis; Anti-inflammatory; Sulfasalazine; *Citrus unshiu* peel and Bupleuri radix mixture; Apoptosis

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Core Tip: Sulfasalazine has been used widely as a standard-of-care in ulcerative colitis; however, it is associated with a spectrum of side effects after long-term and high-dose intake. Since a single dose of sulfasalazine cannot provide satisfactory therapeutic results, we conducted a comparative evaluation of the pharmacological effect of sulfasalazine alone and when used in combination with *Citrus unshiu* peel and Bupleuri radix mixture in an experimentally-induced ulcerative colitis mouse model.

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INTRODUCTION

Inflammatory bowel diseases (IBDs), including ulcerative colitis (UC) and Crohn's disease, are chronic and uncontrolled intestinal disorders that have emerged collectively as an important public health problem worldwide^[1]. The recommended drugs in clinical use for treatment of IBD patients currently include corticosteroids, sulfasalazine, immunosuppressants, antibiotics, and anti-tumor necrosis factor (TNF)- α antibodies. Conventional therapies also involve combinations of these agents^[2,3]. Unfortunately, the incidence and prevalence of IBDs are continuing to increase^[4] and the plethora of data from cases treated with the commonly used drugs have revealed a number of side effects and troubling issues, such as blood disorders, hepatotoxicity, hypospermia, male infertility, and economic burden^[5]. Thus, alternatives for a safer, cheaper, and more efficacious approach to managing and/or treating IBDs is needed.

Diverse mixtures of herbal medicines have been screened as candidates for alleviating various inflammatory disorders^[6,7]. Toki-shakuyaku-san, which is a traditional kampo medicine, was found to down-regulate the inflammatory and apoptotic signaling during colitis^[8]. The rhizome mixture of *Anemarrhena asphodeloides* and *Coptidis chinensis* was found to exert an anti-colitic effect by inhibiting nuclear factor-kappa B (NF- κ B) activation^[9]. Moreover, Hange-shashin-to was found to suppress IBD in a rat model of experimental colitis^[10]. Ultimately, the collective research findings support the potential benefit of anti-inflammatory herbal combinations in colitis.

Citrus unshiu peel has been used widely throughout East Asia for improving the common cold, dyspepsia, and blood circulation^[11]. The *Citrus unshiu* peel – a seedless and easy-peeling citrus fruit – contains various flavonoids, such as hesperidin, naringin, and nobiletin^[12-14]. These active compounds have been reported to exert potent anti-inflammatory, antioxidant, anti-adipogenic, anti-diabetic, anti-microbial, and anti-allergic activities^[15,16]. On the other hand, Bupleuri radix has been mainly applied in clinical use for liver-related disease, and the recent pharmacological research has demonstrated its renoprotective and hepatoprotective effects^[17,18]. Saikosaponins isolated from Bupleuri radix possess valuable pharmacological activities, including those of anti-inflammatory, antitumor, antiviral, and anti-allergic, working mainly through NF- κ B or mitogen-activated protein kinase (MAPK) pathways^[19-21]. On the basis of these reports, we estimated that *Citrus unshiu* peel according to its anti-inflammatory effect and Bupleuri radix according to its hepatoprotective and renoprotective effects may be able to exert therapeutic benefits in UC.

To date, there are no studies on the potential anti-inflammatory effect of a treatment

mixture of *Citrus unshiu* peel and *Bupleuri radix* nor on its underlying mechanisms. The present study was conducted to evaluate the pharmacological effect of sulfasalazine alone and in combination with *Citrus unshiu* peel and *Bupleuri radix* mixture in UC, using a well-established experimentally-induced UC mouse model system.

MATERIALS AND METHODS

Materials

Dextran sodium sulfate (DSS) (molecular weight: 36000-50000 Da) was purchased from MP Biologicals (Santa Ana, CA, United States). Sulfasalazine (purity $\geq 98\%$) and phenylmethylsulfonyl fluoride (commonly known as PMSF) were purchased from Sigma-Aldrich (St. Louis, MO, United States). Protease inhibitor mixture solution and ethylenediaminetetraacetic acid (commonly known as EDTA) were purchased from Wako Pure Chemical Industries, Ltd. (Osaka, Japan). 2',7'-dichlorofluorescein diacetate (referred to as DCF-DA) was obtained from Molecular Probes (Eugene, OR, United States). Pierce bicinchoninic acid protein assay kit was obtained from Thermo Fisher Scientific (Waltham, MA, United States). Enhanced chemiluminescence (commonly known as ECL) western blotting detection reagents and pure nitrocellulose membranes were supplied by GE Healthcare (Chicago, IL, United States). The following antibodies were obtained from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA, United States): (mouse polyclonal) nuclear factor-kappa B p65 (NF- κ Bp65) (1:1000; SC-372), p47^{phox} (1:1000; SC-14015), Rac 1 (1:1000; SC-217), superoxide dismutase (SOD) 1:1000; SC-11407), glutathione peroxidase-1/2 (GPx-1/2) 1:1000; SC-30147), Bax (1:1000; SC-7480), Bcl-2 (1:1000; SC-7382), monocyte chemoattractant peptide-1 (MCP-1) (1:1000; SC-28879), and intercellular adhesion molecule-1 (ICAM-1) (1:1000; SC-1511-R); (goat polyclonal) tumor necrosis factor- α (TNF- α) (1:1000; SC-1351) and interleukin-1 β (IL-1 β) (1:1000; SC-1252); (mouse monoclonal) phosphor-extracellular signal-regulated kinase 1/2 (p-ERK1/2) (1:1000; SC-7383), phosphor-p38 (p-p38) (1:1000; SC-7973), cyclooxygenase-2 (COX-2) (1:1000; SC-19999), inducible nitric oxide synthase (iNOS) (1:1000; SC-7271), histone (1:1000; SC-8030), and β -actin (1:1000; SC-4778); and rabbit anti-goat (1:3000; SC-2774), goat anti-rabbit (1:3000; SC-2004), and goat anti-mouse (1:3000; SC-2005) immunoglobulin G (IgG) horseradish peroxidase (HRP)-conjugated secondary antibodies. Mouse monoclonal anti-caspase-3 (1:1000; 3004-100) was purchased from BioVision Inc. (Mountain View, CA, United States). Rabbit polyclonal anti-reduced nicotinamide adenine dinucleotide phosphate oxidase 4 (NOX4) was purchased from LifeSpan BioSciences (Seattle, WA, United States). All other chemicals and reagents were purchased from Sigma-Aldrich (St. Louis, MO, United States).

Plant materials

Bupleuri radix was supplied by Bonchowon (Yeongcheon-si, Gyeongsangnam-do, South Korea) and two herbs were produced according to Korean Good Manufacturing Practice. Dried *Bupleuri radix* (100 g) was extracted with 10 volumes of water and boiled in distilled water (100°C for 2 h). After filtration, the water extracts were evaporated using a rotary evaporator at 45°C and the solvent was evaporated *in vacuo* to give an extract with a yield of 26%. In addition, a crude drug preparation of *Citrus unshiu* peel (*Citri unshiu* pericarpium) (1 kg; Wansan Medicinal Herbs Co. Ltd., Jeonju-si, South Korea) was extracted with ethanol: H₂O (1:1) under reflux (2 L \times 3). After the solvent was evaporated under reduced pressure, the crude extract (220 g) was obtained. The two prepared herbs were kept at -80°C until use in animal experiments.

Experimental animals and induction of colitis

All procedures involving animals were reviewed and approved by the Institutional Animal Care and Use Committee of the Daegu Haany University (No. DHU2017-043). Eight-week-old male BALB/c mice, weighing 22-24 g, were purchased from Orient Bio Animal Center (Seongnam-si, South Korea). Mice were maintained under a 12h light/dark cycle, housed at a controlled temperature of 24 \pm 2°C and humidity of approximately 60%. After adaptation (1 wk), acute colitis was induced by oral administration of 5% (*w/v*) DSS dissolved in drinking water, for 7 d^[15]. The colitic mice were divided into four groups (*n* = 9 each) for use as DSS controls, DSS + sulfasalazine (30 mg/kg)-treatment experimentals, DSS + sulfasalazine (60 mg/kg)-treatment experimentals, DSS + sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and *Bupleuri radix* mixture (30 mg/kg) (SCPB)-treatment experimentals. A group of 9 untreated (normal)

mice received drinking water without DSS throughout the entire experimental period. Sufasalazine was used as the positive reference agent and it was given at doses of 30 mg/kg/d or 60 mg/kg/d. The 30 mg/kg *Citrus unshiu* peel and *Bupleuri radix* mixture was comprised of 25 mg/kg *Citrus unshiu* peel and 5 mg/kg *Bupleuri radix* (for a 5:1 ratio) and mixed just before application as the drug treatment. At 18 h after the last dosage was given, 2.5% isoflurane (Troikaa Pharmaceuticals Ltd., India) was administered for blood sample collection (cardiac puncture), sacrifice, and removal of the entire colon. All collected specimens were snap-frozen in liquid nitrogen and stored at -80°C until analysis. Symptomatic index of colitis, such as body weight loss, rectal bleeding, and mucus or watery diarrhea, were observed during experimental periods (before sacrifice).

Measurement of serum reactive oxygen species

Serum reactive oxygen species (ROS) concentration was measured by employing the method of Ali *et al.*^[21]. Briefly, 25 mmol/L DCF-DA was added to the serum and allowed to incubate for 30 min, after which the changes in fluorescence values were determined at an excitation wavelength of 486 nm and emission wavelength of 530 nm.

Hematoxylin and eosin staining of colon tissue

For microscopic evaluation, intestine tissue was fixed in 10% neutral-buffered formalin and, after embedding in paraffin, cut into 2 mm sections and stained using hematoxylin and eosin (H&E), for microscopic evaluation. The stained slices were subsequently observed under an optical microscope and analyzed using the iSolution Lite software program (InnerView Co., Seongnam-si, Gyeonggi-do, South Korea).

Preparation of cytosol and nuclear fractions

Protein extraction was performed according to the method of Komatsu^[23], with minor modifications. Briefly, colon tissues were processed to obtain the cytosol fraction by homogenization with ice-cold lysis buffer A (250 mL; containing 10 mmol/L HEPES (pH 7.8), 10 mmol/L KCl, 2 mmol/L MgCl₂, 1 mmol/L DTT, 0.1 mmol/L EDTA, 0.1 mmol/L PMSF, and 1250 µL protease inhibitor mixture solution). After incubation for 20 min at 4°C, the homogenate was mixed with 10% NP-40 and centrifuged (13400 × g for 2 min at 4°C; 5415R Centrifuge from Eppendorf, Hamburg, Germany). The supernatant liquid (cytosol fraction) was separated into a new e-tube and the pellets were washed twice with buffer A (wash supernatants were discarded). The washed pellets were resuspended with lysis buffer C (20 mL; containing 50 mmol/L HEPES (pH 7.8), 50 mmol/L KCl, 300 mmol/L NaCl, 1 mmol/L DTT, 0.1 mmol/L EDTA, 0.1 mmol/L PMSF, 1% (v/v) glycerol and 100 µL protease inhibitor mixture solution) and incubated for 30 min at 4°C. After centrifugation (13400 × g for 10 min at 4°C), the nuclear fraction was prepared to collect the supernatant. Both cytosol and nuclear fractions were stored at -80°C until analysis.

Immunoblotting analysis

For the estimation of NF-κBp65 and histone, 12 µg of protein from each nuclear fraction was electrophoresed through 10% sodium dodecylsulfate polyacrylamide gel (commonly known as SDS-PAGE). The electro-separated proteins were then transferred to a nitrocellulose membrane, blocked with 5% (w/v) skim milk solution for 1 h, and incubated with primary antibodies (NF-κBp65 and histone) overnight at 4°C. After the blots were washed, they were incubated with anti-rabbit or anti-mouse IgG HRP-conjugated secondary antibody for 1 h at room temperature. In addition, 7.5 µg protein of each cytosol fraction was electrophoresed through 8%-12% SDS-PAGE for detection of NOX4, p47^{phox}, Rac1, Bax, Bcl-2, caspase-3, SOD, catalase, GPx-1/2, COX-2, iNOS, TNF-α, IL-1β, MCP-1, ICAM-1, and β-actin. Each antigen-antibody complex was visualized using the ECL western blotting detection reagents and measured by chemiluminescence with Sensi-Q 2000 Chemidoc (Lugen Sci Co., Ltd., Gyeonggi-do, South Korea). Band densities were measured using ATTO Densitograph Software (ATTO Corp., Tokyo, Japan) and quantified as the ratio to histone or β-actin. The protein levels of the groups are expressed relative to those of the normal mice group (represented by the value of 1.0).

Statistical analysis

The data are expressed as the mean ± standard error of the mean. Statistical analysis was performed by one-way ANOVA followed by Least-significant differences (LSD) test using SPSS version 22.0 software (SPSS Inc., Chicago, IL, United States). *P* values

less than 0.05 were considered to indicate statistical significance.

RESULTS

SCPB attenuated the progression of DSS-induced colitis in mice

Compared with the normal (non-DSS) group, the DSS control group showed considerably greater body weight loss over the experimental period ($P < 0.001$). However, oral administration of SCPB and sulfasalazine mildly ameliorated the severity of body weight loss in the DSS control group (Figure 1A). As shown in Figure 1B, the DSS control group showed colon length reduction of 57.94% compared with that of the normal group ($P < 0.001$); however, the group treated with SCPB showed a 2.8% increase compared with that of the DSS control group but the difference did not reach the threshold for statistical significance.

Colonic inflammation involves the disruption of crypt morphology, resulting in the infiltration of inflammatory cells and thickening of the lamina propria^[24]. As shown in Figure 1C, the colons of the DSS control group showed histologic alterations such as infiltration of numerous inflammatory cells, goblet cell degeneration, and crypt distortion consistent with UC. Treatment with sulfasalazine or SCPB appeared to preserve the broad crypt distortion and ameliorate the infiltration of inflammatory cells.

SCPB ameliorated biomarkers associated with oxidative stress in DSS-induced colitis in mice

As shown in Figure 2A, serum ROS levels in the DSS control group were markedly higher than that in the normal (non-DSS) group ($P < 0.001$); however, the administration of sulfasalazine or SCPB appeared to lead to a marked decrease in the DSS-induced elevated levels ($P < 0.001$). As shown in Figure 2B, the protein expressions of nicotinamide adenine dinucleotide phosphate (NADPH) oxidase enzymes in the DSS control group were significantly elevated compared with those in the normal (non-DSS) group (NOX4, $P < 0.05$; p47^{phox}, $P < 0.01$; Rac 1, $P < 0.001$). However, the SCPB administration appeared to decrease and ameliorate the levels of each, in a manner superior to that of sulfasalazine alone (NOX4, $P < 0.05$; p47^{phox}, $P < 0.05$; Rac 1, $P < 0.001$). The 60 mg/kg sulfasalazine dosage, especially, showed a remarkable tendency towards effecting this decrease, but the difference did not reach the threshold for statistical significance.

SCPB up-regulated antioxidant enzymes in DSS-induced colitis in mice

Oxidative stress plays a vital role in IBD^[25]. The activities of SOD and catalase showed a significant decrease in the DSS control group compared to those in the normal (non-DSS) group (SOD, $P < 0.05$; catalase, $P < 0.001$). However, the SCPB treatment significantly elevated the activities of SOD and catalase, but not of GPx-1/2 and the differences did not reach the threshold for statistical significance. These results indicated that SCPB supplementation may decrease the extent of colonic injury *via* its antioxidant effect (SOD, $P < 0.05$; catalase, $P < 0.01$) and do so in a manner superior treatment with sulfasalazine alone (Figure 3).

SCPB suppressed MAPK-related protein expressions in DSS-induced colitis mice

The MAPK pathways can be activated by oxidative stress, leading to inflammation processes and apoptosis^[26]. MAPK-related protein expressions showed augmentation in the colons of mice in the DSS control group compared to those of the normal (non-DSS) group (p-p38, $P < 0.05$; p-ERK1/2; $P < 0.01$); in contrast, the oral administration of SCPB significantly decreased the expression of both p-p38 and p-ERK1/2, which reached nearly normal levels ($P < 0.05$), as shown in Figure 4.

SCPB abrogated NF- κ B activation and expressions of NF- κ B-related inflammatory proteins in DSS-induced colitis mice

It has been confirmed that NF- κ B is the central transcription factor in the regulation of proinflammatory mediators (*i.e.*, COX-2 and iNOS), proinflammatory cytokines (*i.e.*, TNF- α and IL-1 β), and at least one chemokine (*i.e.*, MCP-1), and one adhesion molecule (*i.e.*, ICAM-1) during inflammation^[27]. The DSS control group showed enhanced phosphorylation of NF- κ B in colon ($P < 0.01$), whereas the elevation was significantly reversed upon SCPB ($P < 0.05$). As important downstream targets of NF- κ B, the expressions of COX-2 and iNOS were increased in the DSS control group and

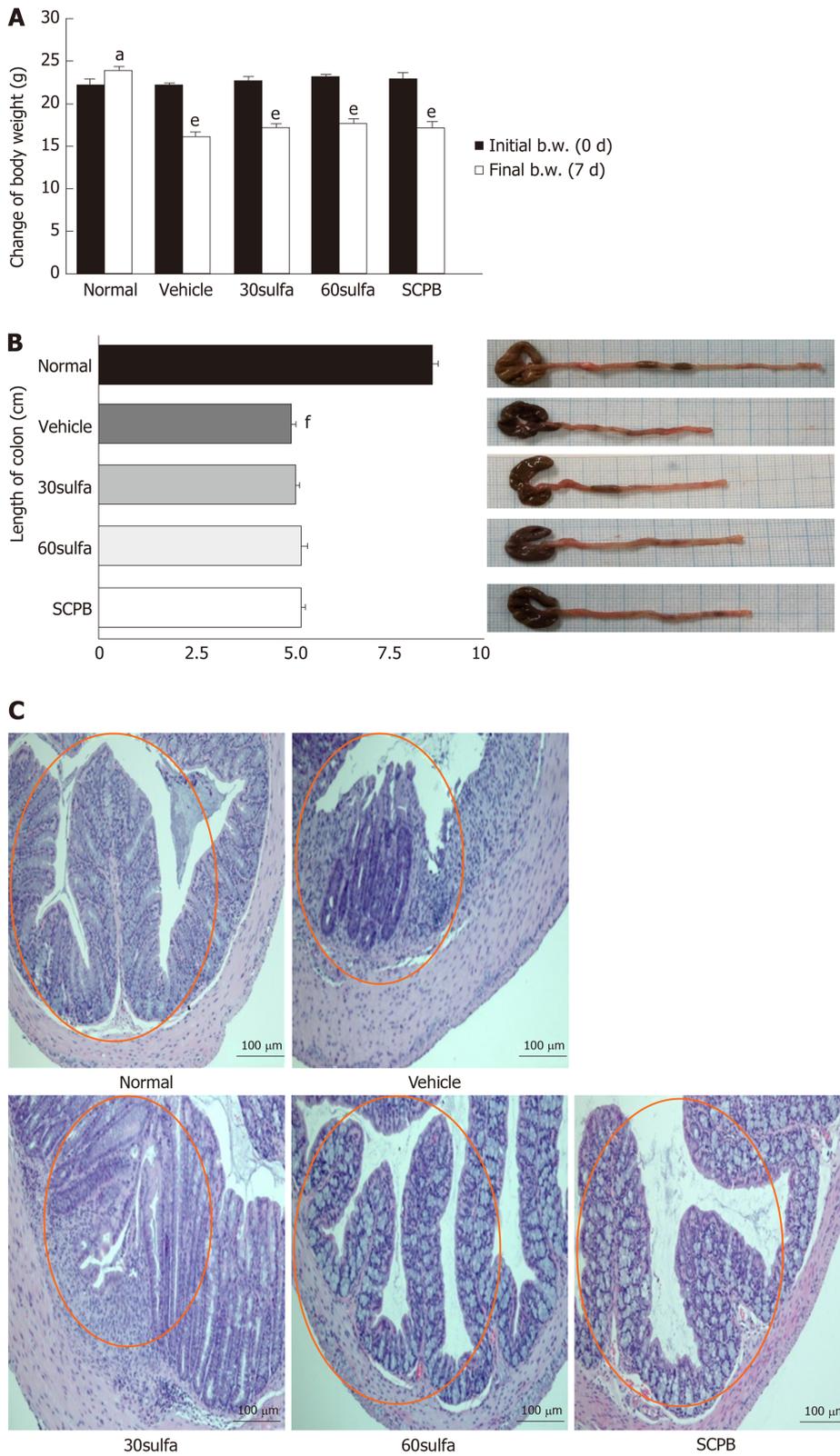


Figure 1 Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg) alleviated Dextran Sodium Sulfate-induced experimental ulcerative colitis. A: Change of body weight after induction of colitis by DSS; B: Length of colon and macroscopic viewpoint; Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated); C: Hematoxylin and eosin staining of colon (magnification $\times 200$), orange line meaned crypt destruction and loss. Data are presented as mean \pm standard error of the mean for $n = 7$. ^a $P < 0.05$, ^e $P < 0.001$ vs initial body weight (b.w.) per group; ^f $P < 0.001$ vs normal (non-DSS) mice. SCPB: Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg).

markedly blocked in mice given SCPB supplementation ($P < 0.05$). In contrast, treatment with sulfasalazine alone merely showed a tendency to decrease the

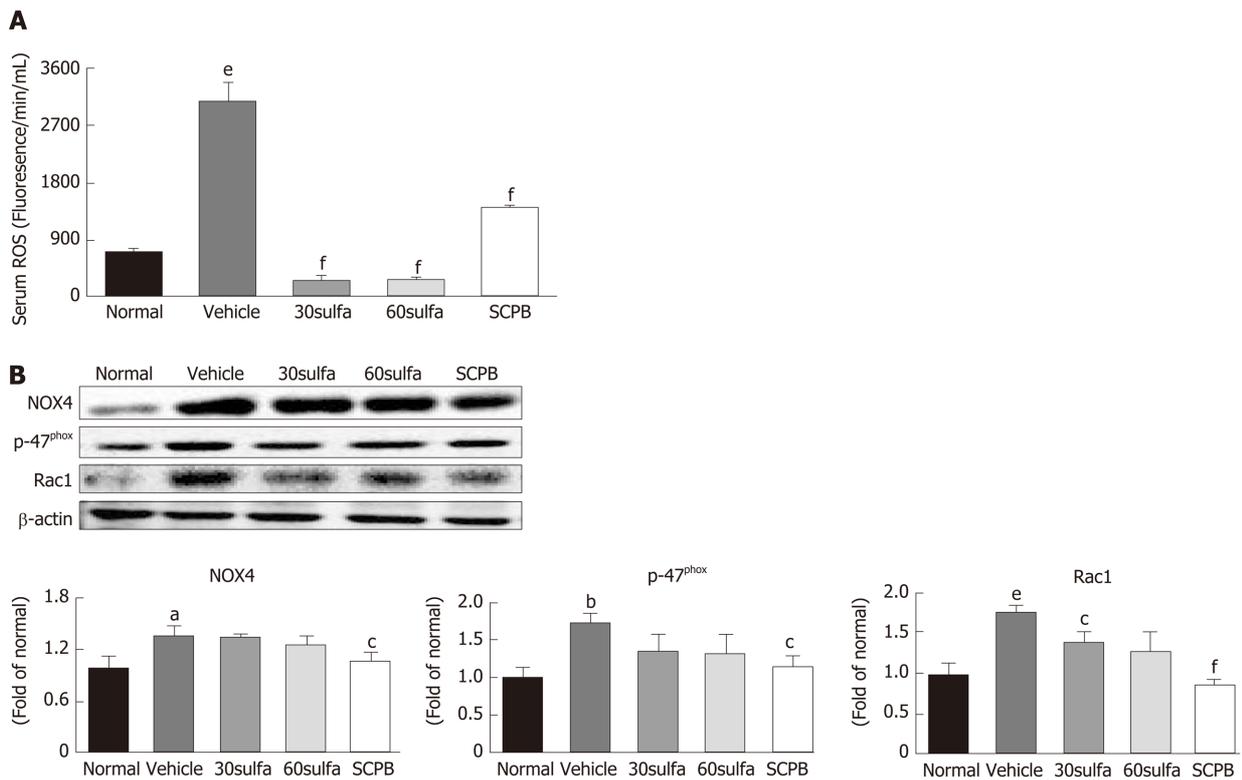


Figure 2 Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg) reduced Serum reactive oxygen species and NADPH oxidase activity in colon. A: Serum reactive oxygen species (ROS); B: Western blot detection of NADPH oxidase proteins; NOX4, p47^{phox}, and Rac 1 protein expressions in mice from the groups of Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated). Data are presented as mean ± standard error of the mean for n = 7. ^aP < 0.05, ^bP < 0.01, ^eP < 0.001 vs normal (non-DSS and untreated) mice; ^cP < 0.05, ^fP < 0.001 vs DSS control mice. SCPB: Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg); ROS: Reactive oxygen species.

expression of the two factors. Moreover, expressions of TNF- α and IL-1 β as well as COX-2 and iNOS were noticeably amplified in the DSS control group but administration of both SCPB and sulfasalazine significantly inhibited this effect. These protein levels were down-regulated similarly or to an extent lower than normal levels (Figure 5). Furthermore, the level of MCP-1 and ICAM-1 protein expressions were decreased in the mice who received SCPB.

SCPB inhibited apoptosis in DSS-induced colitis mice

The excess exposure of ROS in the colonic mucosa is known to trigger apoptosis of colon epithelial cells, leading to progression of IBD^[28]. The DSS control group showed the disease-characteristic apoptosis features of inflamed colon epithelial cells, supported by an observable increase in Bax and caspase-3 activities (Figure 6). In contrast, the SCPB treatment appeared to lead to marked down-regulation of the DSS-induced Bax and caspase-3 activities ($P < 0.001$ and $P < 0.05$, respectively). These findings suggest that SCPB may protect the colon mucosa from apoptosis in DSS-induced colitis. Meanwhile, Bcl-2 protein expression during UC didn't show a significant difference as only a mild increase.

DISCUSSION

UC is a type of IBD characterized by chronic inflammation of the intestinal mucosa, manifesting body weight loss, bloody diarrhea, tenesmus, abdominal pain, and fatigue. The incidence and prevalence of UC have been reported over many years and both continue to show a rapid increase worldwide^[29]. Nowadays, sulfasalazine, a prodrug of 5-aminosalicylic acid, is currently used as the first-line therapy for mild-to-moderate UC^[30]. Although its clinical prescription is executed routinely, the ratios of refractory and relapsed cases are comparatively high^[31] and it remains at the limit of poor tolerability due to frequent gastrointestinal side effects^[32]. DSS, used for the

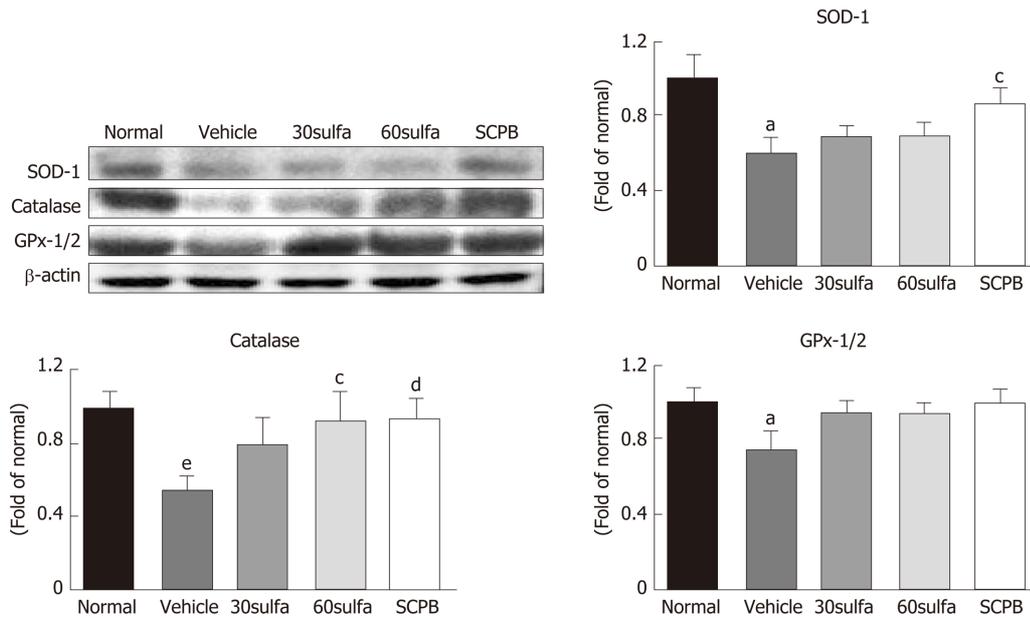


Figure 3 Effect of sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg) on antioxidant proteins in Dextran Sodium Sulfate-induced colitis mice. Western blot detection of the antioxidant proteins; SOD, Catalase, and GPx-1/2 protein expression levels in mice from the groups of Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated). Data are presented as mean ± standard error of the mean for $n = 7$. ^a $P < 0.05$, ^e $P < 0.001$ vs normal (non-DSS and untreated) mice; ^c $P < 0.05$, ^d $P < 0.01$ vs DSS control mice. SCPB: Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg).

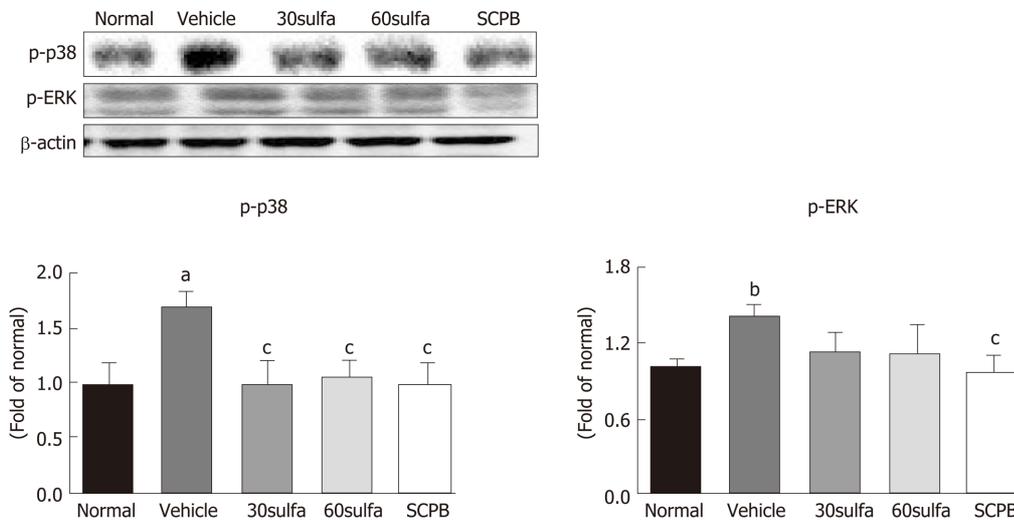


Figure 4 P-p38 and p-ERK protein expressions in Dextran Sodium Sulfate-induced colitis. Western blot detection of the mitogen-activated protein kinase-related proteins; p-p38 and p-ERK in mice from the groups of Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated). Data are presented as mean ± standard error of the mean for $n = 7$. ^a $P < 0.05$, ^b $P < 0.01$ vs normal (non-DSS) mice; ^c $P < 0.05$ vs DSS control mice. SCPB: sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg).

induction of UC in animal models, causes a marked inflammatory and immune response by affecting DNA replication, inhibiting the overgrowth of epithelial cells, inducing macrophage activation, increasing the release of cytokines, and breaking the balance of gut microflora. The gut microflora itself is a critical player in intestinal permeability with imbalance between beneficial and pathogenic bacteria being implicated in IBD pathogenesis^[33]. Consequently, DSS supplementation results in acute UC, which is similar to human UC and making it is an ideal model that has been widely used to study the mechanism of UC and for screening of potential drugs^[34,35].

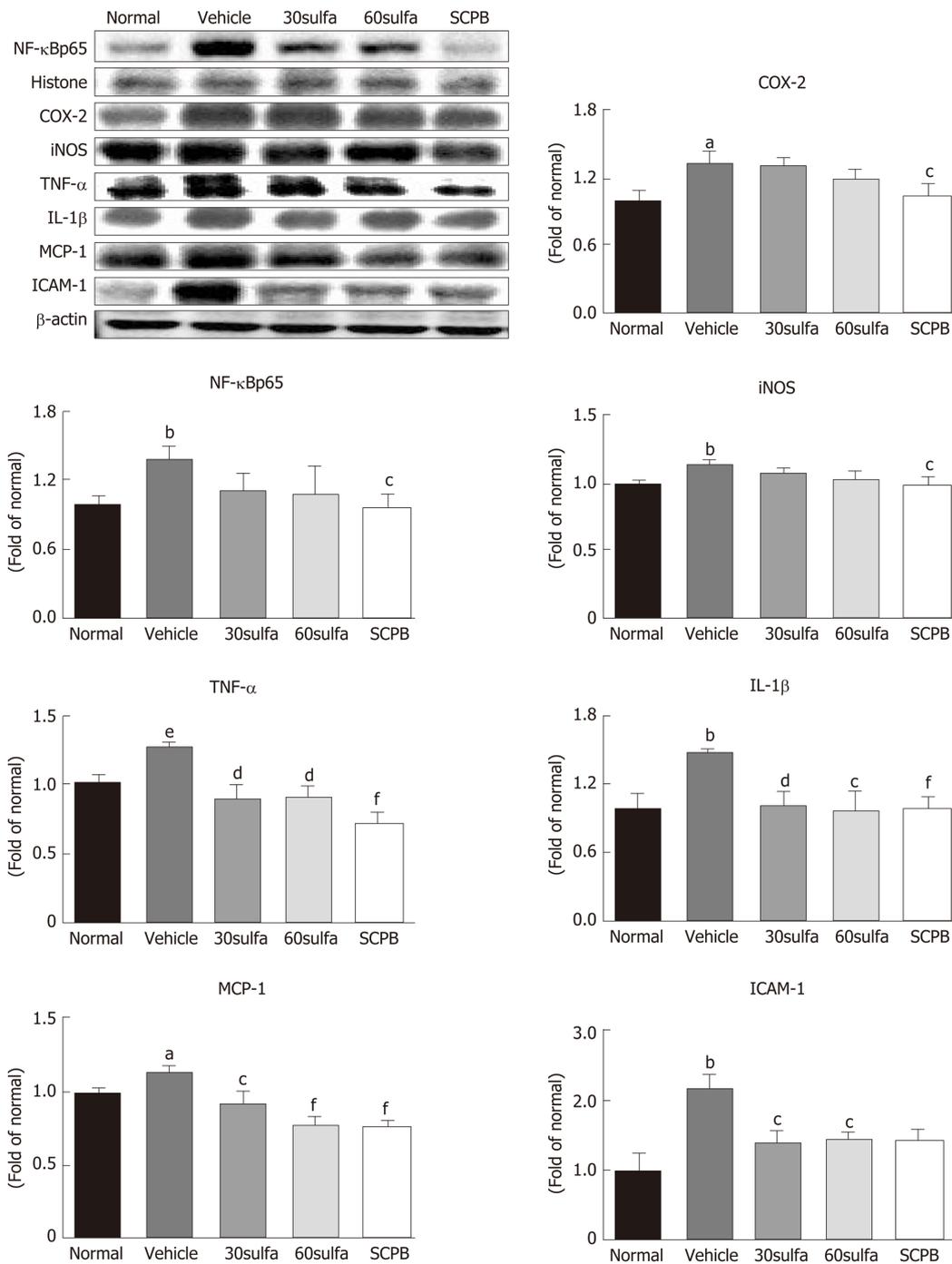


Figure 5 NF-κB p65, COX-2, iNOS, TNF-α, IL-1β MCP-1, and ICAM-1 protein expressions in Dextran Sodium Sulfate-induced colitis.

Western blot detection of the inflammatory proteins; NF-κBp65, COX-2, iNOS, TNF-α, IL-6, MCP-1, and ICAM-1 in mice from the groups of Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated). Data are presented as mean ± standard error of the mean for n = 7. ^aP < 0.05, ^bP < 0.01, ^eP < 0.001 vs normal (non-DSS) mice; ^cP < 0.05, ^dP < 0.01, ^fP < 0.001 vs DSS control mice. SCPB: sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg).

The present study provided, for the first time, a comparative evaluation of the pharmacological efficacy of sulfasalazine combined with *Citrus unshiu* peel and Bupleuri radix mixture (the ‘SCPB’ treatment described herein), as compared with sulfasalazine alone, in a mouse model of UC. While our the DSS control mice had significantly increased body weight loss and decreased colon length, previous studies have showed length of colon to be inversely correlated with severity of the experimental colitis^[6]. In our study, the DSS-induced mice showed significantly decreased final body weight and both the sulfasalazine and SCPB treatments curtailed the body weight loss and the shortening of the colon length. Herein, each groups showed the improvement effect like 30sulfa (1.96%), 60sulfa (5.36%), and SCPB (4.79%)

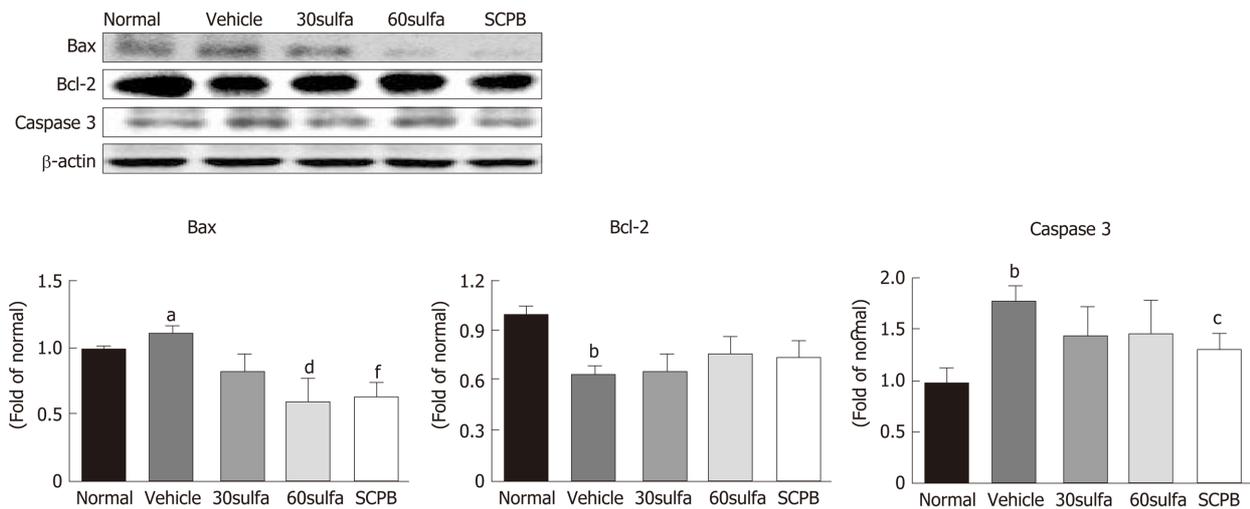


Figure 6 Bax, Bcl-2, and caspase-3 protein expressions in Dextran Sodium Sulfate-induced colitis. Western blot detection of the apoptotic and anti-apoptotic proteins; Bax, Bcl-2, and caspase-3 in mice from the groups of Normal (non-DSS), Vehicle (DSS control), 30sulfa (sulfasalazine 30 mg/kg-treated), 60sulfa (sulfasalazine 60 mg/kg-treated), and SCPB (30sulfa plus *Citrus unshiu* peel and Bupleuri radix mixture at 30 mg/kg-treated). Data are presented as mean \pm standard error of the mean for $n = 7$. ^a $P < 0.05$, ^b $P < 0.01$ vs normal (non-DSS) mice; ^c $P < 0.05$, ^d $P < 0.01$, ^f $P < 0.001$ vs DSS control mice. SCPB: sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg).

on the colon length compared to the DSS control mice although it was not significant. The DSS-induced colonic mucosal damage persisted till day 7, evidenced by epithelial necrosis, impaired mucosa integrity (with submucosa showing hyperemia and edema), and ulceration, accompanied by infiltration of numerous inflammatory cells, such as monocytes and macrophages^[37]; importantly, these pathogenic features appeared to be alleviated by the SCPB treatment.

Excessive ROS, including superoxide radicals (O_2^-), hydroxyl radicals, hydrogen peroxide and singlet oxygen, may have detrimental effects on such basic cellular components as DNA, proteins, and lipids. The enzymatic process that can generate ROS is the reaction catalyzed by NADPH oxidase^[38]. In resting cells, the subunits of NADPH oxidase are present in the cytosol and the membranes. Upon cell activation, the subunits are assembled on a membrane-bound vesicle, which then fuses with the plasma membrane, resulting in the release O_2^- ^[38,39]. Accumulation of O_2^- causes an elevation of the detectable ROS, leading to acceleration of an inflammatory cascade. The influence of ROS in the pathogenesis of gastrointestinal diseases, such as colon cancer and acute and chronic pancreatitis, has been demonstrated^[40]. Above all, the previous studies have indicated the importance of ROS-induced oxidative stress in the development of UC^[41,42] and overproduction of ROS *via* NADPH oxidases, including NOX4, p47^{phox}, and Rac 1, has been implicated in tissue damage observed in chronic inflammatory disorders^[42]. In the current study, the DSS injury was accompanied by an elevated level of serum ROS, which was decreased upon treatment with either sulfasalazine or SCPB. The protein expressions of NOX4, p47^{phox}, and Rac 1 (the markers of NADPH oxidase activity) were augmented in the colons of the DSS control mice. While the 60 mg/kg sulfasalazine-alone treatment down-regulated the NADPH oxidase activity, the SCPB treatment did so to a much greater extent. Generally, ROS are neutralized by endogenous antioxidant enzymes^[43]; namely, SOD converts O_2^- to hydrogen peroxide, which is subsequently neutralized to water by the actions of catalase and GPx-1/2. IBD patients present with serious impairment in antioxidant enzyme levels in their intestinal mucosa^[44]. In our study, the SOD, catalase, and GPx-1/2 enzymic antioxidants were markedly decreased in the mice with DSS-induced colitis. SCPB administration significantly increased the activities of SOD and catalase but not of GPx-1/2. Overall, these results indicate that SCPB regulates antioxidant enzyme activity against oxidative stress in DSS-induced colitis mice; moreover, this effect was superior to that effected by sulfasalazine alone.

NF- κ B participates in controlling the activation of various proinflammatory cytokine genes, such as IL-1 β , IL-6, and TNF- α , underlying its critical role in the pathogenesis of UC. MAPKs are also implicated in the pathogenic mechanism, and their activity leads to the activation of various nuclear transcription factors. ROS overproduction activates MAPKs, including p38 and ERK1/2. Phosphorylation of p38 has been confirmed after induction of experimental colitis, wherein activation of p38

can greatly promote the activation of immune cells and aggravate inflammation^[45]. In particular, p38 MAPK has numerous direct and indirect interactions with NF- κ B. Namely, the phosphorylation of p38 MAPK is implicated by leading to the activation of NF- κ B. Moreover, the phosphorylation of ERK1/2 MAPKs are also stimulated upon activation of NF- κ B^[46,47]. In the present study, the colons of DSS-induced colitis mice showed the expected increases in expressions of ERK1/2 and p38, which SCPB treatment was able to decrease significantly. The NF- κ B transcription factor plays a critical role in inflammation, facilitating the expression and secretion of various proinflammatory cytokines, mediators, and chemokines to mediate a series of subsequent inflammatory cascades^[48]. Blocking NF- κ B activation is known to reduce the release of proinflammatory cytokines, thereby alleviating development of the inflammatory response and achieving a therapeutic effect. In this study, we evaluated the inhibitory effect of SCPB on NF- κ B activation in DSS-induced colitis mice. The DSS-induced elevation in NF- κ B levels was suppressed upon SCPB treatment but the inhibitory effect of SCPB was much lower than that of sulfasalazine alone. These results suggest that SCPB could ameliorate DSS-induced acute colitis by inhibiting NF- κ B activation. NF- κ B activation exerts a strong influence on the inflammatory response.

Our results also indicate that SCPB significantly inhibited the induction of COX-2 and iNOS expressions and the production of the proinflammatory cytokines TNF- α and IL-1 β . Moreover, the SCPB treatment remarkably down-regulated the MCP-1 chemokine and attenuated the adhesion molecule ICAM-1. Excessive exposure of ROS under inflammatory conditions is known to increase epithelial cell apoptosis^[49], which is likely to deteriorate epithelial barrier integrity and has an influence on intestinal damage. Thus, we postulated that DSS treatment is responsible for inducing apoptosis through activation of apoptosis proteins, specifically Bax and caspase-3, and suppression of anti-apoptotic protein, namely Bcl-2, as reported by other researchers^[50,51]. Indeed, our DSS-induced colitis mice showed a considerable down-regulation of Bax and caspase-3 upon SCPB treatment. However, Bcl-2 just showed a tendency to increase without a significance. Maybe it judged that other anti-apoptotic protein such as survivin must have been involved in apoptosis.

CONCLUSION

As a result, the administration of SCPB to mice treated with DSS ameliorated acute inflammation and apoptosis in the colon, as shown in [Figure 7](#). Taken together, the present findings suggest that SCPB is an effective inhibitor of DSS-induced colitis in mice. The SCPB treatment showed enhanced therapeutic effect compared to that of the standard sulfasalazine treatment. Nevertheless, the underlying mechanism of SCPB is still ambiguous and further profound researches are needed.

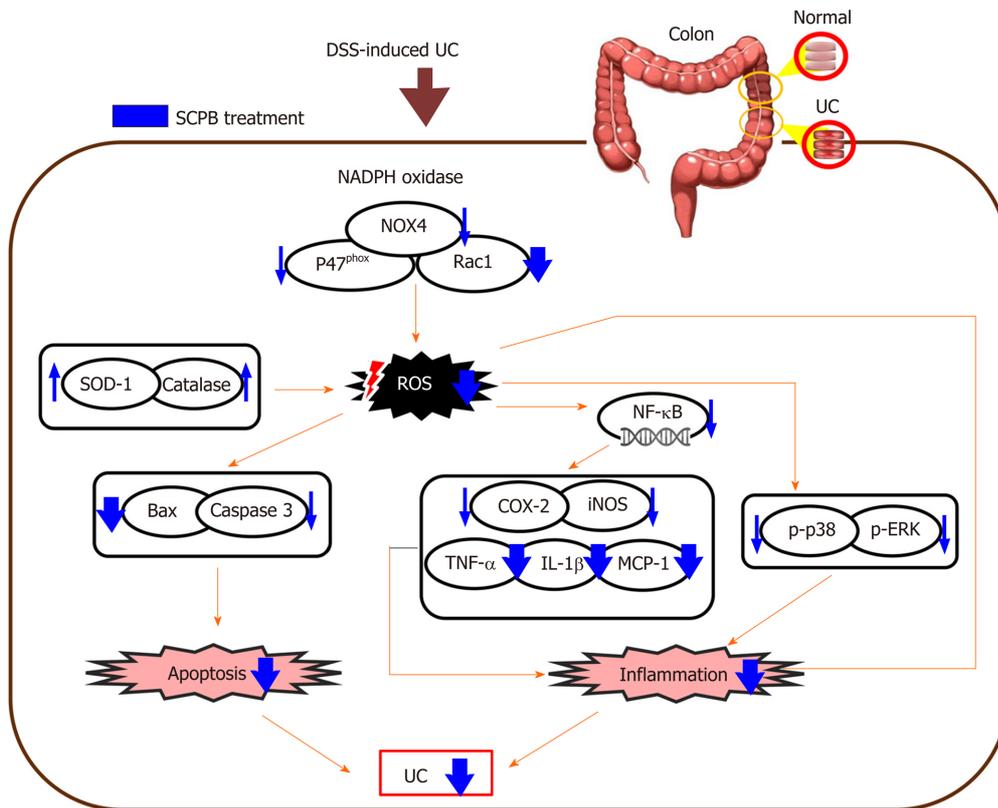


Figure 7 Possible mechanism of *Citrus unshiu* peel and Bupleuri radix mixture combined with sulfasalazine in Dextran Sodium Sulfate-induced ulcerative colitis. SCPB: 30sulfalazine plus *Citrus unshiu* peel and Bupleuri radix mixture 30 mg/kg-treated mice. DSS: Dextran Sodium Sulfate; SCPB: Sulfasalazine (30 mg/kg) + *Citrus unshiu* peel and Bupleuri radix mixture (30 mg/kg); ROS: Reactive oxygen species; UC: Ulcerative colitis.

ARTICLE HIGHLIGHTS

Research background

Ulcerative colitis (UC) has high incidence worldwide and is characterized by unintentional weight loss, abdominal pain, mucous and bloody diarrhea, and anemia. Generally, the recommended therapies for UC include anti-inflammatory drugs, antibiotics, immunosuppressants, and anti-tumor necrosis factor- α antibodies. Sulfasalazine, a drug composed of 5-aminosalicylic acid and sulfapyridine, has been prescribed as a standard-of-care in UC treatment. Otherwise, it can produce a variety of side effects upon long-term and high-dose intakes. Hence, an alternative approach for a safer, cheaper, and more efficacious management or treatment of UC is needed.

Research motivation

UC is chronic and complex autoimmune inflammatory disorder. The incidence of UC has grown worldwide over the recent decades and the quality of life for patients suffering from UC has been falling quickly, in tandem. The findings from our research will give essential help towards dealing with the problems of these patients, with sulfasalazine with *Citrus unshiu* peel and Bupleuri radix mixture (referred to as SCPB), one of more safe and effective herbal medicine mixtures, contributing to improving their quality of life.

Research objectives

The present study was conducted to evaluate the pharmacological effect of sulfasalazine alone and as the SCPB combination using an experimentally-induced UC mouse model.

Research methods

Ulcerative colitis was induced by 5% dextran sodium sulfate in drinking water for 7 d. The pharmacological effect of sulfasalazine alone and SCPB was evaluated using serum analysis, histological exam, and western blotting. The colon tissue was selected

as the region of interest for data analysis. One-way ANOVA followed by Least-significant differences (LSD) test were used for statistical inference.

Research results

The SCPB treatment significantly inhibited the induction of COX-2 and iNOS expressions and the production of the proinflammatory cytokines TNF- α and IL-1 β . Moreover, the SCPB treatment remarkably down-regulated the MCP-1 chemokine and attenuated the adhesion molecule ICAM-1. The SCPB treatment exerted anti-apoptotic effect though a considerable down-regulation of Bax and caspase-3 upon SCPB treatment.

Research conclusions

The SCPB supplementation showed enhanced therapeutic effect compared to that of the standard sulfasalazine treatment. Accordingly, SCPB may represent a promising alternative therapeutic against ulcerative colitis without inducing adverse effects.

Research perspectives

A single dose of sulfasalazine cannot provide satisfactory therapeutic results because of a spectrum of side effects after long-term and high-dose intake. However, when we used in combination with *Citrus unshiu* peel and *Bupleuri radix* mixture in an experimentally-induced ulcerative colitis mouse model, its inflammation was alleviated significantly. SCPB therapy may be more efficacious for symptom improvement of patients with ulcerative colitis in future.

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Basic Study

Immune infiltration-associated serum amyloid A1 predicts favorable prognosis for hepatocellular carcinoma

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Abstract**BACKGROUND**

Serum amyloid A1 (SAA1) is an acute-phase protein involved in acute or chronic hepatitis. Its function is still controversial. In addition, the effect of the expression of SAA1 and its molecular function on the progression in hepatocellular carcinoma (HCC) is still unclear.

AIM

To demonstrate the expression of SAA1 and its effect on the prognosis in HCC and explain further the correlation of SAA1 and immunity pathways.

METHODS

SAA1 expression in HCC was conducted with The Cancer Genome Atlas-Liver Hepatocellular Carcinoma (TCGA-LIHC) in GEPIA tool, and the survival analysis based on the SAA1 expression level was achieved in the Kaplan-Meier portal. The high or low expression group was then drawn based on the median level of SAA1 expression. The correlation of SAA1 and the clinical features were conducted in the UALCAN web-based portal with TCGA-LIHC, including tumor grade, patient disease stage, and the TP53 mutation. The correlation analysis between SAA1 expression and TP53 mutation was subjected to the TCGA portal. The tumor purity score and the immune score were analyzed with CIBERSORT. The correlation of SAA1 expression and tumor-infiltrating lymphocytes was achieved in TISIDB web-based integrated repository portal for tumor-immune system interactions. GSE125336 dataset was used to test the SAA1 expression in the responsive or resistant group with anti-PD1 therapy. Gene set enrichment analysis was applied to evaluate the gene enrichment signaling pathway in HCC. The similar genes of SAA1 in HCC were identified in GEPIA, and the protein-

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protein interaction of SAA1 was conducted in the Metascape tool. The expression of C-X-C motif chemokine ligand 2, C-C motif chemokine ligand 23, and complement C5a receptor 1 was studied and overall survival analysis in HCC was conducted in GEPIA and Kaplan-Meier portal, respectively.

RESULTS

SAA1 expression was decreased in HCC, and lower SAA1 expression predicted poorer overall survival, progression-free survival, and disease-specific survival. Furthermore, SAA1 expression was further decreased with increased tumor grade and patient disease stage. Also, SAA1 expression was further downregulated in patients with TP53 mutation compared with patients with wild type TP53. SAA1 expression was negatively correlated with the TP53 mutation. Lower SAA1 predicted poorer survival rate, especially in the patients with no hepatitis virus infection, other than those with hepatitis virus infection. Moreover, the SAA1 expression was negatively correlated with tumor purity. In contrast, SAA1 expression was positively correlated with the immune score in HCC, and the correlation analysis between SAA1 expression and tumor-infiltrating lymphocytes also showed a positive correlation in HCC. Decreased SAA1 was closely associated with the immune tolerance of HCC. C-X-C motif chemokine ligand 2 and C-C motif chemokine ligand 23 genes were identified as the hub genes associated with SAA1, which could also serve as favorable prognosis markers for HCC.

CONCLUSION

SAA1 is downregulated in the liver tumor, and it is closely involved in the progression of HCC. Lower SAA1 expression indicates lower survival rate, especially for those patients without hepatitis virus infection. Lower SAA1 expression also suggests lower immune infiltrating cells, especially for those with immune cells exerting anti-tumor immune function. SAA1 expression is closely associated with the anti-tumor immune pathways.

Key Words: Serum amyloid A1; Hepatocellular carcinoma; Low expression; Prognosis; Hepatitis; Immune pathways

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Core Tip: In this study, we identified the downregulation of serum amyloid A1 (SAA1) in hepatocellular carcinoma (HCC). SAA1 expression could predict the favorable prognosis for HCC patients, especially for those patients without hepatitis virus infection. SAA1 expression was closely associated with anti-tumor immune signaling pathways. We also identified two signature genes associated with SAA1, suggesting a favorable prognosis function of SAA1 for HCC patients.

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INTRODUCTION

Serum amyloid A1 (SAA1) is a kind of acute-phase protein that is also a member of the coding gene of serum amyloid A (SAA) protein, which consists of SAA2, SAA3, and SAA4^[1,2]. SAA1, SAA2, and SAA3 contribute to the acute phase response, and SAA4 expression is constitutively expressed^[3]. At present, SAA protein is regarded as the most important biomarker in acute inflammation and tissue injury, and it could serve as a marker for viral or bacterial infection. The sensitivity of SAA1 for inflammatory infection diagnosis is superior to C-reaction protein, which was confirmed in the diagnosis of several diseases, such as tuberculosis, leprosis, Crohn's disease, and

rheumatoid arthritis^[4-6]. In recent years, the importance of SAA in the malignant tumor has attracted much more attention. Some studies reported that serum SAA is a biomarker for some solid tumors, such as stomach, colon, pancreas, breast, and lung cancers, and that elevated SAA is also correlated with tumor stage^[7-10]. SAA protein is mainly synthesized by the liver, and some literature has revealed its expression changes in liver diseases, such as liver injury and virus infection^[11]. However, the expression and clinical correlation of SAA in hepatocellular carcinoma (HCC) are still unclear. SAA1, which is an important preproprotein of SAA, should also be examined. Thus, this study mainly focused on the significance of SAA1 in HCC.

HCC is a major malignant tumor of the digestive system with a high lethality rate, especially in Asians^[12]. Clinical data have shown that hepatitis virus infection could be an important reason for the high frequency of HCC in Asians^[13,14]. The clinical treatment for HCC includes chemotherapy, radiotherapy, immunotherapy, and interventional treatment^[15]. The representative chemotherapy drug is sorafenib, from which some patients benefit in prolonging survival. However, clinical practice also revealed the true frequency of drug resistance, which contributed to the poor outcome of HCC patients^[16]. The complex tumor microenvironment and side effects also interfered with the effect of radiotherapy or interventional therapy^[17]. In recent years, immune-based treatments have attracted much attention. Immune checkpoint blockade therapy has been widely conducted in clinical trials (*e.g.*, the PD-1 blockade antibody^[18]) with unsatisfactory outcomes. Considering the significance of the anti-PD1 antibody in other tumors, some researchers hypothesized that immune tolerance might contribute to the poor outcome. Researchers had been trying to explore solutions to overcome immune tolerance. Driving immune cytotoxic cells to kill tumor cells could be an encouraging strategy.

In this study, SAA1 expression was decreased in HCC, and its lower expression represented poorer prognosis, especially in those without hepatitis virus infection, suggesting that immune signaling pathways might be involved in SAA1-mediated HCC progression. The molecular mechanism exploration also confirmed the close association between SAA1 and immune tolerance. In summary, downregulation of SAA1 in HCC may be a candidate target for HCC therapy, especially in the practice of anti-tumor immunity.

MATERIALS AND METHODS

The cancer genome atlas analysis

The expression of SAA1, C-X-C motif chemokine ligand 2 (CXCL2), C-C motif chemokine ligand 23 (CCL23), and complement C5a receptor 1 (C5AR1) in the HCC tumor tissues and normal liver tissues was conducted in the GEPIA portal (<http://gepia2.cancer-pku.cn/#index>)^[19]. Normal liver tissues were comprised of surrounding non-tumor and genotype-tissue expression liver tissues. The correlation of SAA1 with the clinical features (*e.g.*, tumor grade, patient disease stage, and TP53 mutation) was subjected to UALCAN (<http://ualcan.path.uab.edu/index.html>)^[20]. The correlation of SAA1 expression with the frequency of TP53 mutation was conducted in Liver Hepatocellular Carcinoma (LIHC) of The Cancer Genome Atlas (TCGA) portal (www.tcgaportal.org).

Survival analysis

The overall survival (OS), progression-free survival (PFS), recurrence-free survival (RFS), and disease-specific survival (DSS) were subjected to Kaplan Meier plotter (<http://kmplot.com/analysis/>)^[21]. The portal can assess the effect of SAA1 on the survival rate in HCC. The TCGA samples and gene expression omnibus (GEO) series samples were included in the liver tumor of the Kaplan Meier plotter portal. The standard level of high or low expression group was achieved by the best cutoff, which was between the lower and upper quartiles, and the best performing threshold was used as a cutoff.

Immune infiltration analysis

The correlation between SAA1 expression and the tumor purity of HCC was measured in TIMER (<http://timer.cistrome.org/>)^[22], a comprehensive resource for systematic analysis of immune infiltrates. The interaction between SAA1 and the immune system was assessed in TISIDB^[23], an integrated repository portal for tumor-immune system interactions. In this study, the transcriptomics data of SAA1 and clinical data of LIHC from TCGA were included to evaluate the correlation, elucidating the potential

interaction between SAA1 and the immune system.

Gene set enrichment analysis

The enrichment analysis of the Kyoto encyclopedia of genes and genomes pathways (KEGG) was conducted with gene set enrichment analysis (GSEA)^[24]. The standard of sample clustering was based on the median level of SAA1 expression. The number of permutations was set as 1000, and the enrichment statistic was weighted. The Signal2Noise was used as a metric for ranking genes. The minimum sets were above 15 genes. The normalized enrichment score (NES) was used to evaluate the enrichment intensity of SAA1 in indicated pathways. A *P* value < 0.05 and a false discovery rate < 0.05 for an enrichment gene sets were considered as the statistically significant.

GEO analysis

GSE125336 data set was from GEO, a public functional genomics data repository portal. The sequencing data were downloaded *via* the SangerBox tool (<https://shengxin.ren/>). This dataset was collected from the GPL21103 platform (Illumina HiSeq 4000).

Protein-protein interaction network construction

Similar genes that have a similar expression pattern with SAA1 in HCC were obtained from GEPIA. The top 300 similar genes were subjected to protein-protein interaction (PPI) analysis in Metascape^[25].

Statistical analysis

The data were shown as mean ± standard deviation, and the difference between the two groups was determined by student's *t*-test. The correlation analysis was assessed by the Spearman method. The log-rank method was used to perform survival analysis. *P* value < 0.05 was considered a significant statistical difference.

RESULTS

SAA1 was downregulated in HCC and predicted the favorable prognosis for HCC patients

SAA1 as an acute-phase protein, which was reported to be involved in the regulation of pro-inflammation or anti-inflammation signaling, is controversial^[4,26]. Furthermore, the expression of SAA1 in HCC was also unclear. Firstly, we evaluated the expression of SAA1 in HCC and found that SAA1 expression was decreased in liver tumor tissues compared with normal liver tissues (Figure 1A). Then, to determine the clinical significance of the downregulated SAA1 in HCC, we conducted survival analysis. As shown in Figure 1B-D, the patients with lower SAA1 showed poorer survival rates from OS, PFS, and RFS analysis. In detail, the median survival time of HCC patients with low SAA1 expression was significantly shorter than those with high SAA1 expression (OS: 33.5 mo *vs* 70.5 mo; PFS: 11.33 mo *vs* 29.3 mo; DSS: 81.87 mo *vs* 84.83 mo; RFS: 11.97 mo *vs* 34.4 mo). The Cox proportional hazards model also showed favorable prognosis of low SAA1 expression, and the hazard ratio value with 95% confidence interval (CI) of low SAA1 expression in OS, PFS, DSS, and RFS was 0.6 (0.43-0.85), 0.59 (0.43-0.81), 0.59 (0.37-0.91), 0.58 (0.41-0.83) respectively (Table 1). These results demonstrated that the decreased level of SAA1 in HCC could serve as a good prognostic biomarker for HCC patients.

SAA1 is closely involved in the development of HCC

SAA1 expression is downregulated in the liver tumor tissues, as above demonstrated, and the clinical significance of SAA1 in survival time was also confirmed, as shown in Figure 1. To understand further the expression of SAA1 in the development of HCC, we analyzed SAA1 expression in some clinical features, such as tumor grade, patient disease stage, and the TP53 mutation or not. As shown in Figure 2A, SAA expression was further decreased with the increase of tumor grade. Similarly, SAA1 expression was also decreased with increased patient disease stage (Figure 2B), suggesting that SAA1 was closely involved in the progression of HCC. Moreover, TP53 mutation is an important risk factor contributing to the poor prognosis in HCC^[27]. Thus, this study included the TP53 mutation in the analysis of SAA1 in HCC, suggesting interestingly that SAA1 expression was further decreased in tumor tissues with TP53 mutation than those without TP53 mutation (Figure 2C). The correlation analysis between SAA1

Table 1 The survival analysis based on the serum amyloid A1 expression

Survival analysis	Median time in mo		HR (95%CI)	P value
	SAA1 high	SAA1 low		
OS	70.5	33.5	0.6 (0.43-0.85)	0.004
PFS	29.3	11.33	0.59 (0.43-0.81)	0.00091
DSS	84.73	81.87	0.59 (0.37-0.91)	0.017
RFS	34.4	11.97	0.58 (0.41-0.83)	0.0021

SAA1: Serum amyloid A1; OS: Overall survival; PFS: Progression-free survival; DSS: Disease-specific survival; RFS: Recurrence-free survival.

expression and the frequency of TP53 mutation also showed that lower SAA1 expression was accompanied by the high incidence of TP53 mutation ($P < 0.05$, [Figure 2D](#)).

SAA1 is a specific prognostic marker for HCC patients without hepatitis virus infection

As shown in [Figure 1](#), SAA1 could be a favorable prognostic biomarker for HCC. Considering the importance of SAA1 in the regulation of inflammation and the interaction between hepatitis virus infection and tumor in HCC, we evaluated the potential application of SAA1 as a prognostic biomarker in HCC patients with and without hepatitis virus infection. The patients with high SAA1 presented with a good possibility to survive in OS, PFS, and RFS analysis ([Figure 3](#)). On the contrary, there was no significant difference in the HCC patients with hepatitis virus infection ([Figure 3D-F](#)), suggesting that hepatitis virus infection could affect the value of SAA1 in the prediction of HCC prognosis.

SAA1 expression is closely associated with immune infiltration in HCC

SAA1 was downregulated in HCC, and the decreased SAA1 expression could predict the poor prognosis of HCC patients, especially in patients without hepatitis virus infection ([Figure 3](#)). However, there was no statistical significance in those patients with hepatitis virus infection. As an inflammation-responsive gene, some reports confirmed the expression difference of SAA1 in the physiological response, and the hepatitis virus infection was the most important driving factor in the development of HCC. Thus, it was easy to understand the difference of SAA1 as a prognosis factor in HCC patients with and without hepatitis virus infection.

As attention increases regarding immune regulation in the development of HCC, we further evaluated the importance of SAA1 in the tumor immunomodulation. Firstly, the correlation of SAA1 expression and tumor purity was analyzed, and the negative correlation between SAA1 and tumor purity was confirmed ([Figure 4A](#)), which was also consistent with the downregulated SAA1 expression in HCC (as mentioned in [Figure 1](#)). Moreover, the CIBERSORT method was applied to evaluate the correlation between SAA1 and immune score. The results showed a significant positive correlation ($P < 4.93 \times 10^{-11}$, [Figure 4B](#)), suggesting that the lower expression of SAA1 in HCC was followed with a low immune score. Next, this study analyzed the correlation between SAA1 and 27 kinds of tumor-infiltrating lymphocytes (TILs) across human pan-cancers. As shown in [Figure 4C](#), SAA1 expression was widely positively correlated with TILs in many human cancer types, especially in bladder urothelial carcinoma, glioblastoma multiforme, kidney chromophobe, kidney renal papillary cell carcinoma, testicular germ cell tumor, and thyroid carcinoma. The positive correlation between SAA1 expression and TILs was also observed in LIHC. SAA1 was remarkably correlated with the abundance of activated CD8 T cells ($r = 0.292$, $P = 1.12 \times 10^{-8}$, [Figure 5A](#)), natural killer (NK) cells ($r = 0.289$, $P = 1.48 \times 10^{-8}$, [Figure 5B](#)), natural killer T (NKT) cells ($r = 0.324$, $P = 1.87 \times 10^{-10}$, [Figure 5C](#)), T helper (Th)1 cells ($r = 0.424$, $P = 2.2 \times 10^{-16}$, [Figure 5D](#)), and Th17 cells ($r = 0.251$, $P = 9.46 \times 10^{-7}$, [Figure 5F](#)), but there was no significant correlation between SAA1 and the abundance of Th2 cells ($P = 0.619$, [Figure 5E](#)).

Decreased SAA1 is closely associated with the immune tolerance of HCC

The decreased SAA1 expression was followed by lower immune score, especially with the lower cytotoxic T cell infiltration in the HCC, suggesting that SAA1 might

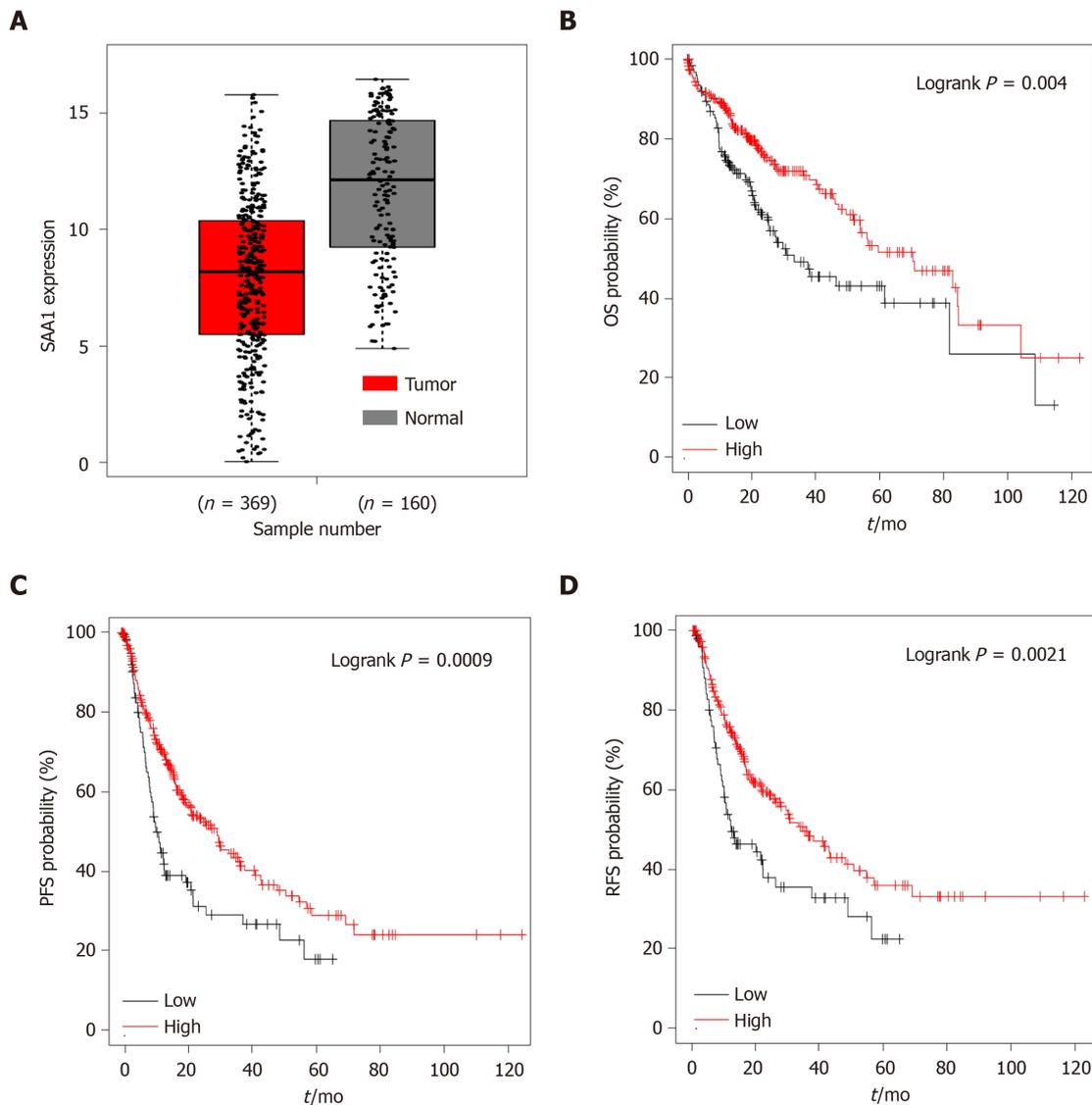


Figure 1 Serum amyloid A1 expression in hepatocellular carcinoma tumor and surrounding non-tumor or genotype-tissue expression liver tissues and its effect on the survival rate of hepatocellular carcinoma patients. A: A total of 160 hepatocellular carcinoma (HCC) tumor samples and 369 normal liver tissues were included to evaluate the serum amyloid A1 (SAA1) transcript expression level. Normal liver tissues are comprised of surrounding non-tumor and genotype-tissue expression liver tissues; B: HCC patients were divided into two groups based on the SAA1 expression level, and conducted the overall survival (OS); C: Progression-free survival (PFS); D: Recurrence-free survival analysis (RFS). The log-rank P value was subjected to evaluate the statistical difference.

contribute to the immune tolerance of HCC. To explain the hypothesis, the GSE125336 dataset was included, and the data showed that SAA1 expression was decreased in the patient group resistant to anti-PD1 therapy than those responsive to anti-PD1 therapy (Figure 6A). The GSEA was included to evaluate the significant pathways of SAA1 in LIHC. The results showed that the most enriched pathways related to decreased SAA1 included cytokine-cytokine receptor interaction (NES = -2.43, Figure 6B), NK cell-mediated cytotoxicity (NES = -2.15, Figure 6C), and antigen processing and presentation (NES = -2.08, Figure 6D).

Two signature genes associated with SAA1 were identified as favorable for prognosis of HCC

The gene enrichment analysis showed that higher SAA1 was enriched in the anti-tumor immunity pathways, including cytokine-cytokine receptor interaction, NK cell-mediated cytotoxicity, and antigen processing and presentation (Figure 6). High SAA1 predicted the favorable prognosis for HCC patients. To evaluate further the importance of SAA1 in the prognosis of HCC, we first conceived the similar genes of SAA1, which were analyzed with PPI analysis. As Figure 7A shows, SAA1 closely interacted with CXCL2, CCL23, and C5AR1. To determine the role of the three

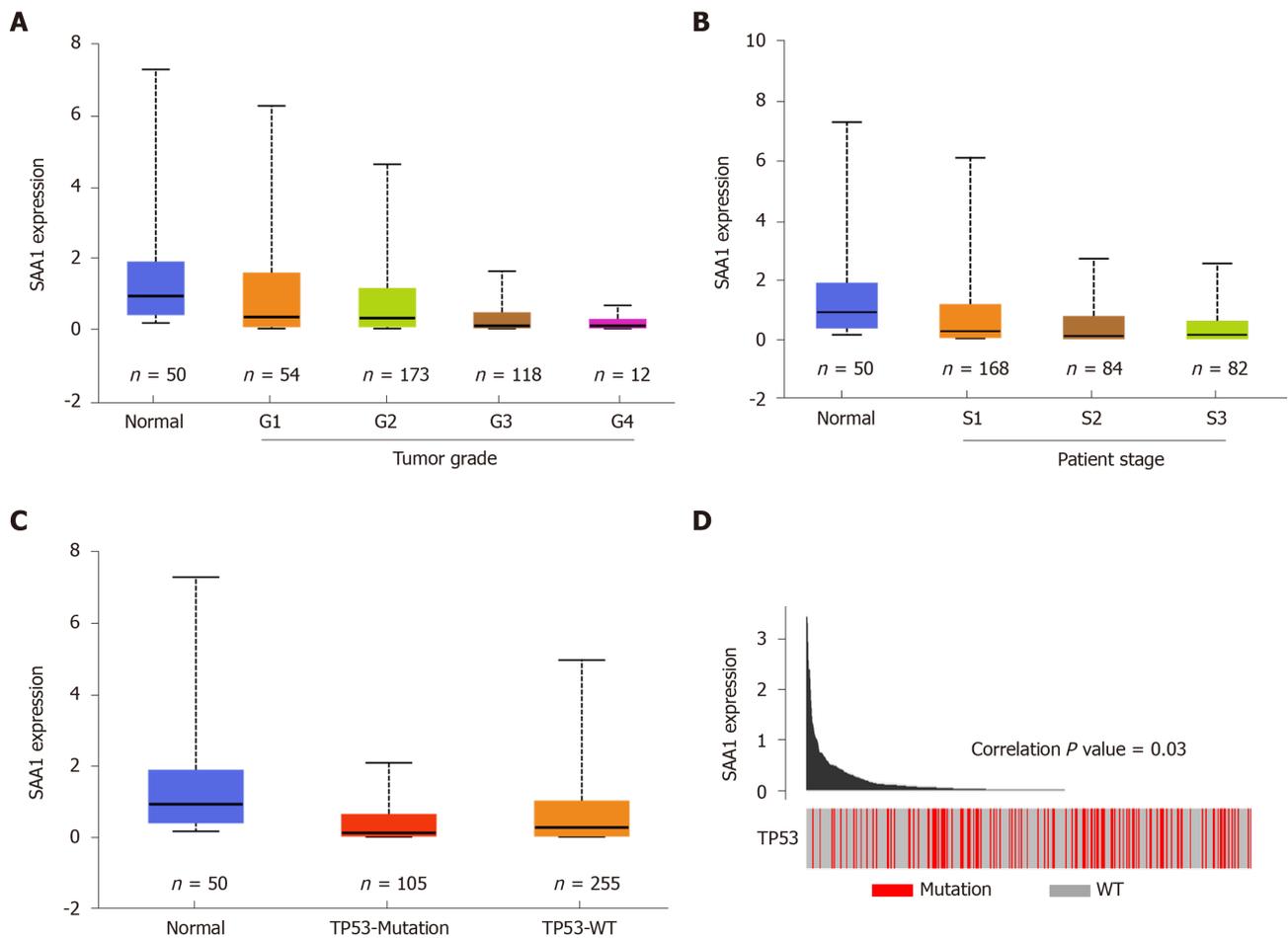


Figure 2 Serum amyloid A1 expression was correlated with hepatocellular carcinoma development. A: The tumor tissues with different grades and surrounding non-tumor tissues were included to analyze the serum amyloid A1 (SAA1) expression; B: The tumor tissues with different disease stage and non-tumor tissues were conducted with the SAA1 expression analysis; C: The SAA1 expression was analyzed in tumor tissues with TP53 mutation or wild type, the non-tumor tissues were used as control; D: The correlation of SAA1 expression and the TP53 mutation was analyzed in the cancer genome atlas portal. SAA1: Serum amyloid A1; WT: Wild type; G1: Tumor grade 1; G2: Tumor grade 2; G3: Tumor grade 3; G4: Tumor grade 4; S1: Patient disease stage 1; S2: Patient disease stage 2; S3: Patient disease stage 3.

associated genes in HCC, their expression levels were assessed (Figure 7B). CXCL2, CCL23, and C5AR1 were all decreased in HCC, which was similar to SAA1. Furthermore, the results of the overall survival analysis of the three genes are presented in Figure 7C and show that higher CXCL2 or CCL23 predicted better survival time. However, there was no clinical value of C5AR1 in the prediction of prognosis for HCC. Taken together, these results indicated that CXCL2 and CCL23, as an interacted protein of SAA1, could be complementary prognostic biomarkers for HCC patients.

DISCUSSION

SAA1, as the most important preproprotein of SAA, is an acute-phase protein involved in viral and bacterial infection, autoimmune disease, and some tumor pathogenesis^[28]. To date, most SAA1 research focuses on its application as a disease marker. As an inflammation-related gene, SAA1 has been reported as a biomarker for the detection of stroke, ankylosing spondylitis, and acute aortic and acute hepatic injury^[29-31]. However, whether SAA1 exerts * pro-inflammatory or anti-inflammatory role is still controversial. Lee *et al*^[4] reported that SAA1 protein could promote inflammatory intestinal disease by inducing pro-inflammatory Th17 cell differentiation^[4]. On the contrary, Cheng *et al*^[26] identified that SAA1 could decrease lipopolysaccharide (LPS)-induced intestinal inflammation by directly binding to LPS to form a complex and induce LPS clearance by macrophage.

Similar to the inflammatory disease, the biological functions of SAA1 in tumors are

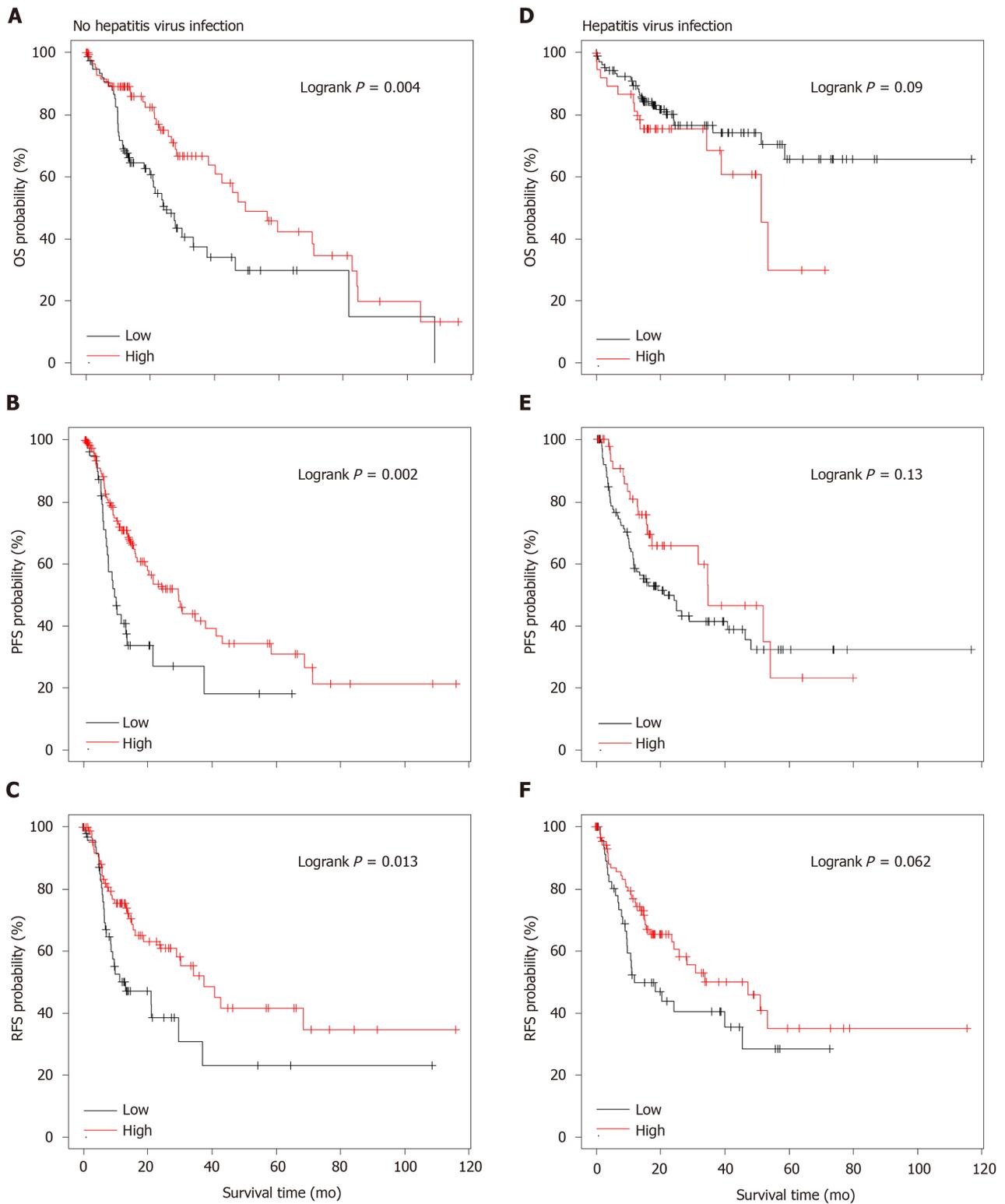


Figure 3 Serum amyloid A1 expression was a specific prognostic biomarker for hepatocellular carcinoma. A: The patients without hepatitis virus infection were subjected to overall survival (OS); B: Progression-free survival (PFS); C: Recurrence-free survival (RFS) analysis based on SAA1 expression level; D: The patients with hepatitis virus infection were subjected to OS; E: PFS; F: RFS analysis based on SAA1 expression level.

different. SAA1 was reported to be overexpressed in ovarian and renal cell carcinoma^[32,33]; and serum SAA1 expression is positively correlated with the development of melanoma. Besides, SAA1 induced interleukin-10 production in neutrophils from melanoma patients, suggesting that SAA1 is a negative prognostic marker in melanoma^[34]. In HCC, SAA1 was identified as the hub gene in the PPI analysis of differentially expressed genes^[35], with unclear expression.

Hence, this study aimed to evaluate the expression of SAA1 and its clinical

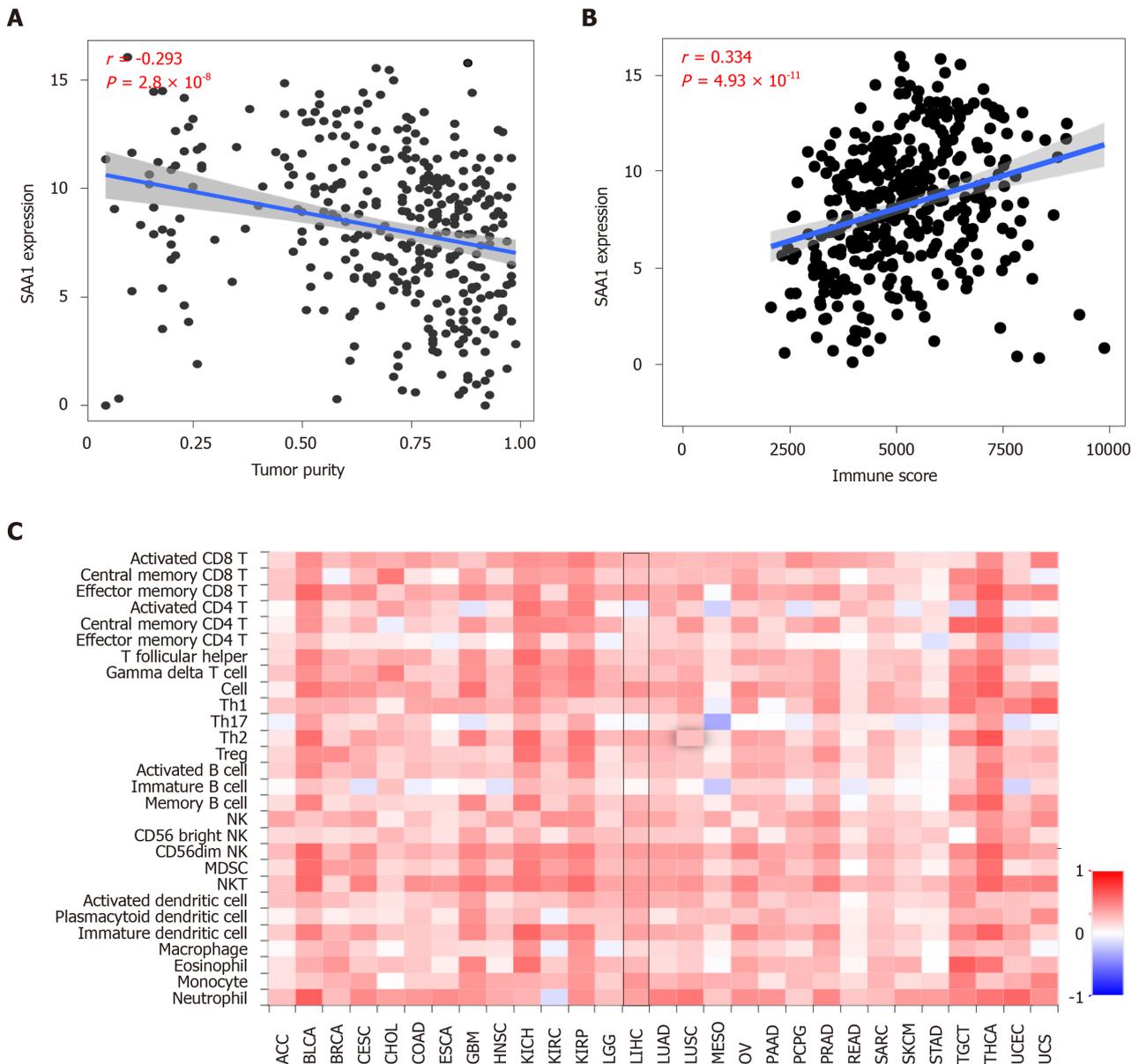


Figure 4 Serum amyloid A1 expression was correlated with immune infiltration in hepatocellular carcinoma. A: The correlation between serum amyloid A1 (SAA1) expression level and the tumor purity was analyzed with CIBERSORT; B: The correlation between SAA1 expression and the immune score was analyzed with CIBERSORT; C: The correlation between SAA1 expression and tumor-infiltrating lymphocytes across human cancer was conducted in TISIDB with Spearman method. SAA1: Serum amyloid A1; TILs: Tumor-infiltrating lymphocytes; NK: Natural killer cell; NKT: Natural killer T cell; ACC: Adrenocortical carcinoma; BLCA: Bladder Urothelial Carcinoma; BRCA: Breast invasive carcinoma; CESC: Cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL: Cholangiocarcinoma; COAD: Colon adenocarcinoma; ESCA: Esophageal carcinoma; GBM: Glioblastoma multiforme; HNSC: Head and Neck squamous cell carcinoma; KICH: Kidney chromophobe; KIRC: Kidney renal clear cell carcinoma; KIRP: Kidney renal papillary cell carcinoma; LGG: Brain lower-grade glioma; LIHC: Liver hepatocellular carcinoma; LUAD: Lung adenocarcinoma; LUSC: Lung squamous cell carcinoma; MESO: Mesothelioma; OV: Ovarian serous cystadenocarcinoma; PAAD: Pancreatic adenocarcinoma; PCPG: Pheochromocytoma and paraganglioma; PRAD: Prostate adenocarcinoma; READ: Rectum adenocarcinoma; SARC: Sarcoma; SKCM: Skin cutaneous melanoma; STAD: Stomach adenocarcinoma; TGCT: Testicular germ cell tumors; THCA: Thyroid carcinoma; UCEC: Uterine corpus endometrial carcinoma; UCS: Uterine carcinosarcoma.

significance in HCC. Firstly, we confirmed the downregulated expression of SAA1 in HCC tumor tissues (Figure 1A). The correlation analysis between SAA1 expression and tumor purity further confirmed its decreased expression in HCC tumor tissues (Figure 4A). Moreover, SAA1 expression decreased with increased tumor grade and disease stage (Figure 2A and B); and the lower SAA1 expression was accompanied with the higher frequency of TP53 mutation (Figure 2C and D), a marker of poor prognosis in HCC. The above results suggested that decreased SAA1 expression was closely involved in the progression of HCC. In the further study of clinical significance, the effect of SAA1 on the survival rate revealed that the lower SAA1 expression in HCC predicted worse survival time (Figure 1B-D), especially in HCC patients without hepatitis virus infection (Figure 3).

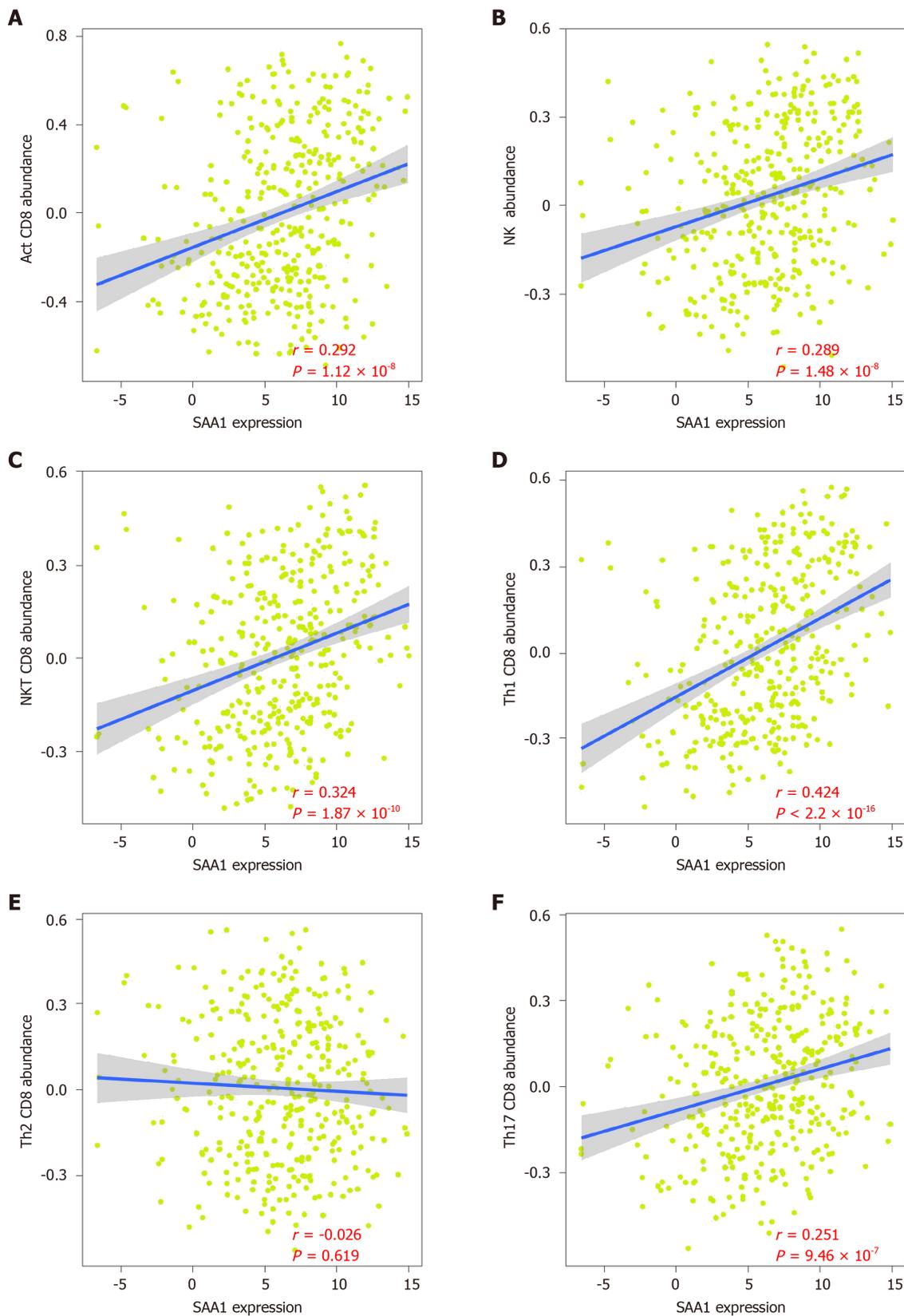


Figure 5 The association between serum amyloid A1 expression and immune cell abundance in hepatocellular carcinoma. A: A total of 373 hepatocellular carcinoma samples were included to analyze the correlation between SAA1 expression and activated CD8 T cell; B: Natural killer (NK) cell; C: Natural killer T (NKT) cell; D: Th1; E: Th2; F: Th17 cells abundance. SAA1: Serum amyloid A1.

Considering the induction of SAA1 in hepatitis by virus infection or tissue injury, the hepatitis virus infection-induced SAA1 expression could interfere with the prognostic value of SAA1 in HCC. This data also indicated that the immune signaling pathways might be closely associated with SAA1-mediated HCC progression.

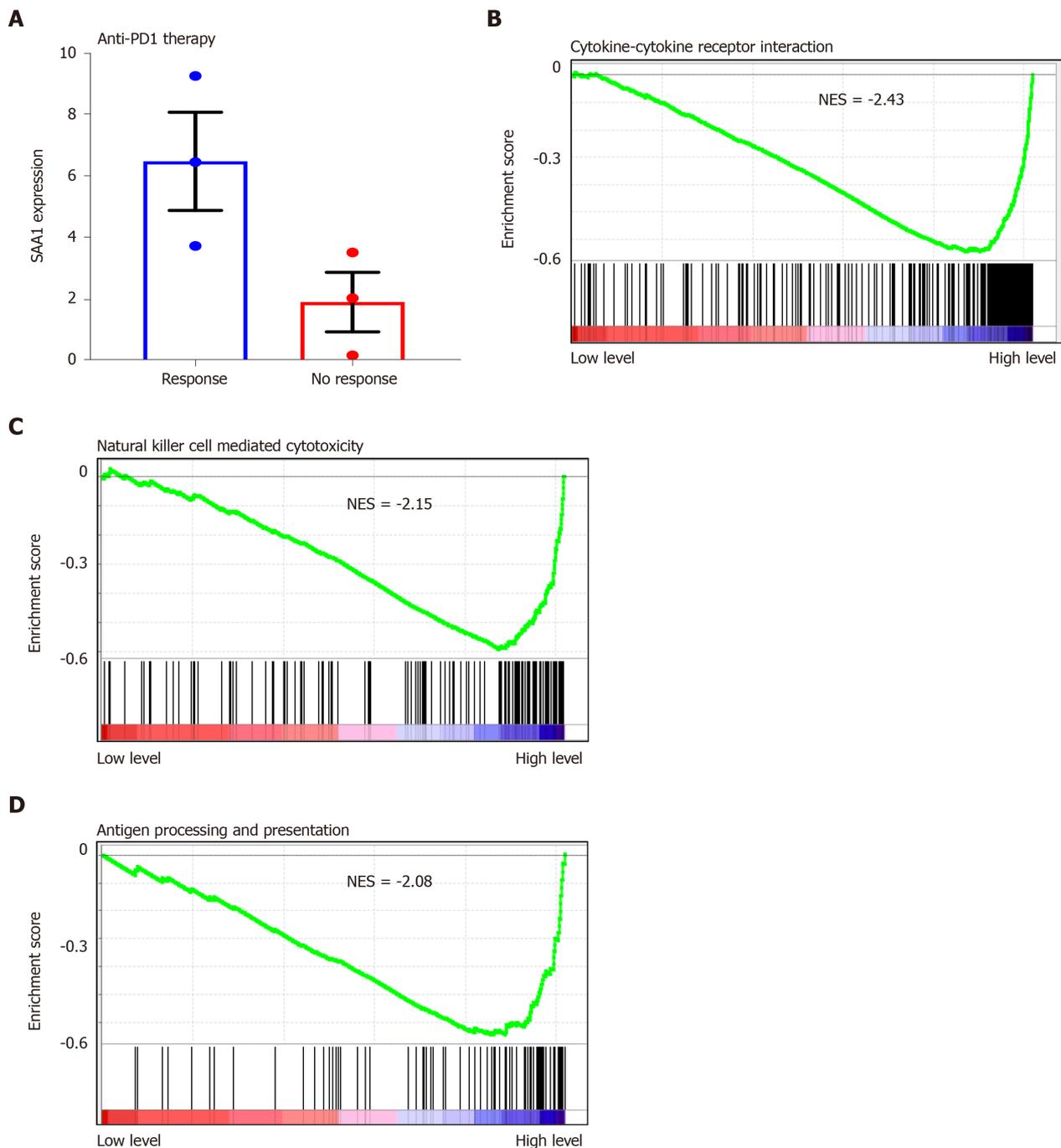


Figure 6 Low serum amyloid A1 expression was negatively correlated with the anti-immunity signaling. A: GSE125336 was used to evaluate the serum amyloid A1 expression in patients who were responsive and resistant to the anti-PD1 antibody; B-D: The gene set enrichment analysis in hepatocellular carcinoma revealed the top three pathways with KEGG. SAA1: Serum amyloid A1; NES: Normalized enrichment score; GSEA: Gene set enrichment analysis.

Interestingly, the immune infiltrating analysis showed that lower SAA1 expression represented lower immune score and immune cells infiltration (Figure 4B and C), especially in the cytotoxic T cells and anti-tumor associated immune cells, including activated CD8 T, NK, NKT, Th1, and Th17 cells (Figure 5). In the exploration of potential molecular mechanisms, the lower SAA1 might contribute to immune tolerance (Figure 6), which could be a potential therapeutic target for enhanced anti-tumor immunity. More significantly, this study also identified two signature genes that interacted with SAA1 as compensative prognostic biomarkers (Figure 7), which could enhance the prognostic value of SAA1 in HCC.

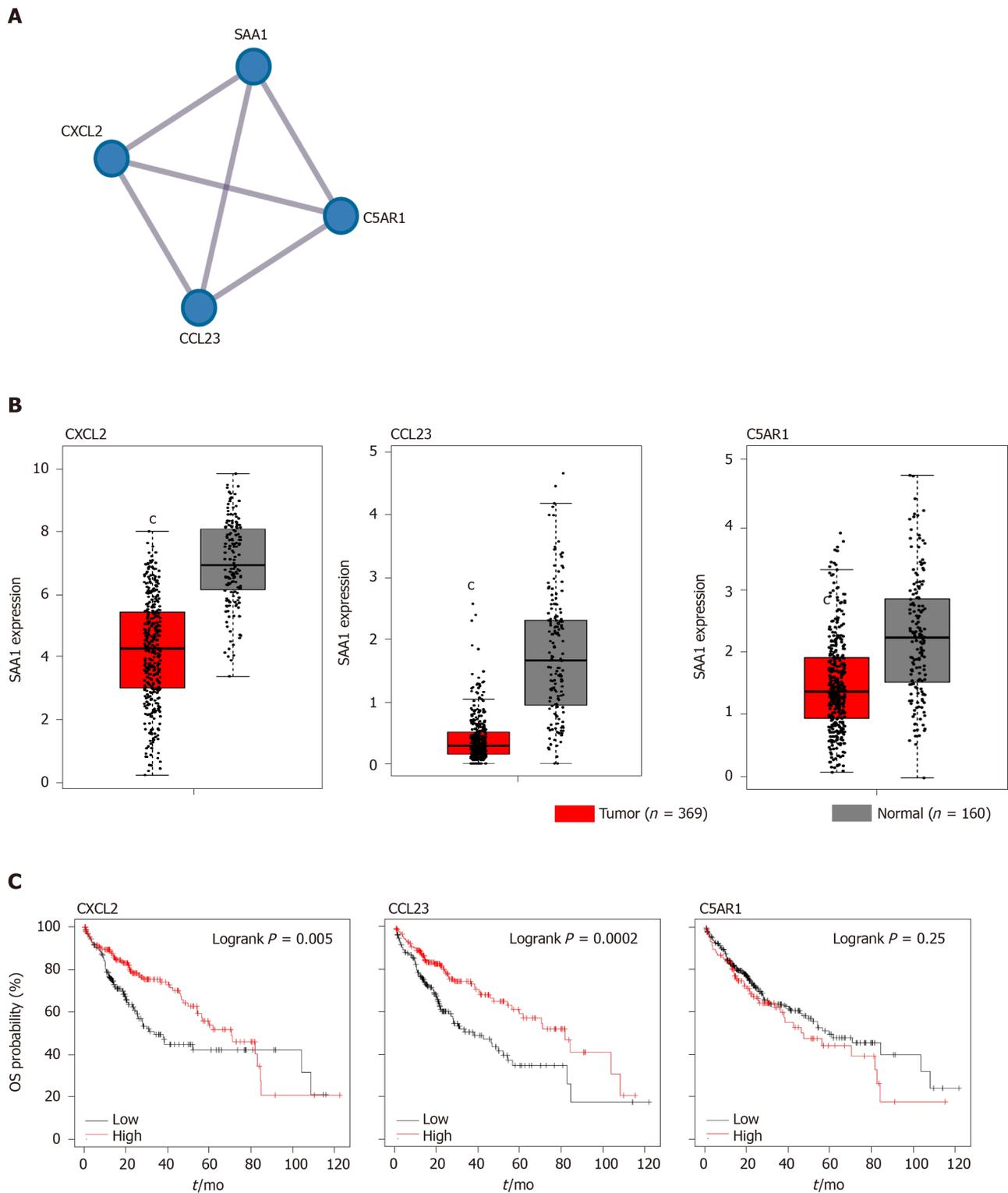


Figure 7 The two signature genes interacted with serum amyloid A1 and acted as a prognostic marker for hepatocellular carcinoma. A: The similar genes of serum amyloid A1 were achieved in GEPIA, and the similar genes were conducted in protein-protein interaction analysis; B: The expression of CXCL12, CCL23, and C5AR1 in hepatocellular carcinoma and non-tumor tissues were analyzed in GEPIA portal; C: The overall survival analysis was conducted based on the expression level of CXCL12, CCL23, and C5AR1. SAA1: Serum amyloid A1; OS: Overall survival; CXCL2: C-X-C motif chemokine ligand 2; CCL23: C-C motif chemokine ligand 23; C5AR1: Complement C5a receptor 1.

CONCLUSION

In summary, this study identified the downregulated expression of SAA1 as a potential prognostic biomarker for HCC, and decreased SAA1 was closely associated with immune tolerance signaling pathways. SAA1 could be an encouraging drug target for anti-tumor immunity. More experiments should be conceived to confirm the

significance of SAA1 in HCC immunotherapy.

ARTICLE HIGHLIGHTS

Research background

Serum amyloid A1 (SAA1) is regarded as an important regulator in the immune network. Recently, SAA1 was reported to regulate the development of some cancers, and it may function as a biomarker for some cancers.

Research motivation

SAA1 is a potential biomarker in some cancers, but its expression and function in hepatocellular carcinoma (HCC) are still unclear.

Research objectives

The project was designed to determine the expression level of SAA1 in HCC and to analyze the association between SAA1 expression and prognosis of HCC patient and its potential regulation on the immune network.

Research methods

GEPIA web-based analytical tool was subjected to evaluate the expression of SAA1 in HCC. The patients from The Cancer Genome Atlas-Liver Hepatocellular Carcinoma (TCGA-LIHC) were sub-grouped according to the median expression level of SAA1. Then, the Kaplan-Meier portal was used to analyze the survival curve of the high or low SAA1 expression groups. UALCAN tool was used to evaluate the expression of SAA1 in different tumor grades, stages, and TP53 mutation or not. The CIBERSORT method was subjected to test the correlation between SAA1 expression and immune infiltration score in HCC. TISIDB integrated portal was conducted to reveal the association between SAA1 level and the tumor-infiltrating lymphocytes. GSE125336 dataset was subjected to analyze the SAA1 level according to the anti-PD1 response. Gene set enrichment analysis method was subjected to analyze the enriched signaling pathways based on SAA1 in HCC. The co-expression genes of SAA1 was subjected to Metascape to evaluate the hub genes. These hub genes were subjected to GEPIA and Kaplan-Meier to analyze the expression and overall survival.

Research results

SAA1 level was downregulated in the liver tumor, and the lower expression could function as a prognostic biomarker in overall survival, progression-free survival, and disease-specific survival of HCC. Besides, the SAA1 expression level was closely associated with tumor grades and patient stages. More interestingly, the HCC patients with TP53 mutation showed a lower expression of SAA1. SAA1 could act as a good prognostic marker in HCC patients without hepatitis infection. SAA1 expression was positively correlated with the immune infiltration score and tumor-infiltrating lymphocytes. Low SAA1 expression was negatively correlated with anti-immune signaling, including cytokine-cytokine receptor interaction, natural killer cell-mediated cytotoxicity, and antigen processing and presentation. CXCL2 and CCL23 were identified as the hub genes that interacted with SAA1 and acted as prognostic markers for HCC.

Research conclusions

SAA1 expression is low in HCC, and its expression is closely associated with the progression of HCC. Besides, SAA1 can act as a poor prognostic biomarker for HCC patients. More interestingly, SAA1 is closely involved in the regulation of the immune infiltrating process.

Research perspectives

In this study, SAA1 was identified as a negative regulator for HCC, and its expression might be a poor prognostic biomarker for HCC patients. Interestingly, the SAA1 expression was closely related to the tumor-infiltrating immune cells network. However, these findings were based on the expression levels. SAA1 is a secreted protein from the liver, and the secreted levels could be much more practical clinically, especially in the prognosis analysis.

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Retrospective Cohort Study

Epidemiology of perforating peptic ulcer: A population-based retrospective study over 40 years

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Institutional review board

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Abstract

BACKGROUND

The incidence of peptic ulcer disease has decreased during the last few decades, but the incidence of reported peptic ulcer complications has not decreased. Perforating peptic ulcer (PPU) is a severe form of the disease.

AIM

To assess trends in the incidence, presentation, and outcome of PPU over a period of 40 years.

METHODS

This was a single-centre, retrospective, cohort study of all patients admitted to Levanger Hospital, Norway, with PPU from 1978 to 2017. The patients were identified in the Patient Administrative System of the hospital using International Classification of Diseases (ICD), revision 8, ICD-9, and ICD-10 codes for perforated gastric and duodenal ulcers. We reviewed the medical records of the patients to retrieve data. Vital statistics were available for all patients. The incidence of PPU was analysed using Poisson regression with perforated ulcer as the dependent variable, and sex, age, and calendar year from 1978 to 2017 as covariates. Relative survival analysis was performed to compare long-term survival over the four decades.

RESULTS

Two hundred and nine patients were evaluated, including 113 (54%) men. Forty-six (22%) patients were older than 80 years. Median age increased from the first to the last decade (from 63 to 72 years). The incidence rate increased with increasing age, but we measured a decline in recent decades for both sexes. A significant increase in the use of acetylsalicylic acid, from 5% (2/38) to 18% (8/45), was

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observed during the study period. Comorbidity increased significantly over the 40 years of the study, with 22% (10/45) of the patients having an American Society of Anaesthesiologists (ASA) score 4-5 in the last decade, compared to 5% (2/38) in the first decade. Thirty-nine percent (81/209) of the patients had one or more postoperative complications. Both 100-day mortality and long-term survival were associated with ASA score, without significant variations between the decades.

CONCLUSION

Declining incidence rates occurred in recent years, but the patients were older and had more comorbidity. The ASA score was associated with both short-term mortality and long-term survival.

Key Words: Perforated peptic ulcer; American Society of Anaesthesiologists classification; Charlson Comorbidity Index; Gastric ulcer; Duodenal ulcer; Epidemiology; Incidence; Clavien-Dindo classification of complications; Mortality

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Core Tip: We sought to review the epidemiology of perforated peptic ulcer in a stable population at a primary hospital over a period of 40 years. The incidence rate has declined in recent decades for both sexes, though median age and comorbidity have both increased. Complications occurred more frequently and were more serious in recent decades, in older patients, in patients with comorbidities, and in patients with higher American Society of Anaesthesiologists (ASA) scores. Both short- and long-term survival were associated with ASA score, without significant variation between the decades.

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INTRODUCTION

The incidence of peptic ulcer disease (PUD), either gastric or duodenal, has decreased during the last few decades with the discovery of the role of *Helicobacter pylori* (*H. pylori*)^[1-5]. However, the incidence of peptic ulcer complications has not decreased in the same manner^[6,7]. Bleeding and perforation are the most severe complications of PUD^[8]. Due to progress in endoscopic and interventional radiological techniques, bleeding is mostly considered a medical emergency and outcomes have improved^[9]. Although bleeding is far more common than perforated peptic ulcer (PPU), perforation accounts for most deaths associated with PUD^[6,10,11] and PPU remains a surgical emergency, with high short-term mortality of 10%-30%^[12-14].

Surgical repair with closure of the perforation, with or without an omental pedicle, is the preferred treatment for PPU^[11,15,16]. This repair can be achieved through either open repair or laparoscopy^[15,17]. Previous studies have shown a change in the demography of PPU over the last few decades, with an increasing age at diagnosis in recent years^[15,18]. Less is known about the implications of increased age in patients with PPU in regards to treatment, complications, and mortality^[12,13,15,19].

Thus, the aim of this study was to investigate changes in demography and the effect on treatment, complications, and short- and long-term mortality in patients admitted to our hospital with PPU over four decades.

MATERIALS AND METHODS

Study population

Levanger Hospital is located in Middle Norway, with a catchment area of 85000 at the start of the study period and 100000 in recent years. This retrospective study included all patients diagnosed with benign PPU between January 1978 and December 2017.

The patients were identified in the Patient Administrative System using International Classification of Diseases (ICD), ICD-8 codes (531.00-531.09, 532.00, 533.00, 534.00), ICD-9 codes (531.1-531.2, 531.5-531.6, 532- 533 with same decimals as for 531), and ICD-10 codes (K25.1-K25.2, K25.5-K25.6, K26-K28 with same decimals as for K25). Additional searches were done for the surgical codes for gastrophary and duodenography. Demographic and clinical data were collected from the hospital records.

The American Society of Anaesthesiologists (ASA) score was used to compare preoperative comorbidity^[20], which was further classified using the Charlson Comorbidity Index^[21]. Complications were classified according to the Clavien-Dindo classification^[22,23]: Grade I, any small deviation from the normal postoperative course treated at bedside or with certain drugs (*e.g.*, antiemetics); grade II, complications treated with transfusion or medicines other than allowed for grade 1 (*e.g.*, antibiotics); grade III, complications requiring endoscopic, radiological, or surgical intervention; grade IV, life-threatening complications; grade V, complications leading to death of the patient.

Definitions

The incidence of PPU was defined as the number of new cases of PPU in the defined population within 1 year. The incidence rate (IR) was defined as the incidence divided by the total person-time at risk during the same year. The incidence rate ratio (IRR) was defined as the ratio between two incidence rates.

Ulcer localisation was considered gastric when present anywhere in the stomach, including pyloric ulcers. Localisation distal to the pylorus was categorised as duodenal.

Study ethics

The study was approved by the Regional Ethics Committee (REK Midt # 2018/1510). We also performed a data protection impact assessment in accordance with the European General Data Protection Regulation before collecting data^[24].

Statistical analysis

The medians of two samples, such as age in men compared to women, were compared by the Wilcoxon rank sum test. The Cochran-Armitage test was used to test for trends in proportions. The Joncheere-Terpstra test was used to test for the distribution of age as a dependent variable across decade groups as an independent variable. Ordinal logistic regression was used to test associations in doubly ordered $r \times c$ tables, such as for the Charlson Comorbidity Index and ASA score by decades. Logistic regression analysis was used to test for an association between 100-day mortality as a dependent variable and sex, age, year of admittance, Charlson Comorbidity Index, and ASA score as independent variables.

The incidence of PPU was analysed using Poisson regression with perforated ulcer as the dependent variable and sex, age in 5-year intervals (20-24, 25-29, up to 90-94, 95-99), and calendar year from 1978 to 2017 as covariates. Non-linear relationships were explored using fractional polynomials^[25]. Fractional polynomials are a method for checking if the effect of an explanatory variable is linear, as in the basic Poisson regression model.

The age and sex distribution for the 10 municipalities around Levanger Hospital for every year from 1980 to 2016 was obtained from Statistics Norway. To study long-term survival in this patient population over 40 years, we performed the relative survival analysis using the Ederer II method^[26,27]. Multivariable analyses were performed using the full likelihood approach. Survival probabilities by sex and age for the Norwegian population for every year from 1978 were downloaded from the Human Mortality Database^[28].

Two-sided *P* values < 0.05 were considered significant. Medians were reported with the range (minimum to maximum) and standard deviation (SD), as well as 95% confidence intervals (CIs), as appropriate. Analyses were carried out in Stata 16 (Stata Corp LP, College Station, Texas, United States), IBM SPSS Statistics 25 (SPSS Inc., Chicago, IL, United States), and StatXact 9 (1050 Winter St, Waltham, MA, United States).

RESULTS

Patient characteristics

Over 40 years, 209 patients with PPU were treated, including 113 (54%) men and 46 (22%) patients older than 80 years. In the first two decades of the observation period, PPU occurred more frequently among men than women (ratio 3:2). In the last two decades, this has evened out to nearly 1:1. Eighty-five percent of the patients presented within 24 h after the onset of pain. Only 7 patients (3.3%) were admitted with a systolic blood pressure < 90 mmHg.

Trends in patient characteristics according to decade of treatment are shown in [Table 1](#). The median age increased from 63 to 72 years from the first 10 years to the last 10 years of study ($P = 0.018$). The mean time from debut of symptoms until hospital admission increased from 7 (SD 9) h in the first 10 years to 13 (SD 14) h in the last 10 years ($P = 0.019$).

Incidence rates

The IR varied between 3.3-5.3 and 4.2-8.7 per 100000/year for women and men, respectively, throughout the observation period. The IR increased with increasing age, without an upper limit (see [Figure 1](#)), until the second decade of the study period in men and to the third decade of the study period in women. Recent years have shown a declining tendency in both sexes (see [Figure 1](#)). Adjusted IRRs obtained from Poisson regression with calendar year and age as covariates are shown in [Table 2](#). The IR increased significantly with age for both gastric and duodenal PPU.

[Figure 2](#) shows that the incidence of gastric ulcer perforations peaked around 1984, whereas duodenal ulcer perforations peaked approximately 15 years later.

Predisposing factors

The use of acetylsalicylic acid increased significantly over 40 years, from 5% (2/38) the first 10 years, to 18% (8/45) the last 10 years ([Table 1](#)). The proportion of patients with PPU who used non-steroidal anti-inflammatory drugs (NSAIDs) or smoked did not change significantly throughout the course of the study.

Comorbidity

The Charlson Comorbidity Index and ASA score increased significantly in patients with PPU over 40 years ([Table 1](#)). In 1978-1987, 5% (2/38) of the patients had an ASA score 4-5, increasing to 22% (10/45) during 2008-2017.

Treatment

Two hundred and six patients had open surgery; 201 with suture and omental patch, 5 with resections. Three patients were not operated on; one was 90 years old and about to die at admission. Another 90-year-old was deemed too sick to tolerate narcosis and operation. The third patient was 70 years old, multimorbid, and had previously undergone difficult operations involving the upper abdomen. He had localised peritonitis and was treated conservatively with nasogastric suction, intravenous drip, antibiotics, and close clinical supervision. He survived. All three were admitted in the last decade.

The median time from debut of symptoms to operation increased significantly ($P = 0.004$), from 8 h in the first decade to 17 h in the last decade. The median time from admittance to hospital to operation and the duration of the operation and hospital stay were stable through all four decades (see [Table 3](#)).

Complications

One or more complications occurred in 39% of patients (81/209). The two most common complications were pneumonia ($n = 18$, 8.6%) and wound infections ($n = 12$, 5.7%). Reoperation was performed in 14 (6.8%) patients for wound dehiscence ($n = 7$, 3.4%), postoperative leak ($n = 4$, 1.9%), intestinal obstruction ($n = 1$), severe bleeding from duodenal ulcer ($n = 1$), and drainage of subphrenic and pelvic abscesses ($n = 1$). The Clavien-Dindo classification of complications is shown in [Table 3](#). Complications occurred more frequently and were more serious in recent decades, in older patients, and in patients with comorbidities and higher ASA scores.

Mortality and long-term survival

The 100-day mortality was 20.6% (43/209) without significant variations between decades. Based on ASA score, the 100-day mortality was 6% in patients with ASA

Table 1 Trends in patient characteristics according to decade of treatment, *n* (%)

<i>n</i> = 209	1978–1987 (<i>n</i> = 38)	1988–1997 (<i>n</i> = 64)	1998–2007 (<i>n</i> = 62)	2008–2017 (<i>n</i> = 45)	<i>P</i> value
Sex					
Women	14 (36.8)	26 (40.6)	31 (50.0)	25 (55.6)	0.049 ^a
Men	24 (63.2)	38 (59.4)	31 (50.0)	20 (44.4)	
Incidence (No./100000)					
Women	3.3 (1.8 to 5.5)	6.0 (3.9 to 8.8)	7.0 (4.8 to 9.9)	5.3 (3.4 to 7.8)	0.14 ^b
Men	5.5 (3.6 to 8.3)	8.7 (6.2 to 12.0)	7.0 (4.8 to 10.0)	4.2 (2.6 to 6.5)	0.32 ^b
Age, mean ± SD, years	62 ± 17	64 ± 16	67 ± 16	69 ± 17	0.018 ^c
Hours from symptom debut until admission, mean ± SD)	7 ± 9	8 ± 12	16 ± 29	13 ± 14	0.019 ^c
ASA class					
II	30 (78.9)	46 (71.9)	33 (53.2)	24 (53.3)	0.001 ^d
III	6 (15.8)	13 (20.3)	19 (30.6)	11 (24.2)	
IV	2 (5.3)	5 (7.8)	10 (16.1)	9 (20.0)	
V	0	0	0	1 (2.2)	
Ulcer localisation					
Gastric	25 (65.8)	27 (42.2)	26 (41.9)	19 (42.2)	0.059 ^a
Duodenal	13 (34.2)	37 (57.8)	36 (58.1)	26 (57.8)	
Past ulcer history	5 (13.2)	25 (39.1)	16 (26.2)	0	0.022 ^a
Smoker at present	19 (57.6)	40 (64.5)	27 (49.1)	26 (59.1)	0.89 ^a
NSAID use	4 (10.5)	11 (17.2)	19 (31.1)	8 (17.8)	0.18 ^a
Steroid use	2 (5.3)	2 (3.1)	7 (11.5)	3 (6.7)	0.42 ^a
Salicylate use	2 (5.3)	4 (6.3)	10 (16.4)	8 (17.8)	0.025 ^a
Charlson Comorbidity index					
0	26 (68.4)	37 (57.8)	29 (46.8)	18 (40.0)	0.003 ^d
1	5 (13.2)	22 (34.4)	24 (38.7)	13 (28.9)	
2+	7 (18.4)	5 (7.8)	9 (14.5)	14 (31.1)	

^aCochran-Armitage exact trend test.

^bPoisson regression with calendar year as covariate.

^cJonckheere-Terpstra exact test.

^dOrdered logistic regression analysis. SD: Standard deviation; ASA: American Society of Anesthesiologists; NSAID: Non-steroidal anti-inflammatory drugs.

score 2, 39% with ASA score 3, and 59% with ASA score 4-5. We performed a multivariable, logistic regression analysis of 100-day mortality as a dependent variable and sex, age, year of admittance, Charlson Comorbidity Index, and ASA score as independent variables. Only ASA score was significantly associated with 100-day mortality [odds ratio (OR) = 12.5; 95%CI: 3.5-41.8 for ASA score 3 and OR = 31.2 (7.4-132) for ASA score 4-5].

The overall estimated 5-year relative survival was 95% (95%CI: 86-101) with ASA score 2, 56% (95%CI: 37-74) with ASA score 3, and 12% (95%CI: 2-35) with ASA score 4-5.

In those who survived the first 100 days, the estimated 5-year relative survival was 98% (95%CI: 89-104) for ASA score 2, 84% (95%CI: 58-102) for ASA score 3, and 26% (95%CI: 3-63) for ASA score 4 (see [Figure 3](#)).

Table 2 Factors associated with peptic ulcer perforation incidence rate ratios from 1978 to 2017. Data are presented as adjusted incidence rate ratios from Poisson regression with calendar year and age as covariates

	Male	P value	Female	P value
	IRR (CI)		IRR (CI)	
Total peptic ulcer perforation				
Calendar year	0.986 (0.970 to 1.001)	0.074	1.005 (0.988 to 1.023)	0.55
Age (per 5 yr)	1.040 (1.029 to 1.051)	< 0.001	1.060 (1.047 to 1.073)	< 0.001
Gastric ulcer perforation				
Calendar year	0.979 (0.956 to 1.001)	0.063	0.998 (0.973 to 1.024)	0.90
Age (per 5 yr)	1.037 (1.022 to 1.053)	< 0.001	1.056 (1.038 to 1.075)	< 0.001
Duodenal ulcer perforation				
Calendar year	0.992 (0.971 to 1.014)	0.49	1.011 (0.988 to 1.035)	0.36
Age (per 5 yr)	1.043 (1.028 to 1.058)	< 0.001	1.063 (1.045 to 1.080)	< 0.001

IRR: Incidence rate ratio; CI: Confidence interval.

Table 3 Trends in treatment and outcome according to decade of treatment, *n* (%)

<i>n</i> = 209	1978–1987 (<i>n</i> = 38)	1988–1997 (<i>n</i> = 64)	1998–2007 (<i>n</i> = 62)	2008–2017 (<i>n</i> = 45)	P value
Treatment					
Simple closure with or without omentopexy	37 (97)	64 (100)	62 (100)	38 (84)	
Gastric resection	1 (3)	0	0	4 (9)	
No operation	0	0	0	3 (7)	
Hours from admission to operation, mean ± SD	7 ± 9	8 ± 12	16 ± 29	13 ± 14	0.019 ^a
Duration of operation, mean ± SD, min	72 ± 29	78 ± 35	61 ± 24	78 ± 40	0.15 ^a
Re-operation	1 (3)	4 (6)	6 (10)	4 (9)	0.18 ^b
Clavien-Dindo classification of complications					
0	28 (74)	45 (70)	38 (61)	17 (38)	0.001 ^c
1-2	6 (16)	8 (13)	9 (15)	13 (29)	
3	1 (3)	1 (2)	4 (7)	4 (9)	
4	0	4 (6)	3 (5)	3 (7)	
5	3 (8)	6 (9)	8 (13)	8 (18)	
100-day mortality	7 (18)	11 (17)	16 (26)	9 (20)	0.56 ^b
Estimated 10-yr relative survival in patients surviving 100 d, (95%CI)	97 (70-114)	71 (52-87)	86 (64-103)	86 (51-108)	0.44 ^d

^aJonckheere-Terpstra exact test.^bCochran-Armitage exact trend test.^cOrdered logistic regression analysis.^dRelative survival analysis with calendar period as covariate. SD: Standard deviation; CI: Confidence interval.

DISCUSSION

This study demonstrated a trend of increasing age and comorbidity in patients admitted for PPU over 40 years. Complications were more common in recent decades. However, we found no significant variations between short-term mortality between the decennia. Comorbidity measured by through ASA score was a good prognostic factor regarding short-term mortality and long-term survival.

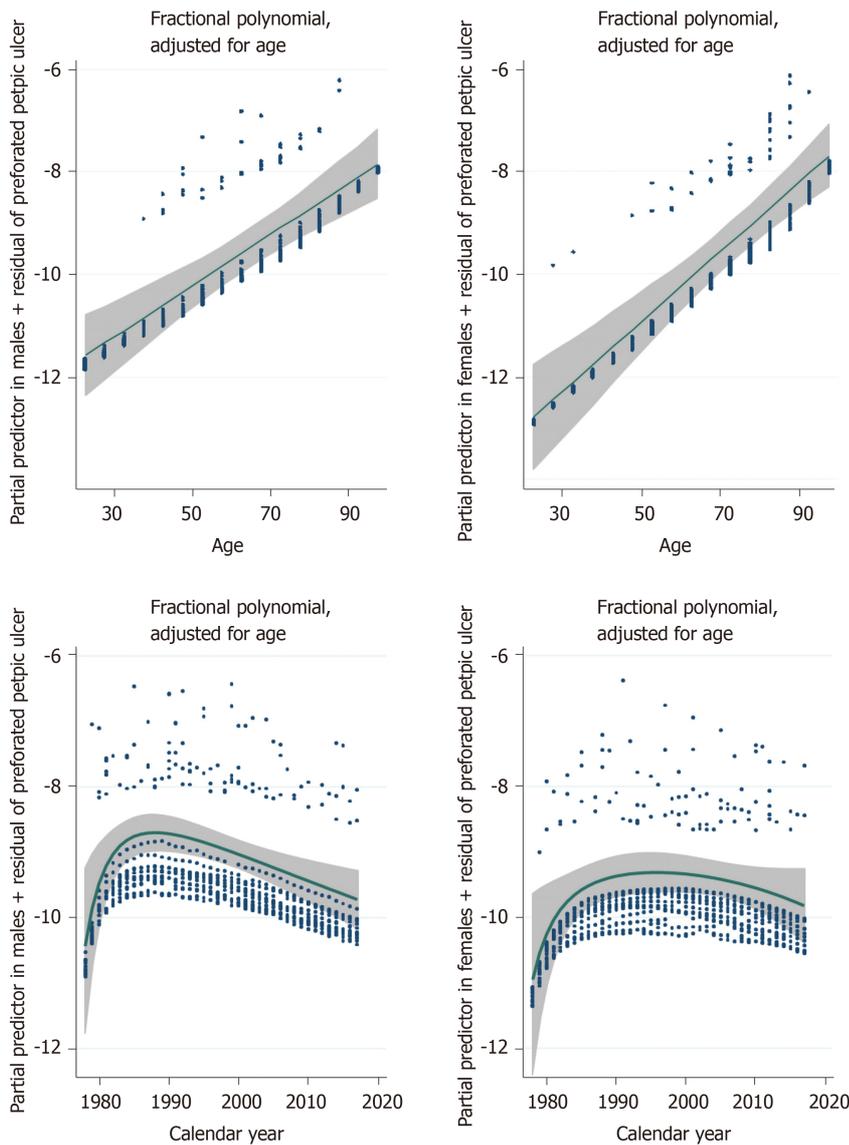


Figure 1 Effects of age and calendar year on the number of patients presenting with perforated peptic ulcer. Data are Poisson regression with fractional polynomials. 95% confidence intervals are shaded grey, and the y-axis is a logarithmic scale. Left, males. The effect of age was linear in both males and females, without an upper limit. Incidence increased, peaking 10 yr earlier in males than in females.

The median age of patients with PPU increased with each decade. In the last decade, more than half of the patients with PPU were > 70 years old. Women constituted a greater share of the patients with PPU with time, surpassing men in the last decade.

The incidence rates for PPU in our population were similar to previous studies, which reported an incidence of 4-15 per 100000/year^[4,7,12]. The IR tended to decline during the last half of the observation period, and this tendency occurred almost one decade earlier for men than women. Over the same period, the IR was similar between the sexes. The Poisson regression with fractional polynomials indicated an increase in IR with increasing age for both sexes.

These epidemiological findings are in agreement with existing data showing a declining trend in PPU, equal gender distribution, and more frequent occurrence among the elderly^[4,15,29,30]. These changes in the epidemiology of PPU may have numerous explanations. The identification and treatment of *H. pylori* as a cause of PUD is considered the main cause of reduced PPU incidence, especially in younger age groups^[1,15]. The introduction of proton pump inhibitors is also postulated to be related to a reduced IR for PPU^[4]. A shift in the occurrence of predisposing factors may also have contributed to these changes.

In addition to *H. pylori* infection, use of NSAIDs, corticosteroids, smoking, and previous history of PUD are known risk factors for PPU^[31,32]. In our study, we found no significant change in trends regarding the use of NSAIDs, corticosteroids, or smoking habits.

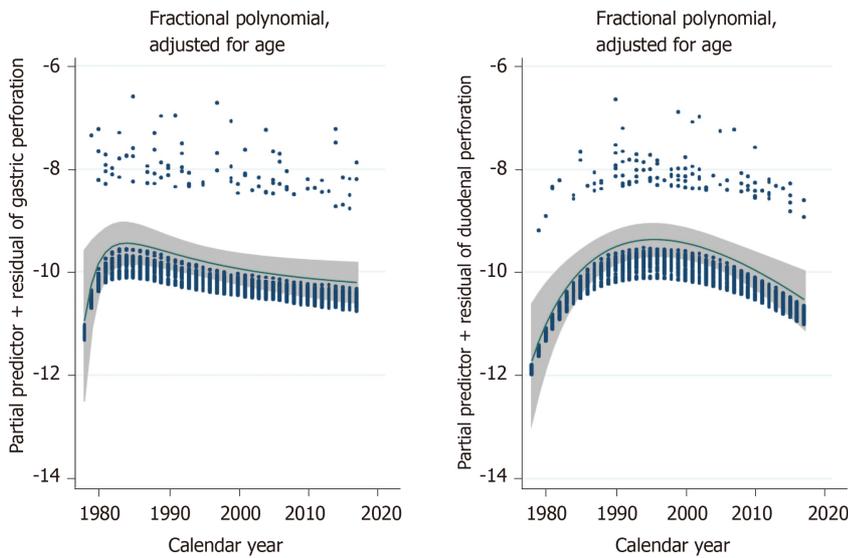
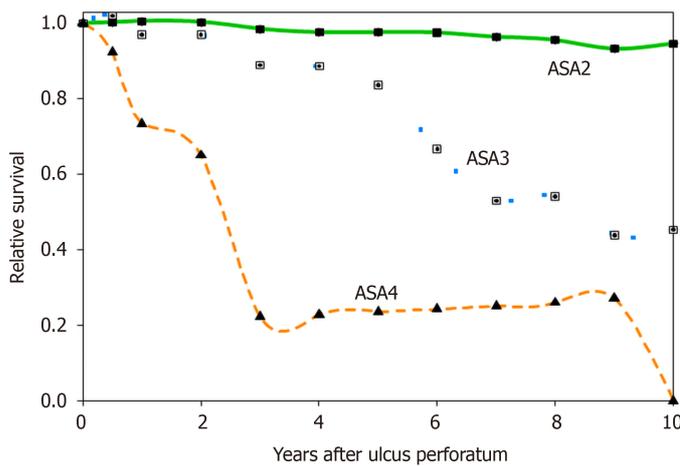


Figure 2 Effect of calendar year on the number of patients presenting with perforated gastric ulcer (left) and duodenal ulcer (right). Data were Poisson regression with fractional polynomials. 95% confidence intervals are shaded grey, and the y-axis is a logarithmic scale. The incidence of gastric ulcer perforations peaked around 1984, whereas the peak of duodenal ulcer perforations was approximately 15 yr later.



Yr	0	1	2	3	4	5	6	7	8	9	10
ASA2	125	124	123	118	112	107	101	96	88	88	75
ASA3	29	29	26	25	22	20	17	13	10	10	7
ASA4	11	9	7	5	1	1	1	1	1	1	0

Figure 3 Relative survival in each American Society of Anesthesiologists group of patients who survived the first 100 postoperative days. ASA: American Society of Anesthesiologists.

Acetylsalicylic acid is also technically considered an NSAID due to similar mechanisms of action^[32,33]. It also has a similar profile regarding adverse events and is associated with an increased risk of PPU^[32]. However, acetylsalicylic acid has a completely different area of use than other NSAIDs, mostly in secondary prevention of thrombotic cardiovascular events^[33]. The significant increase in the use of acetylsalicylic acid through the study period may contribute to the increased IR with increasing age and the elderly being more prone to adverse effects^[15,34].

The patients admitted with PPU had increasing comorbidity in recent decades according to the Charlson Comorbidity Index and ASA class. Increased comorbidity is associated with increased age^[35]. Previous studies have also shown an association between comorbidity, complications, and mortality after PPU^[14]. This is thought to be

related to delayed admittance, diagnosis, and treatment^[15].

The surgical treatment for PPU in our cohort barely changed over four decades, with simple closure with or without omentopexy being the procedure of choice in 98% (201/206) of patients. Only one of the patients were treated with a laparoscopic technique. The length of the operation was stable over all decades, and this could be explained with little variation in surgical access and method.

Three patients in the cohort were treated without an operation, all in the last decade, two of whom died within a short timeframe. This could reflect more frequent “failure-to-rescue” in recent years, especially in elderly patients with severe comorbidity^[29,36].

The increase in time from the debut of symptoms to hospital admission in recent decades may be related to the previously described epidemiological shift in the age of patients with PPU^[4,14,30]. Elderly patients with comorbidity are less likely to present with peritonitis^[29].

Post-operative complications occurred more frequently in recent decades. Increasing age and greater comorbidity in the patients treated for PPU could explain the increase in serious complications (Clavien-Dindo grade 4 and 5)^[37]. We found no significant change in the frequency of reoperation. We also found a substantial increase in the frequency of grade 1-2 complications. This does not necessarily reflect an actual increase in low-grade complications, but may be related to a change in doctors’ habits towards more frequent and detailed descriptions in documentation^[38]. The accuracy of the collected data is limited to the amount of detail in the patient’s journal. This represents a limitation of the retrospective study design.

Short-term mortality measured 100 d post-operatively was stable through all four decades and in concordance with existing data. The short-term mortality was associated with ASA score, supporting the understanding that patient comorbidity affects mortality. A similar association with degree of comorbidity expressed through ASA score was seen regarding long-term survival, measured as 5-year relative survival. This supports previous data suggesting that ASA score can be used as a prognostic factor regarding both short- and long-term survival^[39-41].

The study had some limitations. The retrospective design has weaknesses. The quality of the database was dependent on the quality of the different patient records. Grade 1 Clavien-Dindo complications were often not documented in the patient records. More severe complications were regularly documented, and we expect very few missing grade II to V complications in the database.

CONCLUSION

In conclusion, this study confirmed that the IRR of PPU increased with increasing age, without an upper limit. The IRR increased until the second decade of the study period in men and the third decade in women. Recent years indicate a declining tendency in both sexes. In recent decades, patients were older and had more comorbidity. Post-operative complications increased over the 40 years of the study. ASA score was associated with both short-term mortality and long-term survival.

The results of this study would have external validity for populations similar to the Norwegian population.

ARTICLE HIGHLIGHTS

Research background

The incidence of peptic ulcer disease (PUD) has decreased during the last few decades. However, complicated PUD has not decreased likewise. Perforation is the complication that accounts for most deaths associated with PUD, and it remains a surgical emergency. Perforated peptic ulcer (PPU) has a high short-term mortality.

Research motivation

With the discovery of the role of *Helicobacter pylori* in PUD, it is important to investigate trends and changes in demography in patients with PPU. This will provide more precise characteristics regarding these patients, which in turn might contribute towards more rapid diagnostics and treatment.

Research objectives

The aim of this study was to investigate changes in demography and the effect on treatment, complications, and short- and long-term mortality in patients admitted to our hospital with PPU over four decades.

Research methods

All patients who were admitted to our hospital with PPU from 1978-2017 were retrospectively identified and included. We retrieved their medical records and reviewed them to obtain data concerning patient characteristics, treatment and complications.

Research results

The median age increased from 63 to 72 years from the first to the last decade. The incidence rate increased with increasing age, although we observed a decline in incidence rate in recent decades. Comorbidity increased significantly over the 40 years of the study. The median time from debut of symptoms to operation increased from 8 to 17 h from the first to the last decade. One or more complications occurred in 39 %. Both short- and long-term mortality were associated with American Society of Anaesthesiologists (ASA) score.

Research conclusions

Declining incidence rates occurred in recent years, but the patients were older and had more comorbidity. The ASA score was associated with both short-term mortality and long-term survival.

Research perspectives

This study has shown a demographic shift among patients with PPU. Future research should assess a better understanding of the association of increasing age, comorbidity and other risk factors with PPU. Clinical trials might serve to reduce the high number of complications in these patients.

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Retrospective Study

Investigation of immune escape-associated mutations of hepatitis B virus in patients harboring hepatitis B virus drug-resistance mutations

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Abstract

BACKGROUND

It is unclear whether immune escape-associated mutations in the major hydrophilic region of hepatitis B virus surface antigen (HBsAg) are associated with nucleoside/nucleotide analog resistance.

AIM

To evaluate the association between immune escape-associated mutations and nucleoside/nucleotide analog resistance mutations.

METHODS

In total, 19440 patients with chronic hepatitis B virus infection, who underwent resistance testing at the Fifth Medical Center of Chinese PLA General Hospital between July 2007 and December 2017, were enrolled. As determined by sequence analysis, 6982 patients harbored a virus with resistance mutations and 12458 harbored a virus lacking resistance mutations. Phenotypic analyses were performed to evaluate HBsAg production, replication capacity, and drug-induced viral inhibition of patient-derived drug-resistant mutants with or without the coexistence of sA159V.

and approved the final manuscript.

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Institutional review board

statement: The study was reviewed and approved by the Ethics Committee Approval Document of 302 Hospital, Institutional Review Board Approval No. 2012020D; The study was reviewed and approved by the Ethics Committee Approval Document of 302 Hospital, Institutional Review Board Approval No. 2013052D.

Informed consent statement: All study participants, or their legal guardian, provided informed written consent prior to study enrollment.

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RESULTS

The rate of immune escape-associated mutation was significantly higher in 9 of the 39 analyzed mutation sites in patients with resistance mutations than in patients without resistance mutations. In particular, these mutations were sQ101H/K/R, sS114A/L/T, sT118A/K/M/R/S/V, sP120A/L/Q/S/T, sT/I126A/N/P/S, sM133I/L/T, sC137W/Y, sG145A/R, and sA159G/V. Among these, sA159V was detected in 1.95% (136/6982) of patients with resistance mutations and 1.08% (134/12,458) of patients lacking resistance mutations ($P < 0.05$). The coexistence of sA159V with lamivudine (LAM) and entecavir (ETV)-resistance mutations in the same viral genome was identified during follow-up in some patients with drug resistance. HBsAg production was significantly lower and the replication capacity was significantly higher, without a significant difference in LAM/ETV susceptibility, in sA159V-containing LAM/ETV-resistant mutants than in their sA159V-lacking counterparts.

CONCLUSION

In summary, we observed a close link between the increase in certain immune escape-associated mutations and the development of resistance mutations. sA159V might increase the fitness of LAM/ETV-resistant mutants under environmental pressure in some cases.

Key Words: Hepatitis B virus; Immune escape-associated mutation; Drug-resistance mutation; Nucleoside/nucleotide analogs; Hepatitis B surface antigen; Major hydrophilic region

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Core Tip: A large number of patients were surveyed for immune escape-associated mutations, and the link between immune escape-associated and resistant mutations was identified. Contribution of sA159V to resistance was found in multiple followed up patients, in particular sA159V reduced hepatitis B surface antigen but raised the replication capacity of lamivudine/entecavir-resistant mutants.

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INTRODUCTION

It is estimated that 292 million people worldwide are chronically infected with hepatitis B virus (HBV), including 86 million residing in China^[1]. The treatment of chronic HBV infection is aimed towards the long-term suppression of viral replication to prevent disease progression^[2]. Currently, nucleoside/nucleotide analogs (NAs) including lamivudine (LAM), adefovir dipivoxil (ADV), entecavir (ETV), telbivudine (LdT), tenofovir disoproxil fumarate (TDF), and tenofovir alafenamide (TAF) are approved for the treatment of HBV infection. However, a concern is the drug resistance caused by mutations in the reverse transcriptase (RT) region of the HBV genome. Drug-resistance mutations tend to arise in patients treated with LAM, LdT, and ADV as well as in LAM-refractory patients subsequently treated with ETV^[3,4]. Classical primary resistance mutations include rtM204I/V (LAM-r) for LAM (rtM204I also confers resistance to LdT), rtA181V/rtN236T for ADV as well as LAM-r along with at least one substitution at rt184 (A/C/F/G/I/L/M/S), rt202 (C/G/I), and rtM250 (I/L/V) for ETV^[3,5,6]. In addition, rtS106C+rtH126Y+rtD134E+rtL269I quadruple mutations have recently been reported to confer TDF resistance^[7]. TAF, also known as TDF II, has a higher intrahepatic drug concentration and lower plasma drug concentration than TDF as well as a lower probability of kidney and bone

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abnormalities during therapy^[8].

The rapid selection of drug-resistant HBV mutants may depend on viral fitness, which could be influenced by the host immune response in addition to drug pressure^[9,10,11]. A few drug-resistance mutations, such as rtS78T and rtA181T, introduce a stop codon in the overlapping S region and affect the immune response, thereby influencing the clinical presentation of NA-treated patients^[12-15]. Hepatitis B surface antigen (HBsAg) is diagnostic marker of HBV infection and an important index for predicting the effects of antiviral treatment^[16,17]. HBV immune escape-associated mutations, located mainly in the major hydrophilic region (MHR, amino acids 99–169), have the potential to weaken the immune response. Currently, it is unclear whether these mutations influence drug resistance. Only a few studies on a limited number of patients reference this issue, showing that the frequency of some immune escape-associated mutations is higher in LAM-treated patients than in NA-naive patients, suggesting that selection of drug-resistance mutations is associated with immune escape-associated mutation enrichment^[18,19].

We recently identified several novel immune escape-associated mutations in patients with occult HBV infection; a summary of previously documented immune escape-associated mutations is provided in [Table 1](#)^[20,21]. Notably, for many previously documented mutations, phenotypic information is lacking. In this study, we evaluated a large number of patients to determine whether immune escape-associated mutations are associated with drug-resistance mutations, with a focus on the sA159V mutation.

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MATERIALS AND METHODS

Patient samples

From July 2007 to December 2017, 19440 patients with chronic HBV infection who underwent resistance testing (by direct sequencing) at the Fifth Medical Center of Chinese PLA General Hospital (originally named Beijing 302 Hospital) were enrolled in the study, and their serum samples were collected. All patients were previously treated with NAs. Illness categories included chronic hepatitis B, HBV-related liver cirrhosis, and hepatocellular carcinoma. The diagnostic criteria were based on the guidelines for the prevention and treatment of chronic hepatitis B in China (2005)^[22], and the updated guidelines were used according to the time of patient enrollment. Patients who were co-infected with other hepatitis viruses or human immunodeficiency virus were excluded from the study. All patients were from the Database of Beijing 302 Hospital and provided informed consent for the use of their samples for research before enrollment. The study was approved by the Ethics Committee of Beijing 302 Hospital.

Detection of serological markers and HBV deoxyribonucleic acid

Biochemical and serological markers as well as HBV deoxyribonucleic acid (DNA) levels in the serum samples were routinely detected at the Central Clinical Laboratory of the Fifth Medical Center of the Chinese PLA General Hospital. Roche Elecsys reagents (Basel, Switzerland) were used to measure the serum HBsAg levels, and the threshold for negativity was < 0.05 IU/mL in the quantitative assay or a cut-off index

Table 1 Summary of immune escape-associated mutations in the major hydrophilic region of hepatitis B surface antigen

Region in major hydrophilic region (aa 99–169)	Mutation pattern
Upstream “a” determinant (aa 99–123)	sY100S, sQ101H/K/R, sM103I/T, sL109I/P/R, sP111L/Q/S, sG112K/R, sS114A/L/T, sT115A/N, sT116N, sS117G/N/R, sT118A/K/M/R/S/V, sG119E/R/T, sP120A/L/Q/S/T, sC121R/S, sK122R, sT123A/I/N/S/V
Within “a” determinant (aa 124–147)	sC124R/Y, sT125A/M, sI/T126A/N/P/S, sP127H/L/S/T, sA128T/V, sQ129N/H/P/R, sG130A/K/N/R/S, sT131A/I/K/N, sS132F/P, sM133I/L/T, sF/Y134H/L/R/S/V, sS136F/P/Y, sC137W/Y, sC139R/S/Y, sT140I, sK141E/R, sP142L, sD144A/E, sG145A/R, sC147R/Y
Downstream “a” determinant (aa 148–169)	sS154P, sA159G/V, sV168A

aa: Amino acid.

of < 1.00 in the chemiluminescent immunoassay assay.

Sequence analysis of HBV reverse transcriptase/S genes and phylogenetic tree analysis

Sequence and phylogenetic analyses were performed as previously described^[23,24]. In brief, a 1225-bp fragment [nucleotides (nt) 54–1278] spanning the full-length RT region (nt 130–1161) and S region (nt 155–835) of the viral genome was analyzed. Drug-resistance and immune escape-associated mutations were analyzed by direct sequencing using an in-house nested PCR method with a lower detection limit of 10 IU/mL. Clonal sequencing of the samples of interest was performed (20 clones per sample). Phylogenetic trees were constructed using MEGA 7 software.

Construction of 1.1-mer HBV reverse genome vectors and site-directed mutagenesis

Replication-competent vectors containing various mutant or wild-type (WT) RT/S genes were constructed for a phenotypic analysis based on the pTriEx-mod-1.1 vector, which was used for antigenicity analyses as previously described^[21,24]. Eight recombinant vectors harboring RT/S genes from eight viral strains of a representative patient (patient A) were constructed. The eight strains were: WT, sA159V (M1), rtM204I (M2), sA159V+rtM204I (M3), rtL180M+rtM204V (M4), sA159V+rtL180M+rtM204V (M5), rtL180M+rtT184L+rtM204V (M6), and sA159V+rtL180M+rtT184L+rtM204V (M7). M6 was modified from M7 by the elimination of the sA159V mutation using the QuikChange Lightning Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA, United States). The primer (sense) was 5'-CCTGGGCTTTCGAAAATTCCTATG-3'.

Phenotypic analysis of HBsAg, replication capacity, and drug-induced viral inhibition

Experiments were performed as described previously, with minor modifications^[21,24]. Briefly, recombinant vectors were individually transfected into HepG2 cells. At 3 d after cultivation, the supernatant was harvested for the measurement of HBsAg by two assays, *i.e.* a chemiluminescence immunoassay (Roche) and an enzyme-linked immunosorbent assay (ELISA; Wantai Bio Pharm., Beijing, China).

To assess drug-induced viral inhibition, transfected HepG2 cells were cultured in the presence or absence of NAs for 4 d. Cells were lysed, and viral core particles were immunoprecipitated using anti-HBc/protein A+G. HBV replicative intermediates in the core particles were released and quantified by real-time PCR. The relative replication capacity of a mutant *vs* WT strain was determined in the absence of NAs. Approximately 90% effective concentrations of the four NAs were used, as previously determined^[25,26]. These were 0.05 μmol/L for LAM, 0.05 μmol/L for ETV, 3.0 μmol/L for ADV, and 5.0 μmol/L for TDF. Viral inhibition was determined as the relative value of the NA-treated samples *vs* the NA-untreated samples. Experiments were performed at least three times independently.

Statistical analysis

Data are presented as the means (standard deviation) or medians (interquartile range). Differences between groups were examined by the Student's *t*-test (two-tailed) or chi-squared tests. Multivariate regression was used to determine independent risk factors.

Statistical analyses were performed using SPSS 23.0 for Windows (SPSS Inc., Chicago, IL, United States). A value of $P < 0.05$ was considered statistically significant.

RESULTS

Clinical profile of immune escape-associated mutations in patients with and without resistance mutations

Drug-resistance mutations were detected in 35.92% (6,982/19,440) of all patients included in the study. Moreover, patients harboring resistance mutations had higher HBV DNA levels than patients lacking resistance mutations. The rate of immune escape-associated mutation was significantly higher at 9 of 39 analyzed mutation sites in patients with resistance mutations than in patients without resistance mutations. These mutations were sQ101H/K/R, sS114A/L/T, sT118A/K/M/R/S/V, sP120A/L/Q/S/T, sT/I126A/N/P/S, sM133I/L/T, sC137W/Y, sG145A/R, and sA159G/V. The percentage of patients with MHR mutations was significantly higher in the resistance mutation-positive group than in the resistance mutation-negative group (23.32% *vs* 18.51%, $P < 0.05$) (Table 2). In particular, mutations were detected in 67/63/168 of 298 sQ101H/K/R-positive patients, 39/2/76 of 117 sS114A/L/T-positive patients, 5/5/15/3/1/2 of 31 sT118A/K/M/R/S/V-positive patients, 3/0/0/23/81 of 107 sP120A/L/Q/S/T-positive patients, 94/58/0/214 of 366 sT/I126A/N/P/S-positive patients, 14/46/136 of 196 sM133I/L/T-positive patients, 1/8 of 9 sC137W/Y-positive patients, 77/46 of 123 sG145A/R-positive patients, and 87/136 of 223 sA159G/V-positive patients.

Clinical incidence and features of the sA159V mutation

Restricted by the scale of the study, sA159V was selected as a representative immune escape-associated mutation for further analyses. The detection rate of sA159V was significantly higher in patients with resistance mutations than in patients lacking resistance mutations [1.95% (136/6982) *vs* 1.08% (134/12458), $P < 0.05$]. In contrast, the detection rate of sA159G did not differ significantly between the two patient groups (1.25% (87/6982) *vs* 1.48% (185/12458), $P > 0.05$). The clinical features of the sA159V-positive and sA159V-negative patients are summarized in Table 3. A multivariate analysis showed that age and the coexistence of ADV-r/LAM-r mutations were independently associated with the sA159V mutation. The sA159V-positive patients had higher rates of coexisting drug-resistance mutations than the sA159V-negative patients.

Longitudinal analysis of the clinical course of patients with HBV mutations during nucleotide analog therapy

Five representative sA159V-positive patients with available serial serum samples were subjected to clonal analysis of HBV RT/S genes. The five patients were infected with genotype C HBV and diagnosed with chronic hepatitis B or HBV-related liver cirrhosis.

Patient A, a 52-year-old male, was first admitted in October 2007 with chronic hepatitis B. The patient received LAM (from May 2008 to October 2009) and ETV+ADV (from October 2009 to June 2011). In tested clones of sample A-S1, WT, sA159V, sQ129R, and rtM204I detection rates were 80%, 10%, 5%, and 5%, respectively. In sample A-S2, six mutants were detected, *i.e.* sA159V+rtL180M+rtM204V (35%), rtL180M+rtM204V (35%), sA159V+rtM204I (15%), sA159V+rtL180M+rtM204I (5%), sA159V+rtM204V (5%), and rtM204I (5%). In sample A-S3, sA159V+rtL180M+rtM204V+rtT184L was the most abundant (Figure 1A). Clonal sequencing of sample A-S4 failed due to an extremely low viral load. The 10 viral clonal sequences from the patient were deposited in GenBank (MN642606-MN642615) and used to construct a phylogenetic tree (Figure 2).

Four patients received various NAs: LAM, ADV, or ETV, as monotherapy or in combination. Patient B had seven sA159V-containing mutants in samples B-S1 and B-S2 during ETV therapy. Resistant mutants were subsequently suppressed by ETV+ADV, whereas the sA159V mutation was observed in sample B-S3 (Figure 1B). Patient C and Patient D initially received ADV and failed to exhibit virological breakthrough. In both patients, the sA159V mutant existed before virological breakthrough (samples C-S1 and D-S1), and sA159V-containing ADV-resistant mutants were dominant in samples C-S2 and D-S2 at virological breakthrough (Figure 1C and D). Samples from Patient E included three sA159V-containing

Table 2 Analysis of immune escape-associated mutations in the major hydrophilic region in patients with and without resistance mutations

Clinical features	Resistance mutation (+), n = 6982	Resistance mutation (-), n = 12458	P value	The MHR Mutation occurrence [(+) vs (-)]
Age in year	44.01 ± 11.73	39.01 ± 13.08	< 0.05	
Gender, male	5709 (81.77%)	9982 (80.13%)	< 0.05	
HBV genotype, C%/B%	86.79/12.52	83.00/16.05	< 0.05	
HBV DNA as log ₁₀ IU/mL	4.62 (3.17, 6.47)	4.24 (2.83, 6.16)	< 0.05	
sY100S	20 (0.29%)	29 (0.23%)	NS	
sQ101H/K/R	298 (4.27%)	229 (1.84%)	< 0.05	↑
sM103I/T	8 (0.11%)	14 (0.11%)	NS	
sL109I/P/R	12 (0.17%)	24 (0.19%)	NS	
sP111L/Q/S	10 (0.14%)	21 (0.17%)	NS	
sG112K/R	4 (0.06%)	9 (0.07%)	NS	
sS114A/L/T	117 (1.68%)	137 (1.10%)	< 0.05	↑
sT115A/N	2 (0.03%)	8 (0.06%)	NS	
sT116N	6 (0.09%)	32 (0.26%)	< 0.05	↑
sS117G/N/R	5 (0.07%)	19 (0.15%)	NS	
sT118A/K/M/R/S/V	31 (0.44%)	32 (0.26%)	< 0.05	↑
sG119E/R/T	6 (0.09%)	10 (0.08%)	NS	
sP120A/L/Q/S/T	107 (1.53%)	35 (0.28%)	< 0.05	↑
sC121R/S	1 (0.01%)	1 (0.01%)	NS	
sK122R	154 (2.21%)	315 (2.53%)	NS	
sT123A/I/N/S/V	56 (0.80%)	91 (0.73%)	NS	
sC124R/Y	4 (0.06%)	9 (0.07%)	NS	
sT125A/M	8 (0.11%)	21 (0.17%)	NS	
sT/I126A/N/P/S	366 (5.24%)	534 (4.29%)	< 0.05	↑
sP127H/L/S/T	91 (1.30%)	165 (1.32%)	NS	
sA128T/V	7 (0.10%)	15 (0.12%)	NS	
sQ129N/H/P/R	90 (1.29%)	129 (1.04%)	NS	
sG130A/K/N/R/S	65 (0.93%)	85 (0.68%)	NS	
sT131A/I/K/N	133 (1.90%)	219 (1.76%)	NS	
sS132F/P	2 (0.03%)	9 (0.07%)	NS	
sM133I/L/T	196 (2.81%)	277 (2.22%)	< 0.05	↑
sF/Y134H/L/R/S/V	65 (0.93%)	51 (0.41%)	NS	
sS136F/P/Y	6 (0.09%)	4 (0.03%)	NS	
sC137W/Y	9 (0.13%)	5 (0.04%)	< 0.05	↑
sC139R/S/Y	3 (0.04%)	9 (0.07%)	NS	
sT140I	39 (0.56%)	61 (0.49%)	NS	
sK141E/R	3 (0.04%)	4 (0.03%)	NS	
sP142L	11 (0.16%)	9 (0.07%)	NS	
sD144A/E	17 (0.24%)	26 (0.21%)	NS	
sG145A/R	123 (1.76%)	163 (1.31%)	< 0.05	↑

sC147R/Y	0	0	NS
sS154P	1 (0.01%)	2 (0.02%)	NS
sA159G/V	223 (3.19%)	319 (2.56%)	< 0.05 ↑
sV168A	143 (2.05%)	234 (1.88%)	NS
Average number/patient	0.35	0.27	< 0.05 ↑
Patient percentage with the MHR mutation(s)	23.32% (1628/ 6982)	18.51% (2306/12458)	< 0.05 ↑

(+): Positive; (-): Negative; DNA: Deoxyribonucleic acid; HBV: Hepatitis B virus; MHR: Major hydrophilic region; NS: Not significant.

Table 3 Analysis of clinical features of sA159V-positive and sA159V-negative patients

Clinical features	sA159V-positive, n = 270	sA159V-negative, n = 19170	Univariate, P value	Univariate, P	Multivariate, P value	Multivariate, P
Age in year	46.67 ± 12.19	40.72 ± 12.83	0.00	< 0.05	0.00	< 0.05
Gender, male	214 (79.26%)	15477 (80.74%)	0.54	> 0.05	0.97	> 0.05
Genotype, C%/B%	90.00/10.00	84.31/14.82	0.03	< 0.05	0.40	> 0.05
HBV DNA as log ₁₀ IU/mL	4.54 (3.18, 6.55)	4.37(2.95, 6.27)	0.09	> 0.05	0.40	> 0.05
ALT in U/L	42 (25, 87)	42 (26, 82)	0.67	> 0.05	0.32	> 0.05
AST in U/L	41 (28, 83)	38 (26,71)	0.33	> 0.05	0.61	> 0.05
TBIL in μmol/L	16.10 (10.95, 25.45)	14.30 (10.40, 22.10)	0.13	> 0.05	0.58	> 0.05
CHE in U/L	5940 (3114, 8091)	6764 (4276, 8469)	0.11	> 0.05	0.87	> 0.05
HBsAg, COI	4987.83 ± 3128.43	5064.50 ± 2931.79	0.05	> 0.05	0.15	> 0.05
Coexistent with ADV-r mutation	41 (15.19%)	1663 (8.68%)	0.00	< 0.05	0.00	< 0.05
Coexistent with LAM-r mutation	97 (35.93%)	5316 (27.73%)	0.00	< 0.05	0.01	< 0.05
Coexistent with ETV-r mutation	20 (7.41%)	868 (4.53%)	0.04	< 0.05	0.40	> 0.05

ADV-r: Adefovir resistance; ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; CHE: Cholinesterase; COI: Cut-off index; DNA: Deoxyribonucleic acid; ETV-r: Entecavir resistance; HBsAg: Hepatitis B surface antigen; HBV: Hepatitis B virus; LAM-r: Lamivudine resistance; TBIL: Total bilirubin.

ETV/LAM-resistant mutants (sample E-S2) when the virological response was inadequate upon ETV+TDF therapy (Figure 1E).

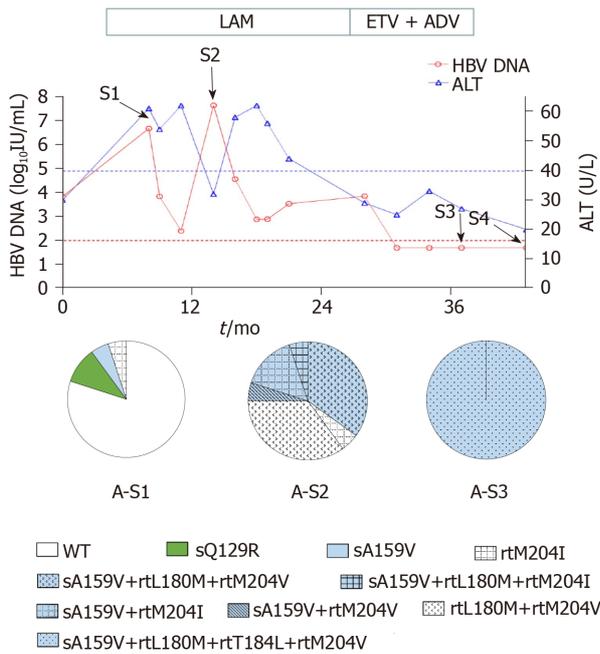
Quantitative HBsAg levels

As determined by the Roche quantitative assay, the HBsAg levels in the supernatant of the seven mutants decreased significantly to 46.2% (M1), 40.8% (M2), 14.0% (M3), 44.9% (M4), 20.6% (M5), 35.1% (M6), and 16.6% (M7) of the WT level. Three sA159V-containing resistant mutants had significantly lower HBsAg levels than their sA159V-lacking counterparts (M2 vs M3, M4 vs M5, M6 vs M7, all P < 0.05) (Figure 3). Consistent results were obtained by ELISA (data not shown).

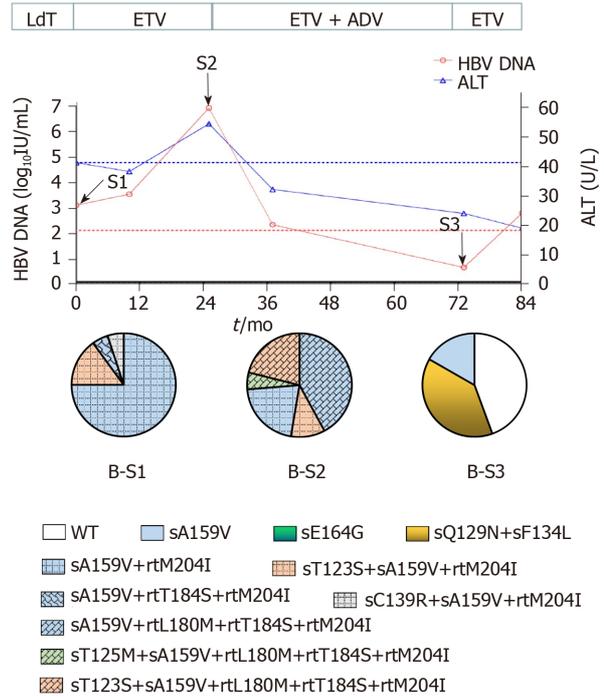
Assessment of viral replication capacity

The replication capacities of the seven mutants (M1–M7) decreased significantly to 49.0% (M1), 16.4% (M2), 37.8% (M3), 22.0% (M4), 46.0% (M5), 15.4% (M6), and 33.0% (M7) of the WT level. Three sA159V-containing resistant mutants had significantly higher replication capacities than their sA159V-lacking counterparts (M2 vs M3, M4 vs M5, M6 vs M7, all P < 0.05) (Figure 4).

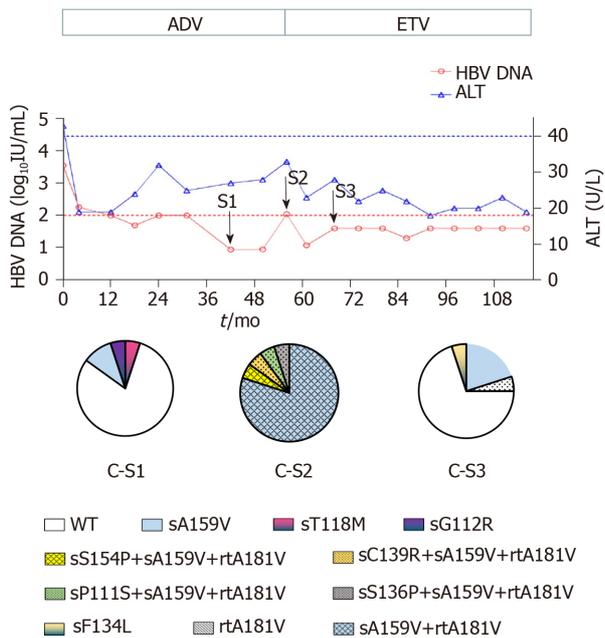
A



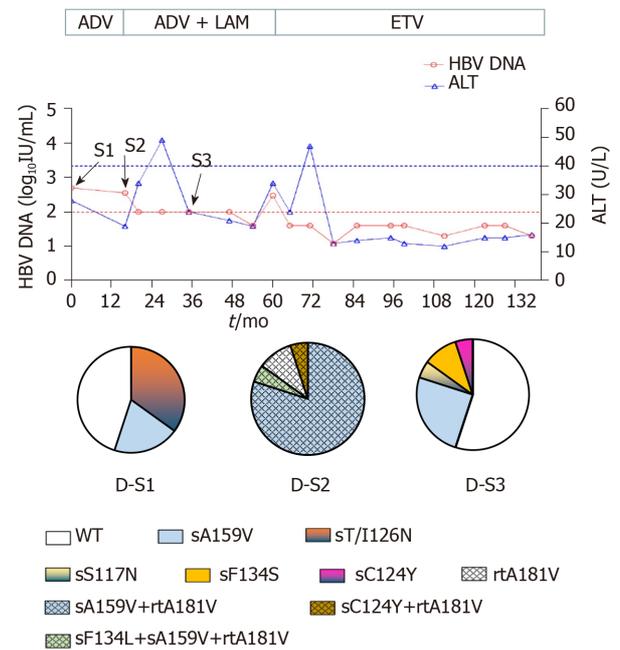
B



C



D



E

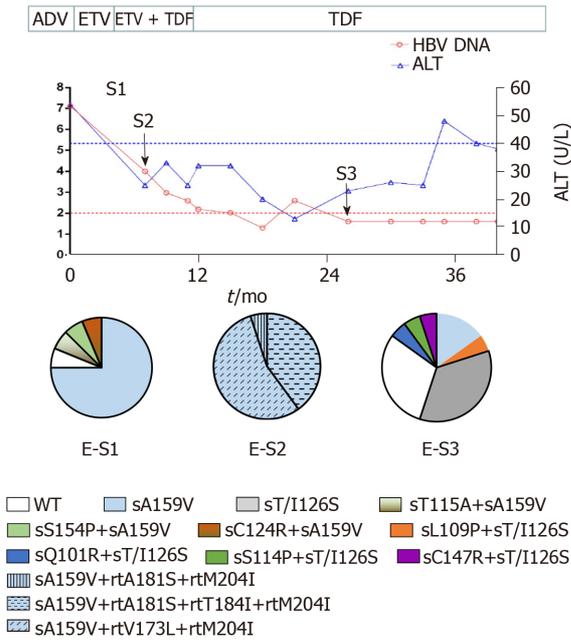


Figure 1 Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in five representative patients. Dynamic changes in serum hepatitis B virus deoxyribonucleic acid (HBV DNA) and alanine aminotransferase (ALT) levels are shown along with antiviral therapies. The duration (months) of antiviral therapy is represented by bars above the graph, and the serum samples from the patient for cloning are indicated by arrows. Two dashed lines show the lower detection limit of HBV DNA (100 IU/mL) and normal ALT levels (40 U/L). Proportions of wild-type and mutant HBV reverse transcriptase from each sample are depicted by a series of pie charts. A: Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in patient A; B: Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in patient B; C: Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in patient C; D: Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in patient D; E: Evolution of drug-resistant hepatitis B virus strains and clinical responses during antiviral therapy in patient E.

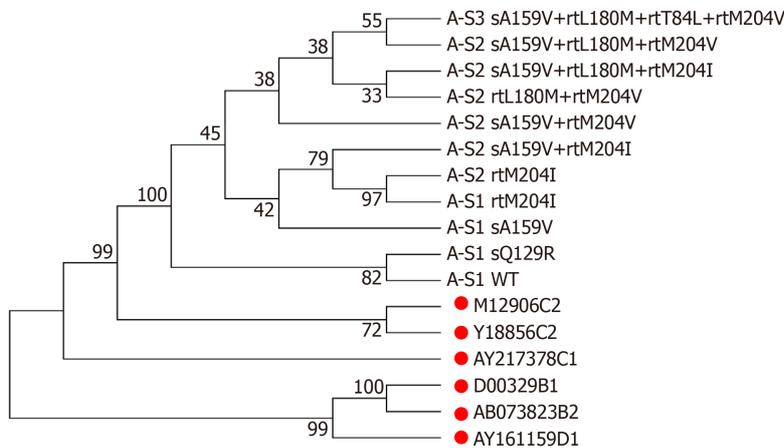


Figure 2 Phylogenetic tree analysis of hepatitis B virus reverse transcriptase sequences from a patient with sA159V + resistance mutations. Reference sequences are marked with solid red circles.

Assessment of drug-induced viral inhibition

A viral inhibition test was performed using the WT and seven mutant strains. Inhibition was evaluated by the levels of HBV replicative intermediates in the samples treated with NAs relative to those in the untreated samples. LAM strongly inhibited WT and M1, with rates of inhibition of 90.5% and 87.5%, respectively. In contrast, LAM-resistant mutants (M2–M5) and ETV-resistant mutants (M6–M7) were highly resistant to LAM, regardless of the presence or absence of the sA159V mutation in the viral genome (Figure 5A). ETV also strongly inhibited WT and M1 with rates of inhibition of 92.5% and 95.6%, respectively. M2–M5 were partially resistant to ETV,

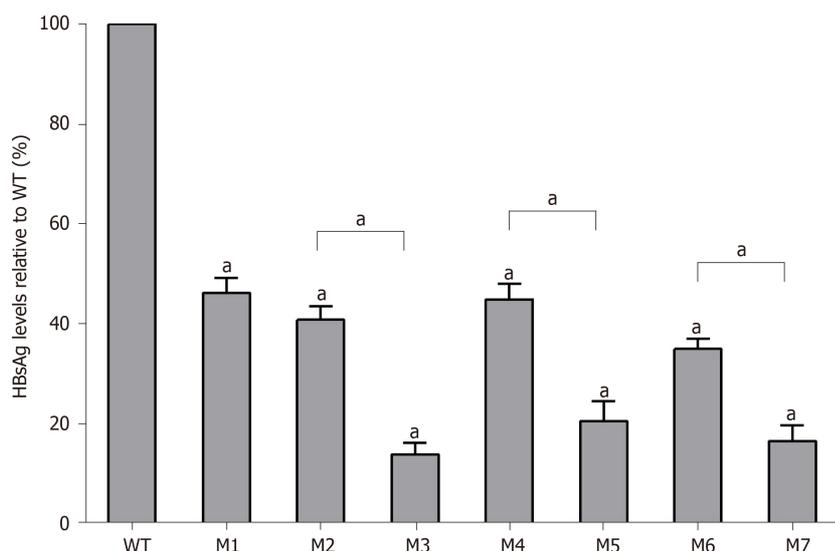


Figure 3 Quantitative analysis of hepatitis B surface antigen levels in individual viral vector-transfected human hepatocellular carcinoma cells. Relative values (%) of mutant hepatitis B surface antigen levels vs wild-type levels are shown. Data are expressed as means \pm standard deviations. M1, sA159V; M2, rtM204I; M3, sA159V+rtM204I; M4, rtL180M+rtM204V; M5, sA159V+rtL180M+rtM204V; M6, rtL180M+rtT184L+rtM204V; M7, sA159V+rtL180M+rtT184L+rtM204V. $^aP < 0.05$ (mutant vs wild-type or other indicated mutant).

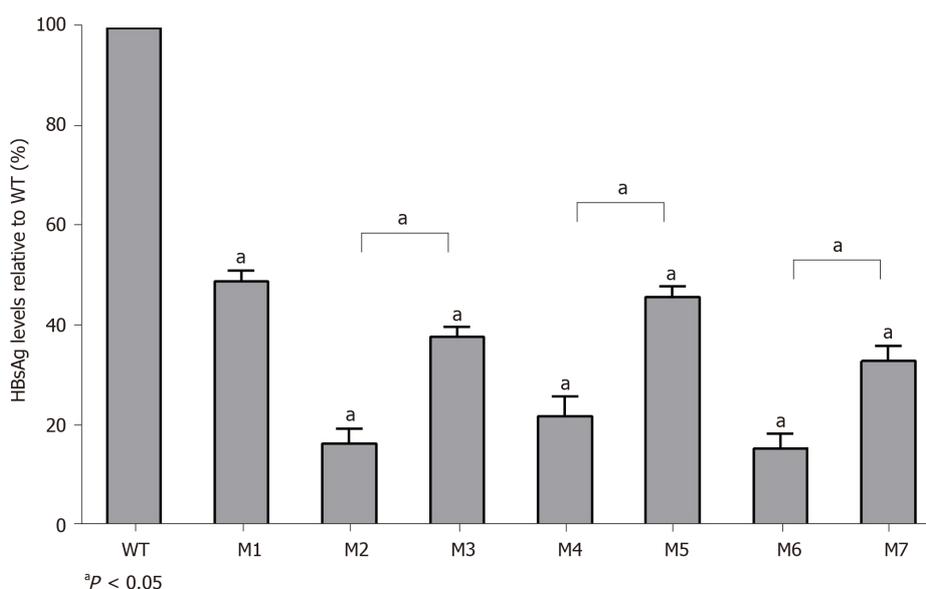


Figure 4 Quantitative analysis of hepatitis B virus deoxyribonucleic acid production levels in individual viral vector-transfected human hepatocellular carcinoma cells. Relative values (%) of mutant hepatitis B virus deoxyribonucleic acid levels vs wild-type levels are shown. Data are expressed as the means \pm standard deviations. M1, sA159V; M2, rtM204I; M3, sA159V+rtM204I; M4, rtL180M+rtM204V; M5, sA159V+rtL180M+rtM204V; M6, sA159V+rtL180M+rtT184L+rtM204V; M7, rtL180M+rtT184L+rtM204V. $^aP < 0.05$ (mutant vs wild-type or other indicated mutants).

with 54.9%-64.7% inhibition. M6-M7 were highly resistant to ETV (Figure 5B). All the tested viral strains were highly sensitive to ADV and TDF, with rates of inhibition of 87.29%-95.04% (Figure 5C and D).

DISCUSSION

The clinical implications of immune escape-associated mutations arise from their relationship with occult HBV infections, HBV reactivation, and HB vaccination failure^[27-30]. There is a paucity of data from population-based clinical investigations about the link between immune escape-associated mutations and drug-resistance

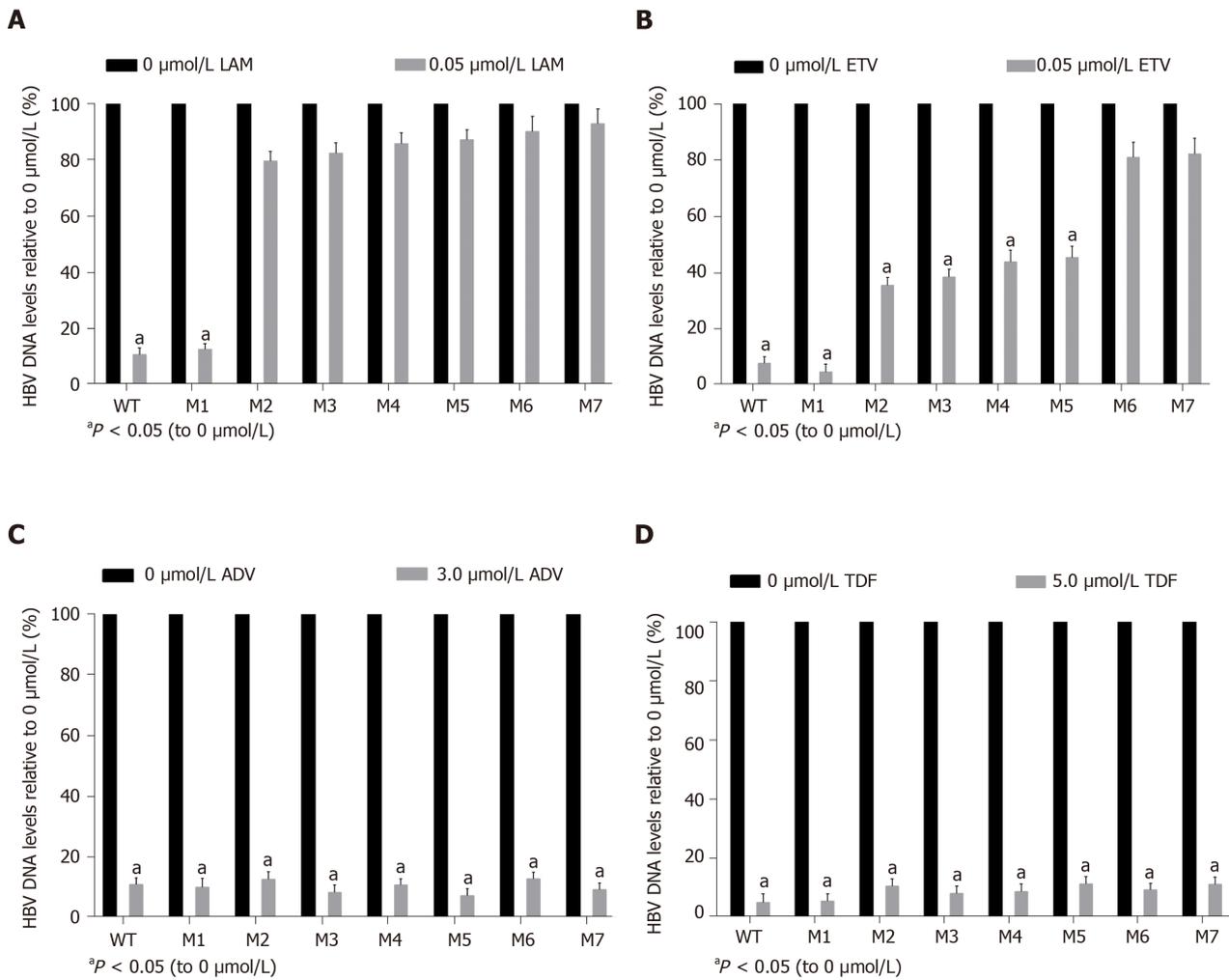


Figure 5 Assessment of drug-induced viral inhibition. Human hepatocellular carcinomas cells were transiently transfected with wild-type or individual viral vectors and cultured with or without one of the following four drugs: (A) 0.05 μmol/L lamivudine, (B) 0.05 μmol/L entecavir, (C) 3.0 μmol/L adefovir, and (D) 5.0 μmol/L tenofovir disoproxil fumarate. Viral inhibition was evaluated as the relative hepatitis B virus deoxyribonucleic acid level of samples with the drug to that without the drug. M1, sA159V; M2, rtM204I; M3, sA159V+rtM204I; M4, rtL180M+rtM204V; M5, sA159V+rtL180M+rtM204V; M6, rtL180M+rtT184L+rtM204V; M7, sA159V+rtL180M+rtT184L+rtM204V. ^aP < 0.05.

mutations. Our analysis of the largest number of resistance mutation-positive patients to date clearly showed that the frequency of immune escape-associated mutations is significantly higher in resistance mutation-positive patients than in resistance mutation-negative patients.

We selected the sA159V mutation for detailed analyses because: (1) Its frequency was significantly higher in resistance mutation-positive patients than in resistance mutation-negative patients; (2) It was frequently detected together with LAM-, ADV-, and ETV-resistance mutations; and (3) Its virological features have not been documented by phenotypic analyses.

In a longitudinal analysis of five patients, the coexistence of sA159V with LAM/ADV/ETV-resistance mutations was frequently detected in the viral pool along with virological breakthrough or an inadequate virological response upon NA therapy. In addition, the sA159V mutation alone was detected before the emergence of the resistance mutation and was recovered after the sA159V-containing resistant mutants were effectively suppressed by rescue therapy. A phylogenetic analysis of Patient A-derived viral strains showed that sA159V+rtM204I (rtL180M) and sA159V+rtM204V (rtL180M) mutants are likely derived from the sA159V mutant as an adaptation to LAM pressure. The sA159V+rtL180M+rtT184L+rtM204V mutant is probably derived from sA159V+rtL180M+rtM204V as an adaptation to ETV pressure.

sA159V mutants had lower HBsAg levels than the WT strain. Viral strains harboring both sA159V and LAM- or ETV-resistance mutations exhibited significantly lower HBsAg levels than their counterpart strains lacking sA159V mutations. In contrast, the HBV DNA levels were partially restored in the LAM- or ETV-resistance viral strains

with sA159V compared to the levels in the WT strain, suggesting that the sA159V mutation has a compensatory effect on replication in resistant viral strains. Notably, the sA159V mutation had no effect on LAM and ETV sensitivity.

In view of these results, it is possible that the sA159V mutation increases the fitness of resistant mutants by alleviating anti-HB immune stress and enhancing viral replication competency rather than by directly increasing drug resistance. This is supported by a previous study demonstrating that two classical immune escape-associated mutations, sG145R and sP120T, significantly reduce HBsAg production and increase the replication capacity of LAM-resistant HBV mutants^[31]. Of note, our study was based on patient-derived viral strains rather than artificially generated strains, thus providing convincing evidence.

Nevertheless, *in vitro* experimental data may not always fully reflect *in vivo* processes. In our study, the sA159V mutant had lower HBsAg production than the WT strain. However, sA159V-positive patients had similar serum HBsAg levels to those of sA159V-negative patients. This bias could be explained by the frequent coexistence of the sA159V mutant with the WT virus in these patients. Although a large number of patients were investigated, the study was restricted by the inability to collect serial samples from many patients.

In summary, we provide evidence supporting the influence of HBV immune escape-associated mutations on drug resistance based on a large-scale clinical investigation. We also found that the sA159V mutation might increase the fitness of LAM/ETV-resistant mutants by decreasing the HBsAg levels and increasing the viral replication capacity. These results provide new insights into the association of HBV immune escape with HBV drug resistance.

ARTICLE HIGHLIGHTS

Research background

A large number of patients were surveyed for both immune escape-associated and drug-resistance mutations.

Research motivation

A link between immune escape-associated and resistance mutations was identified.

Research objectives

The association between immune escape-associated mutations and nucleotide analog resistance mutations was evaluated.

Research methods

Upon follow-up, hepatitis B virus (HBV) sA159V was found to have contributed to resistance in several patients.

Research results

HBV sA159V reduced the hepatitis B surface antigen production but increased the replication capacity of lamivudine (LAM)/entecavir (ETV)-resistant mutants.

Research conclusions

sA159V might increase the fitness of LAM/ETV-resistant mutants under environmental pressure in some cases.

Research perspectives

Immune escape-associated and drug-resistance mutations.

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Retrospective Study

RBBP4 promotes colon cancer malignant progression via regulating Wnt/ β -catenin pathway

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Data sharing statement: Technical appendix, statistical code, and dataset available from the corresponding author at

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Abstract

BACKGROUND

Our previous study demonstrated that RBBP4 was upregulated in colon cancer and correlated with poor prognosis of colon cancer and hepatic metastasis. However, the potential biological function of RBBP4 in colon cancer is still unknown.

AIM

To investigate the biological role and the potential mechanisms of RBBP4 in colon cancer progression.

METHODS

Real-time polymerase chain reaction and western blot analysis were used to detect the expression of RBBP4 in colon cancer cell lines. The cell proliferation and viability of SW620 and HCT116 cells with RBBP4 knockdown was detected by Cell Counting Kit-8 and 5-ethynyl-2'-deoxyuridine staining. The transwell assay was used to detect the invasion and migration capabilities of colon cancer cells with RBBP4 knockdown. Flow cytometry apoptosis assay was used to detect the apoptosis of colon cancer cells. Western blotting analysis was used to detect the expression of epithelial-mesenchymal transition and apoptosis related markers in colon cancer. The nuclear translocation of β -catenin was examined by Western blotting analysis in colon cancer cells with RBBP4 knockdown. The TOPFlash luciferase assay was used to detect the effect of RBBP4 on Wnt/ β -catenin activation. The rescue experiments were performed in colon cancer cells treated

Wfzhu@163.com. Participants gave informed consent for data sharing.

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with Wnt/ β -catenin activator LiCl and RBBP4 knockdown.

RESULTS

We found that RBBP4 was highly expressed in colon cancer cell lines. The 5-ethynyl-2'-deoxyuridine assay showed that knockdown of RBBP4 significantly inhibited cell proliferation. RBBP4 inhibition reduced cell invasion and migration *via* regulating proteins related to epithelial-mesenchymal transition. Knockdown of RBBP4 significantly inhibited survivin-mediated apoptosis. Mechanistically, the TOPFlash assay showed that RBBP4 knockdown increased activity of the Wnt/ β -catenin pathway. Meanwhile, RBBP4 knockdown suppressed nuclear translocation of β -catenin. With Wnt/ β -catenin activator, rescue experiments suggested that the role of RBBP4 in colon cancer progression was dependent on Wnt/ β -catenin pathway.

CONCLUSION

RBBP4 promotes colon cancer development *via* increasing activity of the Wnt/ β -catenin pathway. RBBP4 may serve as a novel therapeutic target in colon cancer.

Key Words: Colon cancer; Wnt/ β -catenin; RBBP4; Epithelial-mesenchymal transition; Apoptosis; Invasion

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Core Tip: Our previous study demonstrated upregulation of RBBP4 in colon cancer and correlation of poor prognosis with colon cancer and hepatic metastasis. This study explored the potential biological function of RBBP4 in colon cancer. We found that RBBP4 was highly expressed in colon cancer cell lines. Knockdown of RBBP4 significantly inhibited cell proliferation and survivin-mediated apoptosis and suppressed nuclear translocation of β -catenin. RBBP4 inhibition reduced cell invasion and migration *via* regulating proteins related to epithelial-mesenchymal transition. Mechanistically, RBBP4 knockdown increased activity of the Wnt/ β -catenin pathway. RBBP4 may serve as a novel therapeutic target in colon cancer.

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INTRODUCTION

Colon cancer is one of the most common malignancies in developed countries. There are more than one million new cases of colon cancer worldwide and 608000 deaths every year^[1]. Although the treatment of colon cancer has made great progress, including surgery or radiotherapy and chemotherapy, the prognosis of patients with colon cancer has shown no marked progress in recent years^[2]. The 5-year relative survival rate of patients with stage IV disease is slightly higher than 10%^[3,4]. Although considerable efforts have been made in the past few years to clarify the mechanisms underlying the development and progression of colon cancer, it is still far from completely understood. Hence, it is necessary to explore the further mechanisms involved in the pathogenesis of colon cancer and to develop new therapeutic targets.

RBBP4 is a new, 48-kD tumor-specific protein found in HeLa cell lysates^[5,6]. RBBP4 belongs to a highly conserved subfamily of nucleoproteins with four WD repeat sequences. RBBP4 binds to retinoblastoma protein *in vivo* and *in vitro*, hence the name^[7]. The *RBBP4* gene encodes a protein that is part of several chromatin-modified protein complexes, such as nucleosome remodeling and deacetylation complex^[8], polycomb repressor complex 2^[9], and SIN3-chromatin modulating complexes^[10], which influence gene transcription, and regulates cell cycle and proliferation^[11]. In recent decades, accumulated research has demonstrated that RBBP4 plays a key role in the pathogenesis of cancers, such as liver^[12], breast^[13], and gastric^[14,15] cancers. In our previous study, we proved that RBBP4 is upregulated in colon cancer and may serve

as a novel predictor for poor prognosis of colon cancer and liver metastasis^[16]. However, its potential role and mechanisms in colon cancer have not been reported.

Therefore, the present study aimed to explore the potential role of RBBP4 in colon cancer aggravation and the underlying molecular mechanisms. We detected expression of RBBP4 in colon cancer cell lines, then investigated the role of RBBP4 in colon cancer cell proliferation, migration, invasion, and apoptosis and finally explored the molecular mechanisms of RBBP4 in colon cancer malignancy characteristics. This study clarifies the role of RBBP4 in colon cancer development through its effect on the Wnt/ β -catenin signaling pathway.

MATERIALS AND METHODS

Cell culture

A normal human colon cell line (NCM640) and colon cancer cell lines (SW620, HT29, LoVo, SW480, and HCT-116) were purchased from the Cell Bank of Type Culture Collection of the Chinese Academy of Sciences (Shanghai, China). These cell lines originated from the American Type Culture Collection (ATCC, Manassas, VA, United States). All the cell lines were cultured in the corresponding medium according to the suggestion of ATCC with 10% fetal bovine serum (FBS). All the cells were maintained in a humidified incubator with 5% CO₂ at 37 °C. The Wnt/ β -catenin activator LiCl was obtained from Sigma-Aldrich (Munich, Germany).

Plasmids, siRNA, and transfection

The plasmids of the human *RBBP4* gene, siRNA targeting human RBBP4, and their controls were synthesized by Genechem (Shanghai, China). The cells were transfected with siRNAs, plasmids, or their controls using Lipofectamine 3000 (Invitrogen, Carlsbad, CA, United States). In total, 2×10^5 – 3×10^5 cells were transfected with 100 pmol siRNA or 2 μ g plasmid DNA. Western blotting was used to detect the transfection efficiency 24 h and 48 h after transfection, and real-time polymerase chain reaction was used for verification.

Real time polymerase chain reaction detection

Total RNA from colon cancer tissues and cells was extracted using TRIzol reagent (Invitrogen). Total RNA (0.5 μ g) was reversed transcribed to cDNA using PrimeScript™ RT reagent Kit with gDNA Eraser (Takara, Dalian, China). SYBR Green Polymerase Chain Reaction Master mix (Takara) was used to determine the mRNA level of *RBBP4* on an ABI 7900Fast Real-time Detection System (Applied Biosystems, Carlsbad, CA, United States) in 20 μ L reaction system. All reactions were performed in triplicate. The relative expression of *RBBP4* was normalized to the internal reference *GAPDH*. The 2^{-DDCT} method was used to analyze the data. The primers used in the study were as follows: *GAPDH* forward primer: 5'-ATG GGG AAG GTG AAG GTC G-3', *GAPDH* reverse primer: 5'-GGG GTC ATT GAT GGC AAC AAT A-3'; *RBBP4* forward primer: 5'-GCT ATG GGC TTT CTT GGA-3', and *RBBP4* reverse primer: 5'-CAC AGG CAG ATG GTA TGG-3'.

Cell Counting Kit-8 assay

Cell viability was assessed by Cell Counting Kit-8 (CCK-8) assay (Dojindo Laboratories, Kumamoto, Japan). Cells were seeded in 96-well plates at 3×10^3 cells per well with 200 μ L culture medium. With supernatant removed, 10 μ L CCK-8 reagent in 100 μ L medium was added to each well at 0 h, 24 h, 48 h, 72 h, and 96 h. The plates were incubated in the dark at 37 °C for 2 h, and absorbance at 450 nm was detected with a microplate reader (BioTek, Winooski, VT, United States). The experiments were performed in triplicate.

5-Ethynyl-2'-deoxyuridine cell proliferation assay

5-Ethynyl-2'-deoxyuridine (EdU) assay was performed using Click-iT™ EdU Imaging Kit with Alexa Fluor™ 488 Azides (Invitrogen). Briefly, 1×10^5 cells were plated in six-well plates and incubated at room temperature overnight. The cells were incubated with 10 μ M EdU for 1 h at 37 °C and fixed in 3.7% paraformaldehyde. After permeabilization with 0.5% Triton X-100 in phosphate buffered saline for 20 min, the cells were reacted with 1 \times Click-iT® reaction cocktail for 20 min. The nuclei were labeled with Hoechst 33342 for 30 min and photographed under a fluorescence microscope. All studies were conducted in triplicate.

Western blotting

Total proteins were extracted using the ice cold radioimmunoprecipitation assay buffer with cocktail protease and phosphatase inhibitors (Cell Signaling Technology, Danvers, MA, United States). NE-PER™ Nuclear and Cytoplasmic Extraction Reagent (Thermo Scientific, Waltham, MA, United States) was used to extract the nuclear and cytoplasmic proteins. Proteins were quantified using a BCA protein assay kit (Thermo Scientific). Then equivalent proteins were separated by 10% SDS-PAGE and transferred to polyvinylidene fluoride membranes (Millipore, Billerica, MA, United States). The membranes were probed with antibodies against RBBP4 (ab92344), survivin (ab134170), GAPDH (ab181620), β -catenin (ab32572), pro-caspase-3 (ab32150) (Abcam, Cambridge, MA, United States), Cleaved caspase-3 (9661), E-cadherin (14472), N-cadherin (13116), vimentin (5741), and histone H3 (14269) (Cell Signaling Technology) overnight at 4 °C and then incubated with horseradish-peroxidase-conjugated secondary antibodies (Cell Signaling Technology) for 1 h at room temperature. The bands were visualized by ECL kit (Millipore).

Migration and invasion assay

The migration and invasion assays were performed by the transwell method. For the invasion assay, the cells were plated on Matrigel-coated upper chambers (24-well inserts; pore size, 8 μ m; BD Biosciences, San Jose, CA, United States). For the migration assay, the cells were plated on uncoated upper chambers. In the lower wells, medium was replaced with fresh medium with 5% FBS. The cells were incubated for 24 h in medium containing 1% FBS, trypsinized, and suspended in medium containing 1% FBS at a final concentration of 1×10^6 cells/mL. Then, 200 μ L cell suspension was placed in each of the upper wells, and the chamber was incubated at 37 °C for 24 h. Cells were fixed and stained with hematoxylin and eosin. The nonmigrating cells from the upper surface of the filter were wiped with a cotton swab. The cells that migrated to the lower side of the filter were counted and photographed with an optical inverted microscope. Five random fields in each assay were counted and averaged.

Flow cytometry analysis of apoptosis

For the assessment of apoptosis, an Annexin V-FITC/propidium iodide (PI) apoptosis detection kit (BD Biosciences) was used. Colon cancer cells were collected in six-well plates at 1×10^6 cells/mL. After transfection for 48 h, the cells were trypsinized and washed once with phosphate buffered saline. After centrifugation at 1000 r/min for 5 min, the cells were stained with 5 μ L Annexin V-FITC and PI in the dark condition for 30 min, and then were analyzed by flow cytometry (BD Biosciences). At least 10000 events were recorded for each sample. The apoptosis data were analyzed by FlowJo V10 software (Tree Star, San Francisco, CA, United States).

Luciferase assays

The TOPFlash assay was performed using the T-cell factor Reporter Plasmid Kit (Millipore). The ratio of luciferase activities from a T-cell factor-responsive reporter (pTOPFlash) *vs* a control luciferase reporter gene construct (pFOPFlash) was determined 48 h after transfection with Lipofectamine 2000 in SW480 and HCT116 cells. Luciferase activities were normalized for transfection efficiency by cotransfection with a β -galactosidase-expressing vector. The cells were transfected with siRBBP4 plasmid or RBBP4 plasmid or control plasmids. The cells were harvested after 24 h and processed for luciferase and β -galactosidase activities, and the data were normalized to β -galactosidase levels.

Statistical analysis

Statistical analyses were performed using GraphPad Prism version 7.0 (GraphPad Software, La Jolla, CA, United States) software and verified by SPSS version 20.0 (SPSS, Chicago, IL, United States). Each experiment was performed at least in triplicate, and the results were expressed as the mean \pm standard deviation. Student's *t* test and one-way analysis of variance were conducted to analyze the differences between groups, and a *P* < 0.05 was considered statistically significant.

RESULTS**RBBP4 is upregulated in human colon cancer cell lines**

In our previous study, we detected the expression pattern of RBBP4 in colon cancer

tissues and proved that RBBP4 was upregulated. In the present study, we examined the protein and mRNA levels of RBBP4 in five human colon cancer cell lines and a normal human colon cell line. mRNA and protein levels of RBBP4 were significantly higher in colon cancer cell lines compared with the normal human colon cell line. We selected SW480 and HCT116 cells with high RBBP4 levels for subsequent experiments (Figure 1A and 1B).

Knockdown of RBBP4 inhibited cell growth in vitro

To investigate the biological function of RBBP4 in colon cancer cells, we knocked down RBBP4 *via* siRNA-mediated gene silencing. The knockdown efficiency was determined by Western blotting (Figure 1C). We then examined the role of RBBP4 in colon cancer cell viability using the CCK-8 assay. Cell viability was decreased in both HCT116 and SW620 cells after RBBP4 knockdown (Figure 1D and 1E). EdU proliferation assay showed that RBBP4 knockdown significantly reduced proliferation of colon cancer cells (Figure 1F and 1G). These results showed that RBBP4 played an essential role in the growth of colon cancer cells.

RBBP4 knockdown receded migration and invasion of colon cancer cells

We examined the effect of RBBP4 knockdown on colon cancer cell migration and invasion *in vitro* using the transwell assay. The number of migrated and invasive cells in RBBP4 knockdown HCT116 and SW620 colon cancer cells was less than that in the control group (Figure 2A and 2B). The epithelial-mesenchymal transition (EMT) pathway has been proved to play a key role in tumor migration and invasion^[17]. To investigate the molecular mechanisms of RBBP4 in regulating colon cancer cell migration and invasion, we performed Western blotting to detect expression of EMT-related proteins including N-cadherin, E-cadherin, and vimentin. RBBP4 knockdown markedly decreased mesenchymal proteins, but upregulated epidermal protein expression (Figure 2C). These results indicated that RBBP4 regulated colon cancer cell migration and invasion *via* the EMT pathway.

RBBP4 knockdown aggravated apoptosis of colon cancer cells

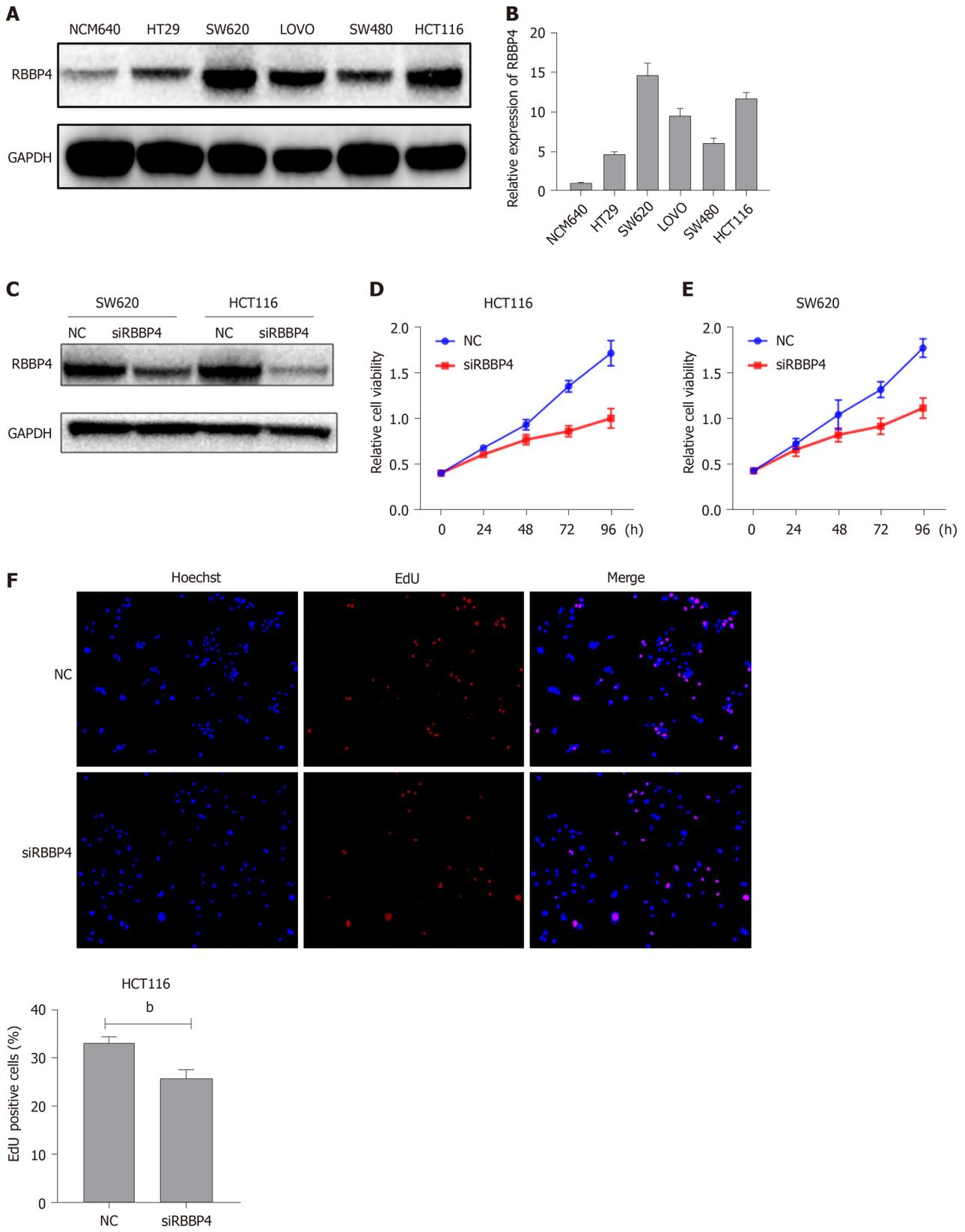
To investigate the mechanism underlying RBBP4-knockdown-induced antiproliferation, we detected the apoptotic rate of colon cancer cells by flow cytometry. Apoptosis rate in HCT116 and SW620 cells with RBBP4 knockdown increased by $42.0\% \pm 2.2\%$ and $33.3\% \pm 2.91\%$, respectively, compared with the control cells ($12.95\% \pm 1.40\%$ and $10.83\% \pm 0.93\%$, $P < 0.01$, Figure 3A and 3B). To investigate the molecular mechanisms of RBBP4 in regulating colon cancer cell apoptosis, we detected apoptosis-related proteins, and showed that survivin, an antiapoptotic protein, was downregulated after RBBP4 knockdown, thus leading to the increase of pro-caspase-3 and cleaved caspase-3.

RBBP4 knockdown suppressed activity of the Wnt/ β -catenin pathway in colon cancer cells

The Wnt/ β -catenin pathway is one of the important signaling pathways inducing EMT, and survivin is a known downstream target of the pathway^[17-19]. We hypothesized that the biological role of RBBP4 was executed through the Wnt/ β -catenin pathway. To clarify this hypothesis, the TOP/FOP flash luciferase reporter assays were used. Compared with the control cells, overexpression of RBBP4 led to an increase of TOP flash luciferase reporter activity in HCT116 and SW620 cells (Figure 4A and 4B). However, RBBP4 knockdown inhibited the activity of the TOP flash luciferase reporter (Figure 4A and 4B). As reported previously, β -catenin nuclear translocation is an essential event for Wnt/ β -catenin pathway activation. To elucidate further the underlying mechanism, we examined the influence of RBBP4 on β -catenin nuclear translocation in colon cancer cells. The level of β -catenin in the nucleus was decreased, while that in cytoplasm was increased by RBBP4 knockdown (Figure 4C). All these data indicated that activity of the Wnt/ β -catenin pathway was regulated by RBBP4 *via* regulation of the nuclear translocation of the β -catenin protein in colon cancer cells.

Function of RBBP4 in colon cancer cells was mediated by the Wnt/ β -catenin pathway

To examine whether the function of RBBP4 in colon cancer was mediated by the Wnt/ β -catenin pathway, we used the Wnt/ β -catenin pathway activator LiCl in a rescue experiment. The role of RBBP4 knockdown on the inhibition of β -catenin



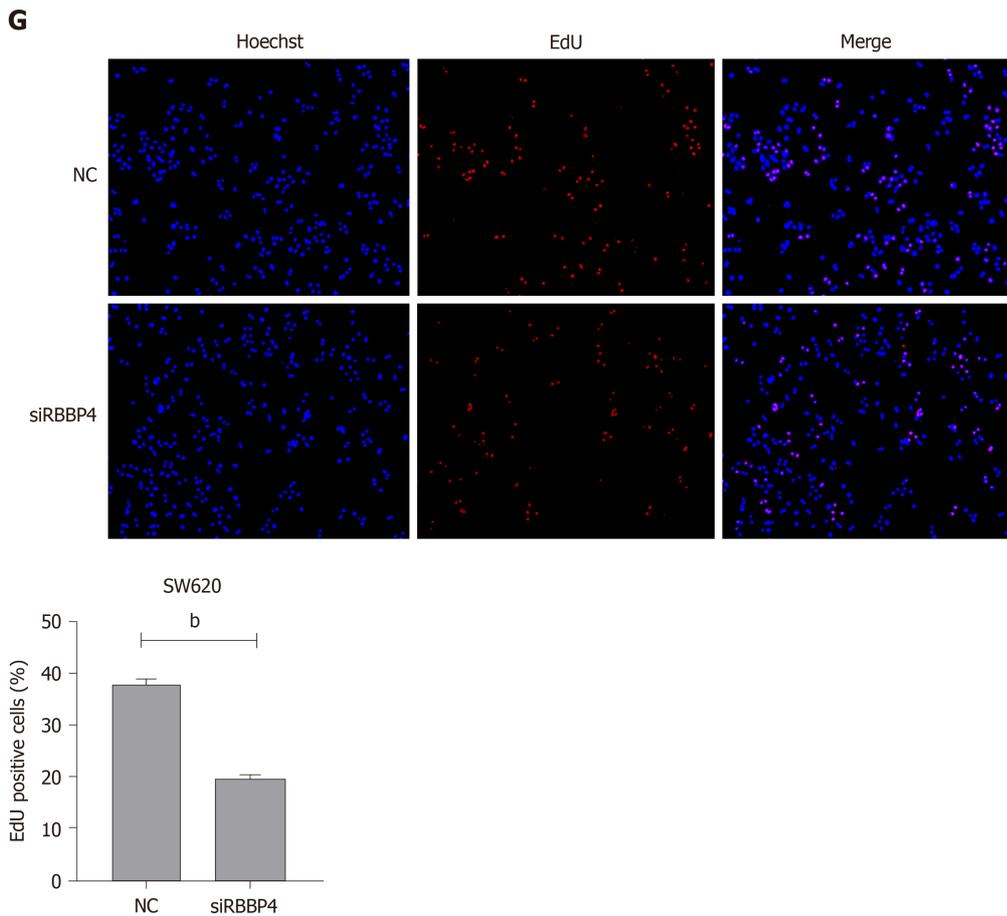


Figure 1 Expression of RBBP4 in colon cancer cell lines and its effect on cell proliferation. A: Protein level of RBBP4 in the colon cancer cell lines quantified by western blotting; B: mRNA level of *RBBP4* in the colon cancer cell lines quantified by polymerase chain reaction; C: RBBP4 siRNA efficiency verified by western blotting in SW620 and HCT116 cells; D: Cell viability was detected by the Cell Counting Kit-8 assay in HCT116 cells; E: Cell viability was detected by the Cell Counting Kit-8 assay in SW620 cells; F and G: Cell proliferation was detected by 5-ethynyl-2'-deoxyuridine assay in HCT116 cells and SW620 cells. ^a $P < 0.01$ vs controls. EdU: 5-Ethynyl-2'-deoxyuridine.

nuclear translocation was partly reversed by LiCl (Figure 5A). CCK-8 assays showed that the viability of HCT116 and SW620 cells treated with RBBP4 siRNA was significantly enhanced when they were cotreated with LiCl compared with untreated cells ($P < 0.05$, Figure 5B and 5C). The transwell assay showed that the inhibition of invasion by RBBP4 knockdown was partly reversed by LiCl ($P < 0.05$, Figure 5C and 5D). The expression of EMT-related proteins was also partly reversed by LiCl compared with the shRBBP4 group (Figure 5E). All these results suggested that the role of RBBP4 in colon cancer progression is mediated by the Wnt/ β -catenin pathway.

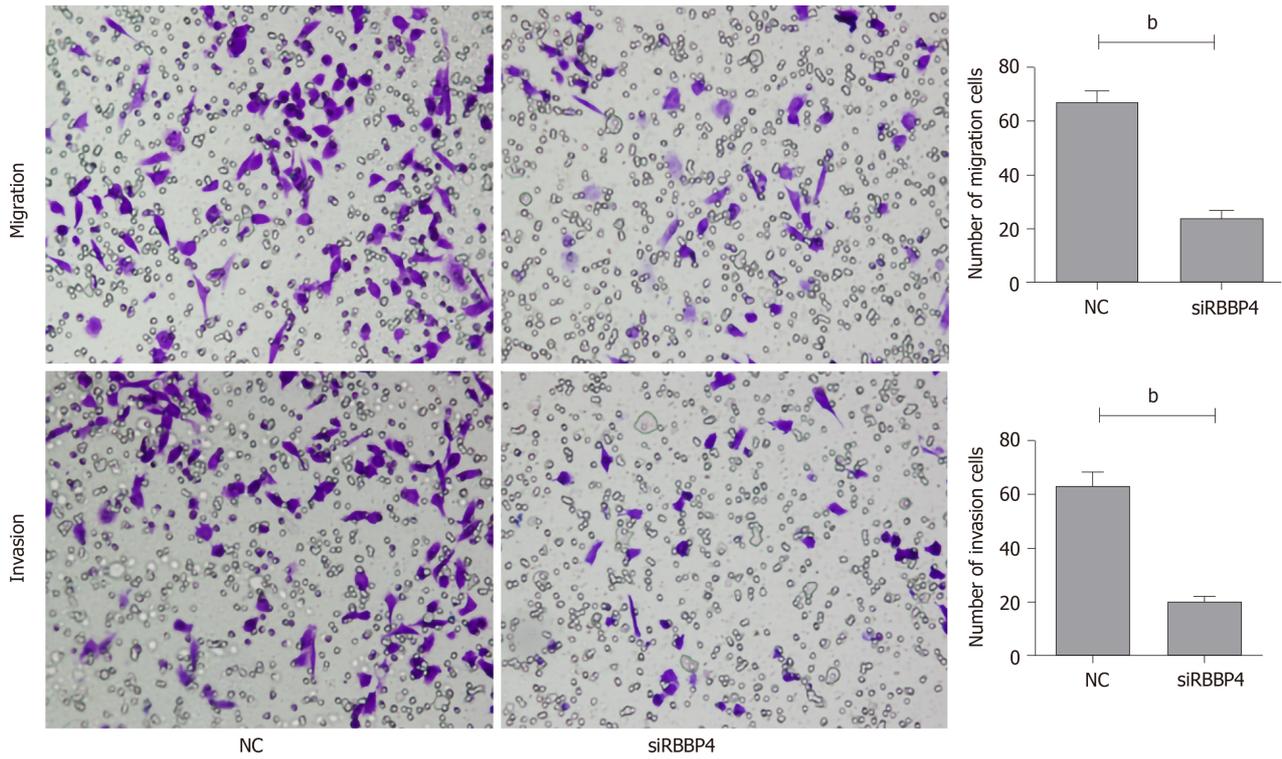
DISCUSSION

RBBP4, also known as RbAp48, is named for its ability to bind to retinoblastoma proteins *in vivo* and *in vitro*^[20]. Previous studies showed that the RBBP4 protein is a component of a variety of complexes involved in chromatin assembly, remodeling, and nucleosome modification, such as SIN3^[21], polycomb repressor complex 2^[22,23], histone acetyltransferase 1^[24], and chromatin assembly factor 1^[25] and plays a different role in each complex. It has been demonstrated that RBBP4 expression is upregulated and correlated with the malignant phenotypes in many types of human tumors, such as lung cancer^[26], liver cancer^[27], thyroid carcinoma^[28], and acute lymphoblastic leukemia^[29]. However, little is known about RBBP4 in colon cancer.

In our previous study, we demonstrated that RBBP4 was upregulated in colon cancer tissues, and elevated RBBP4 level was correlated with poor prognosis and liver metastasis. Nevertheless, the detailed molecular biological function of RBBP4 and the potential mechanisms in colon cancer are unclear. In the present study, our evidence indicated that RBBP4 knockdown decreased the proliferation, apoptosis, and

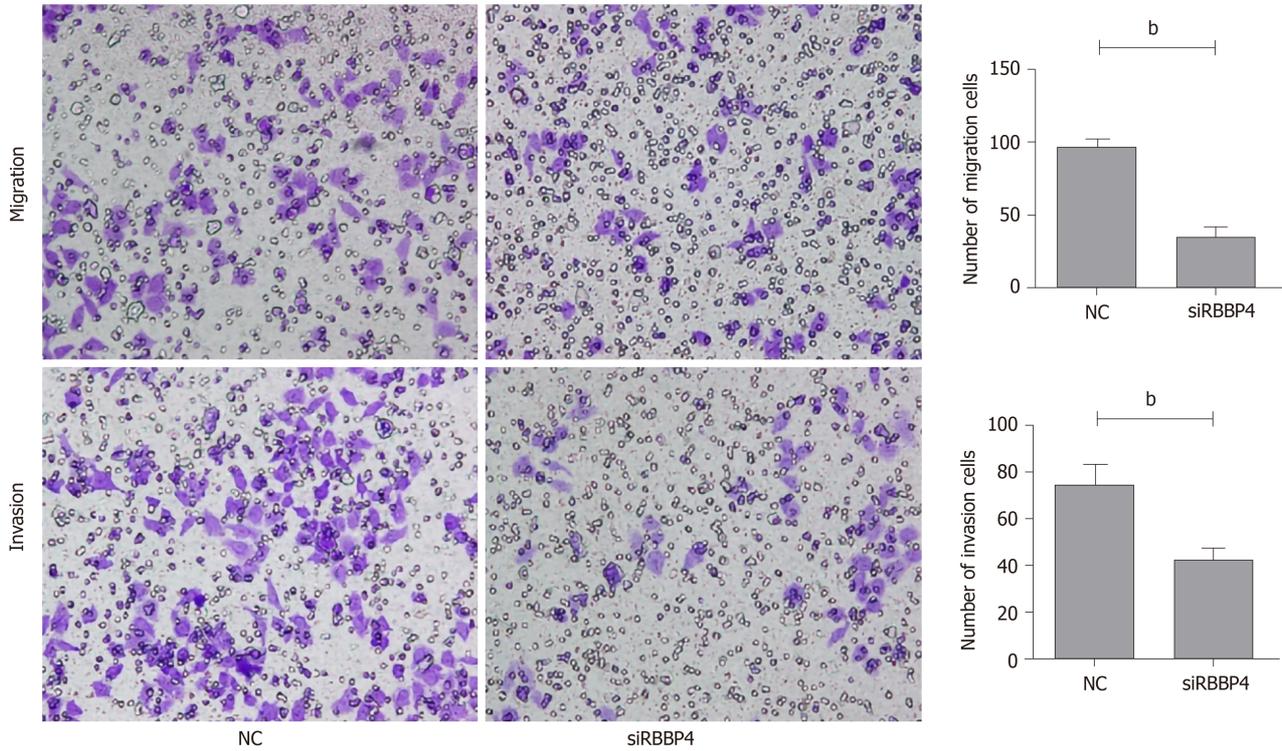
A

SW620



B

HCT116



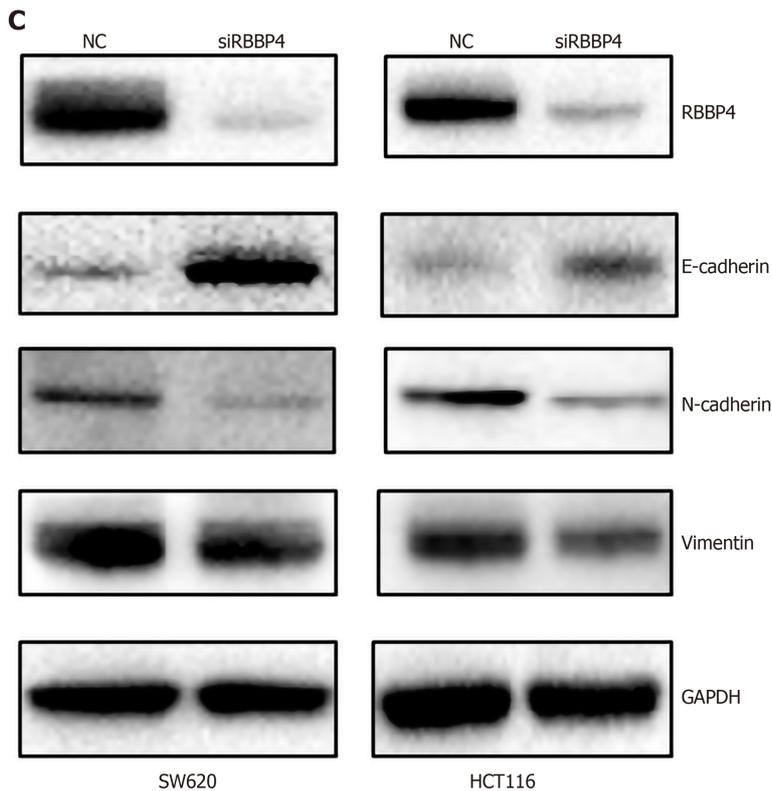


Figure 2 RBBP4 knockdown inhibits migration and invasion of colon cancer cell lines. A: Migration and invasion of RBBP4 knockdown SW620 cells were measured by the transwell assay. Results were quantitated by counting migrating and invasive cells in five randomly chosen high-power fields for each replicate; B: Migration and invasion of RBBP4 knockdown HCT116 cells were measured by the transwell assay; C: Western blotting examination for epithelial-mesenchymal transition related proteins. ^b*P* < 0.01 vs controls.

aggressiveness of colon cancer cells, suggesting its oncogenic functions in colon cancer progression. RBBP4 promoted the nuclear accumulation of β -catenin, thus activating the Wnt/ β -catenin signaling pathway. The role of RBBP4 in colon cancer progression was partially dependent on Wnt/ β -catenin signaling pathway.

Abnormalities in the Wnt signaling pathway are associated with a variety of tumor types, including colon cancer^[30,31]. The Wnt pathway is classified into canonical and noncanonical pathways; the former of which is β -catenin dependent^[32]. For the canonical pathway, in the absence of Wnt ligands, free cytoplasmic β -catenin binds to cytoplasmic complexes containing *Adenomatous Polyposis Coli*, axin, casein kinase 1a, and glycogen synthase kinase 3b, which promotes the phosphorylation of β -catenin leading to β -catenin ubiquitination and subsequent proteasomal degradation. The interaction between Wnt and Frizzled leads to the activation of the Disheveled family proteins. The activated Disheveled proteins cause the inhibition of glycogen synthase kinase 3b, resulting in the accumulation of free cytoplasmic β -catenin, which is then transported to the nucleus. In the nucleus, β -catenin binds to various transcription factors, such as T-cell factor and lymphoid enhancer factor 1, to activate Wnt target genes^[33-35]. However, the relationship between RBBP4 and the Wnt pathway is poorly understood. In our study, for the first time we proved that RBBP4 could enhance the nuclear translocation of β -catenin and activate the Wnt/ β -catenin pathway in colon cancer.

Studies over the past decade have shown that cells that harbor functionally impaired mutations of Wnt signaling cascades, such as *Adenomatous Polyposis Coli*, β -catenin, and axin, are thought to be prevalent in colon cancer^[36]. The mutations lead to abnormal transcriptional induction of Wnt/ β -catenin downstream genes^[37]. Many target genes of Wnt/ β -catenin have been identified, such as survivin^[38]. Survivin was recently identified as an inhibitor of apoptosis that directly inhibits caspase-3 and caspase-7 activity^[39]. The role of survivin in colorectal tumorigenesis has been shown. We found that RBBP4 knockdown inhibited the level of survivin, thus inducing apoptosis of colon cancer cells. This result proved that RBBP4 regulates the Wnt/ β -catenin pathway.

Liver metastasis is an important characteristic of colon cancer, and EMT plays a central role^[40]. A previous study showed that activation of Wnt/ β -catenin signaling

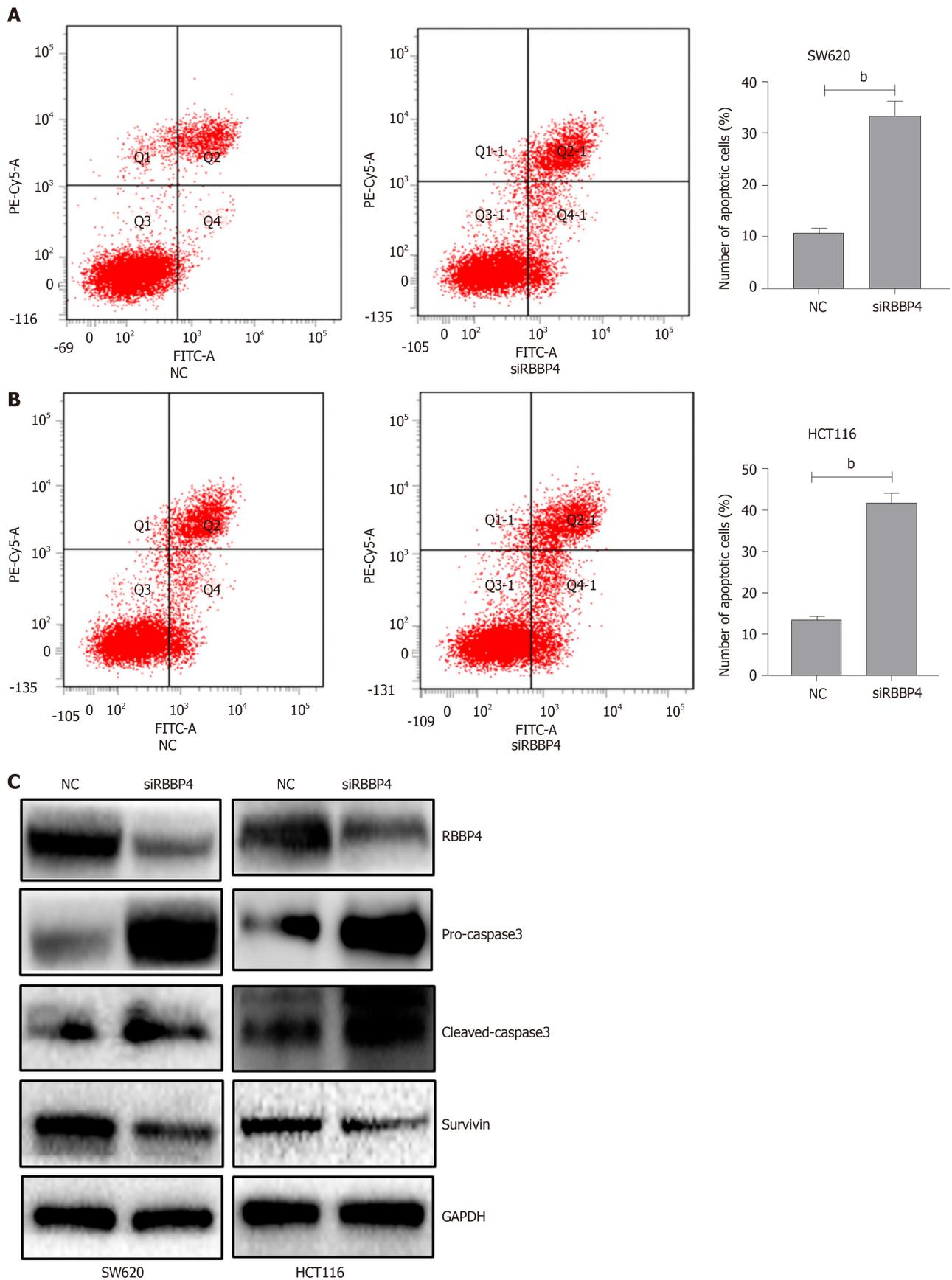


Figure 3 RBBP4 knockdown inhibits apoptosis of colon cancer cell lines. **A:** Apoptosis of SW620 cells examined by flow cytometry with the Annexin V-FITC/propidium iodide kit. The cells in the Q4 quadrant were defined as the apoptotic cells; **B:** Apoptosis of HCT116 cells examined by flow cytometry with the Annexin V-FITC/propidium iodide kit; **C:** Western blotting examination for apoptotic proteins. ^b*P* < 0.01 vs controls.

results in expression of target genes that lead to the dedifferentiated phenotype and

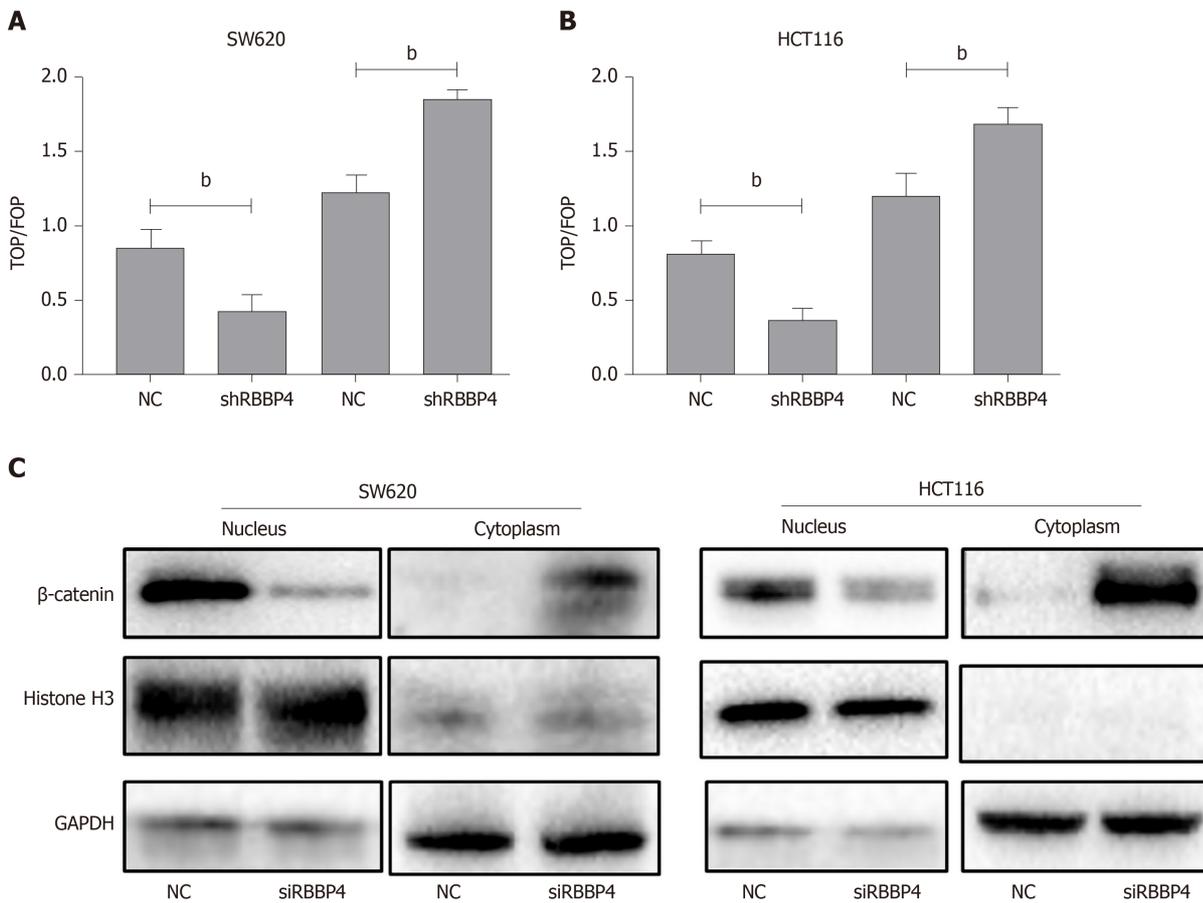
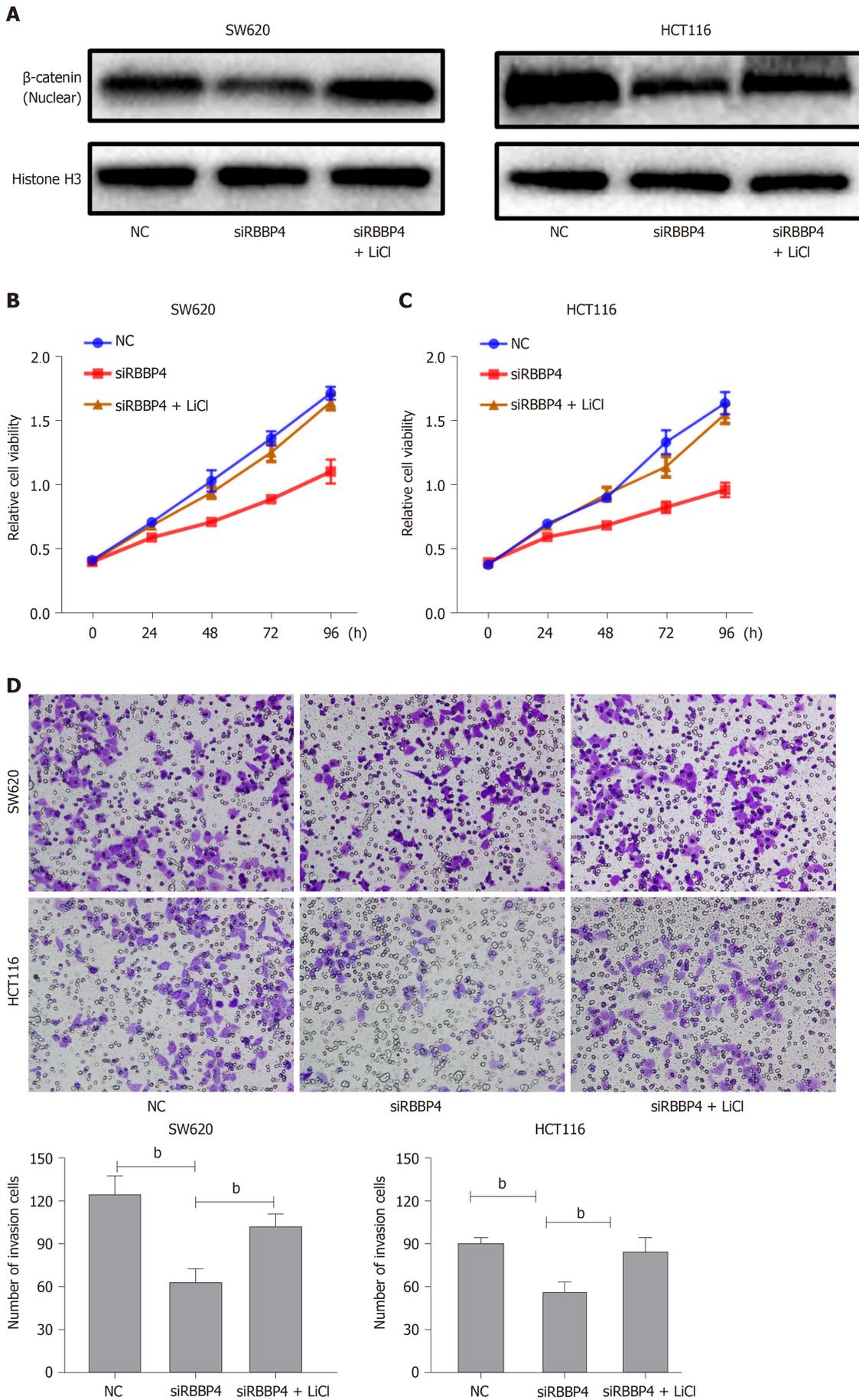


Figure 4 Effect of RBBP4 on activation of Wnt/ β -catenin pathway. A: The TOPFlash experiment in SW620 cells with RBBP4 knockdown or RBBP4 overexpression; B: The TOPFlash experiment in HCT116 cells with RBBP4 knockdown or RBBP4 overexpression; C: Western blotting of the level of β -catenin in cell nucleus and cytoplasm. ^b*P* < 0.01 vs controls.

EMT of colon cancer cells^[41]. The nuclear translocation of β -catenin was reported to induce Slug and inhibit E-cadherin transcription in colon cancer^[42]. However, the relationship between RBBP4 and EMT has not been clarified. In our study, we found that RBBP4 knockdown markedly decreased mesenchymal proteins but upregulated expression of epidermal proteins, indicating inhibition of the EMT pathway. This process may be mediated by the Wnt/ β -catenin pathway.

CONCLUSION

In conclusion, the results presented in this study demonstrated that RBBP4 plays an important role in the malignant progression of colon cancer. This is probably induced *via* inhibiting Wnt/ β -catenin pathway activity and relocating β -catenin from the nucleus to the plasma membrane. Further investigation of the functional mechanism of RBBP4 as a tumor oncogene may provide a potential therapeutic strategy for intervention of colon cancer progression.



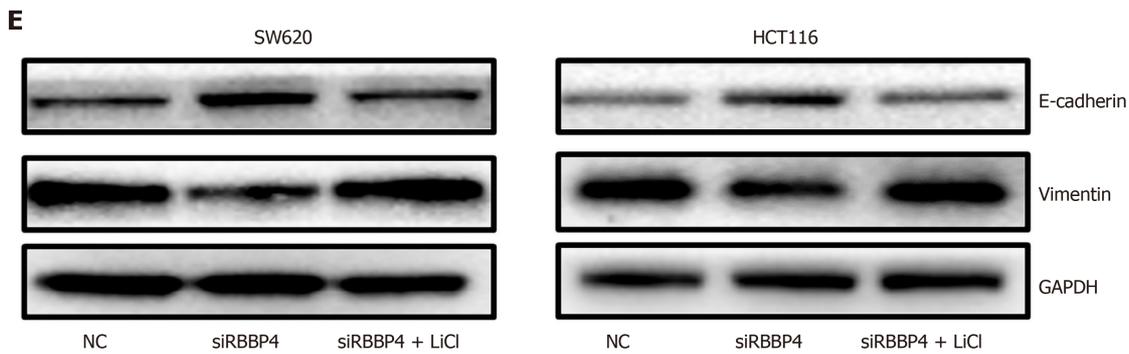


Figure 5 Rescue experiments of RBBP4. A: SW620 and HCT116 cells with RBBP4 siRNA or negative control transfection were incubated with or without 20 mmol/L LiCl, then the level of β -catenin in the nucleus was detected by western blotting; B: The viability of SW620 cells with RBBP4 siRNA or negative control transfection cultured in medium with or without 20 mmol/L LiCl; C: The viability of HCT116 cells with RBBP4 siRNA or negative control transfection cultured in medium with or without 20 mmol/L LiCl; D: Invasion of SW620 and HCT116 cells with RBBP4 siRNA or negative control transfection cultured in medium with or without 20 mmol/L LiCl; E: The protein expression of E-cadherin and vimentin in SW620 and HCT116 cells with RBBP4 siRNA or negative control transfection cultured in medium with or without 20 mmol/L LiCl. ^b $P < 0.01$ vs controls.

ARTICLE HIGHLIGHTS

Research background

Our previous study demonstrated that RBBP4 is upregulated in colon cancer and correlated with poor prognosis of colon cancer and hepatic metastasis. However, the potential biological function of RBBP4 in colon cancer is still unknown.

Research motivation

To explore the potential mechanisms underlying colon cancer development and discover biomarkers for the treatment of colon cancer.

Research objectives

To investigate the underlying mechanisms of RBBP4 in colon cancer malignant development.

Research methods

Real-time polymerase chain reaction and western blot analysis were used to detect the expression of RBBP4 in colon cancer cell lines. The cell proliferation and viability of SW620 and HCT116 cells with RBBP4 knockdown was detected by Cell Counting Kit-8 and 5-ethynyl-2'-deoxyuridine staining. The transwell assay was used to detect the invasion and migration capabilities of colon cancer cells with RBBP4 knockdown. Flow cytometry apoptosis assay was used to detect the apoptosis of colon cancer cells with RBBP4 knockdown. Western blot analysis was used to detect the expression of epithelial-mesenchymal transition and apoptosis related markers in colon cancer with RBBP4 knockdown. The nuclear translocation of β -catenin was examined by western blot analysis in colon cancer cells with RBBP4 knockdown. The TOPFlash luciferase assay was used to detect effect of RBBP4 on Wnt/ β -catenin activation. The rescue experiments were performed in colon cancer cells treated with Wnt/ β -catenin activator LiCl and RBBP4 knockdown.

Research results

We found that RBBP4 was highly expressed in colon cancer cell lines. The 5-ethynyl-2'-deoxyuridine assay showed that knockdown of RBBP4 significantly inhibited cell proliferation. RBBP4 inhibition reduced cell invasion and migration *via* regulating proteins related to epithelial-mesenchymal transition. Knockdown of RBBP4 significantly inhibited surviving-mediated apoptosis. Mechanistically, the TOPFlash assay showed that RBBP4 knockdown increased activity of the Wnt/ β -catenin pathway. RBBP4 knockdown suppressed nuclear translocation of β -catenin. With a Wnt/ β -catenin activator, rescue experiments suggested that the role of RBBP4 in colon cancer progression was dependent on the Wnt/ β -catenin pathway.

Research conclusions

This study demonstrated that RBBP4 promoted colon cancer development *via*

increasing activity of the Wnt/ β -catenin pathway. RBBP4 may serve as a novel therapeutic target in colon cancer.

Research perspectives

In the future, additional research will be carried out to further explore the important role of RBBP4 and whether RBBP4 knockdown can be employed to enhance the sensitivity of chemotherapy of colon cancer and to develop novel anticancer treatments.

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Observational Study

Updated bone mineral density status in Saudi patients with inflammatory bowel disease

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Abstract**BACKGROUND**

Little is known about inflammatory bowel disease (IBD) burden and its impact on bone mineral density (BMD) among adult patients in Saudi Arabia. To the best of our knowledge, our study is the only study to give an update about this health problem in adult Saudi patients with IBD. IBD is a great risk factor for reduced BMD due to its associated chronic inflammation, malabsorption, weight loss and medication side effects. Consequently, screening for reduced BMD among patients with IBD is of utmost importance to curb and control anticipated morbidity and mortality among those patients.

Informed consent statement: All study participants provided informed written consent prior to study enrollment.

Conflict-of-interest statement: The authors declare no conflicts of interest.

Data sharing statement: The datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

STROBE statement: The authors have read the STROBE Statement – checklist of items, and the manuscript was prepared and revised according to the STROBE Statement.

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AIM

To assess the relationship between IBD and BMD in a sample of adult Saudi patients with IBD.

METHODS

Ninety adult patients with IBD - 62 Crohn's disease (CD) and 28 ulcerative colitis (UC) - were recruited from King Fahad Specialist Hospital gastroenterology clinics in Buraidah, Al-Qassim. All enrolled patients were interviewed for their demographic information and for IBD- and BMD-related clinical data. All patients had the necessary laboratory markers and dual-energy x-ray absorptiometry scans to evaluate their BMD status. Patients were divided into two groups (CD and UC) to explore their clinical characteristics and possible risk factors for reduced BMD.

RESULTS

The CD group was significantly more prone to osteopenia and osteoporosis compared to the UC group; 44% of the CD patients had normal BMD, 19% had osteopenia, and 37% had osteoporosis, while 78% of the UC patients had normal BMD, 7% had osteopenia, and 25% had osteoporosis (P value < 0.05). In the CD group, the lowest t -score showed a statistically significant correlation with body mass index (BMI) ($r = 0.45$, $P < 0.001$), lumbar z -score ($r = 0.77$, $P < 0.05$) and femur z -score ($r = 0.85$, $P < 0.05$). In the UC group, the lowest t -score showed only statistically significant correlation with the lumbar z -score ($r = 0.82$, $P < 0.05$) and femur z -score ($r = 0.80$, $P < 0.05$). The ROC-curve showed that low BMI could predict the lowest t -score in the CD group with the best cut-off value at ≤ 23.43 (m/kg^2); area under the curve was 0.73 (95% CI: 0.59–0.84), with a sensitivity of 77%, and a specificity of 63%.

CONCLUSION

Saudi patients with IBD still have an increased risk of reduced BMD, more in CD patients. Low BMI is a significant risk factor for reduced BMD in CD patients.

Key Words: Inflammatory bowel disease; Crohn's disease; Ulcerative colitis; Bone mineral density; Osteoporosis; Fracture risk

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Core Tip: Saudi patients with inflammatory bowel disease still have a high prevalence of reduced bone mineral density. Osteopenia and osteoporosis burdens were 19% and 37% in Crohn's disease (CD) patients, and 7% and 25% in ulcerative colitis patients, respectively. Low body mass index is a significant risk factor for reduced bone mineral density in CD patients.

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INTRODUCTION

Crohn's disease (CD) and ulcerative colitis (UC) are the main subtypes of inflammatory bowel disease (IBD). Europe and North America have the highest burden of CD and UC, approaching more than 0.3% of the population^[1]. However, there has recently been an abrupt rise in the IBD burden in newly industrialized countries worldwide, including socioeconomics and lifestyle changes^[2]. This rising trend is a result of multiple factors, including socioeconomic and lifestyle changes^[2].

Data about the IBD prevalence in Saudi Arabia are very limited in the literature. However, similar to other Asian countries, Saudi Arabia has experienced lifestyle and industrialization changes over the past decades, with the available data pointing to increasing trends of both CD and UC in the eastern, western and central regions of

Saudi Arabia^[3].

IBD is not limited to the gastrointestinal tract (GIT). It also has extraintestinal manifestations that have been recorded in up to half of patients^[4]. One of these manifestations is reduced bone mineral density (BMD), namely osteoporosis and osteopenia^[5]. The literature shows that the burden of reduced BMD is increased among IBD patients, with a variable prevalence ranging from 5% to 37%^[6].

Osteoporosis and osteopenia are well-known predictors of major health problems, including increased fracture risk, and consequently, decreased quality of life. IBD patients' fracture risk is 40% higher than that recorded for non-IBD individuals^[7]. Such increased fracture risk has severe implications for the health care system, with additional burden at the individual, social, and public levels^[8]. Based on this added risk, screening for reduced BMD in IBD patients should be done on a regular basis to curb the anticipated morbidity and mortality of the disease.

Adding to the general risk factors for osteoporosis and osteopenia, IBD-specific factors include genetic predisposition, disease activity, medications (*i.e.*, steroids), small bowel resection, malabsorption, low body mass index (BMI), and pro-inflammatory cytokines^[9].

Little is known about the updated prevalence of reduced BMD and its predisposing factors among adult IBD patients in Saudi Arabia. Additionally, there is a knowledge gap regarding the impact of CD and UC on BMD among Saudi patients in the era of biological therapy. Consequently, our study aimed to investigate these knowledge gaps among IBD patients living in Al-Qassim province, Saudi Arabia.

MATERIALS AND METHODS

Study design and participants

This cross-sectional study took place at King Fahad Specialist Hospital in Buraidah, Al-Qassim, Saudi Arabia between February 2018 and December 2019. The study was approved by the regional ethical committee, and all participants provided informed consent prior to their enrollment in the study.

Ninety adult (> 19 years old) Saudi patients with an IBD diagnosis (62 CD and 28 UC) were recruited from the hospital gastroenterology unit. The IBD diagnosis (either previously established or newly diagnosed) was based on patients' clinical, endoscopic, radiographic, and histopathologic findings according to the European Crohn's and Colitis Organisation (ECCO) diagnostic criteria^[10,11].

IBD patients who had any concomitant malignancy, end organ failure, pregnancy, or a GIT pathology other than IBD were excluded from the study.

Procedure

In their interview in the GIT department, patients received the standard of care according to the Saudi Ministry of Health guideline protocols regarding IBD (based on ECCO criteria), including history taking, physical examinations, investigations, and treatment plan. Moreover, all patients were offered the study questionnaire and given appointments to measure their BMD by dual x-ray energy absorptiometry (DXA) scan.

Data extraction

Clinical data: Clinical data were obtained by interviewing the patients and by reviewing their previous records and investigations. Data included age, gender, smoking status, BMI, physical activity, IBD-related extraintestinal manifestations (affecting the eye, skin, joints, liver, gall bladder and/or blood vessels)^[12], IBD-related data (disease subtype, childhood onset, duration, extent, clinical presentations, perianal disease, malabsorption, hospital/ICU admissions, endoscopic reports, previous surgeries, and prescription drugs used), and IBD activity scores [Crohn's Disease Activity Index (CDAI) for CD^[13] and Mayo Score for UC^[14]].

Biochemical measurements: Following the patients' initial interview, venous blood samples were obtained for their full blood count, erythrocyte sedimentation rate (ESR), C-reactive protein, iron panel tests, liver and kidney function tests, calcium, phosphate, alkaline phosphatase (ALP) and 25-hydroxy-vitamin D [25(OH)D]. Stool analysis was done for fecal calprotectin.

BMD measurements: We adopted the World Health Organization's diagnostic criteria^[15] for measuring BMD as follows: (1) Normal BMD: *t*-score \geq -1 standard deviation (SD); (2) Osteopenia: *t*-score between -1.0 and -2.5 SD; and (3) Osteoporosis: *t*

-score \leq -2.5 SD.

Measurements were conducted on both lumbar spine and left femoral neck. BMD values were expressed as *t*- and *z*-scores^[15]. We considered the lowest *t*-score values, obtained either from lumbar spine or femur neck, for BMD measurement. DXA scans were conducted using Discovery W, QDR series (Hologic, Waltham, MA, United States).

Data synthesis and statistical analysis

The statistical package of MedCalc version 19.0.5 was used in our analysis. Quantitative data is presented as mean \pm SD, and qualitative data is presented as percentages. Comparisons between groups were made using the Mann-Whitney's *u*-test/unpaired *t* test for ordinal and continuous variables, respectively, and the χ^2 -test/Fisher's exact test was used for categorical variables. Correlations between variables were performed using Pearson's/Spearman's rank correlation coefficient when applicable. *P* values less than 0.05 were considered statistically significant.

The statistical methods of this study were reviewed by Nazmus Saquib, PhD, from Sulaiman Al Rajhi University. He attests that the statistical methods in this study are suitable and adequately and appropriately described.

RESULTS

Patient demographics and IBD clinical characteristics

This cross-sectional study included 90 patients (31.5 \pm 8.8, 19-60 years; 49 males, 54%). The patients were divided into 2 groups: CD group [62 patients (29.23 \pm 7.58, 19-51 years; 32 males, 52%)], and UC group [28 patients (33.22 \pm 10.53, 20-60 years; 17 males, 61%)].

Weight loss, malabsorption syndrome, abdominal pain, extraintestinal manifestations, previous related hospital admissions and previous related surgeries were higher, and BMI was lower in the CD group than in the UC group (Table 1).

The disease in the CD group mainly affected the ilio-colic area in 55% of the patients, 39% in the ileum, 3% in the colon, and the remaining 3% in the upper GIT. On the other hand, 50% of the UC group had left side colitis, 46% had pancolitis, and 4% had proctitis.

The CDAI score was 157.26 \pm 98.15 (range: 27-490), and the Mayo score was 3.69 \pm 2.27 (range: 1-11) in the CD and UC groups, respectively. There were more patients with severe clinical disease activity and endoscopic activity in the UC group than in the CD group (7 vs 3 patients).

Regarding medication history, the percentages of steroid, azathioprine, and anti-tumor necrosis factor (anti-TNF) use were not significantly different between the CD group and the UC group. However, mesalamine use was significantly higher in the UC group.

Patients' laboratory profile

Lab investigations showed that most of the variables were comparable between the two study groups. However, ALP, vitamin B12, and fecal calprotectin showed statistically significant higher values in the UC group than in the CD group (Table 2).

Measurements of BMD in CD and UC patients based on the lowest *t*-score

Out of all participants (both groups), 46 patients (51%) had normal *t*-scores (-0.27 \pm 0.54) and 44 patients (49%) had low *t*-scores (-2.15 \pm 0.77, *P* < 0.001). Lower BMD levels, and consequently higher osteopenia/osteoporosis percentages, were detected in the CD group than in the UC group. In the CD group, 44% of the patients had normal BMD, 19% had osteopenia, and 37% had osteoporosis, while in the UC group, 78% of the patients had normal BMD, 7% had osteopenia, and 25% had osteoporosis (*P* value < 0.05) (Table 3, Figure 1).

Risk factors for reduced BMD

In the CD group, the lowest *t*-score showed a statistically significant correlation with BMI (*r* = 0.45, *P* < 0.001) (Figure 2), lumbar *z*-score (*r* = 0.77, *P* < 0.05) and femur *z*-score (*r* = 0.85, *P* < 0.05), but showed inverse correlations with abdominal pain (*r* = -0.35, *P* < 0.05), malabsorption syndrome (*r* = -0.44, *P* < 0.001), extraintestinal manifestations (*r* = -0.28, *P* < 0.05), total number of the symptoms (*r* = -0.29, *P* < 0.05) and with the need for vitamin D therapy (*r* = -0.27, *P* < 0.05).

Table 1 Comparison of demographic characteristics and patients' clinical profile in the Crohn's disease and ulcerative colitis groups

Parameters	CD (62 pts)	UC (28 pts)	P value
Age (yr)	29.23 ± 7.58	33.22 ± 10.53	NS
Sex (males), <i>n</i> (%)	32 (52)	17 (61)	NS
Smoking (%)	10	29	NS
BMI (kg/m ²)	22.2 ± 3.52	25.646 ± 2.87	< 0.05
Abdominal pain (%)	83	17	NS
Bloody diarrhea (%)	67	96	NS
Bleeding per rectum (%)	3	4	NS
Malabsorption syndrome (%)	19	0	< 0.05
Perianal disease (%)	59	4	NS
Weight loss (%)	11	0	< 0.05
Extraintestinal manifestations (%)	21	7	NS
Comorbidities (%)	8	18	NS
Previous IBD-related admission (<i>n</i>)	2.16 ± 1.48	0.7 ± 0.44	< 0.05
Previous related surgeries (%)	33	4	NS
Family history (%)	15	4	NS
Steroid therapy (%)	79	71	NS
Azathioprine (%)	82	37	NS
Mesalamine (%)	10	81	< 0.05
Anti-TNF therapy (%)	65	29	NS

CD: Crohn's disease; UC: Ulcerative colitis; pts: Patients; BMI: Body mass index; IBD: Inflammatory bowel disease; TNF: Tumor necrosis factor; NS: Not significant.

In the UC group, the lowest *t*-score showed only statistically significant correlation with the lumbar *z*-score ($r = 0.82$, $P < 0.05$) and femur *z*-score ($r = 0.80$, $P < 0.05$).

The ROC-curve showed that low BMI could predict low *t*-score much better in the CD rather than the UC group. In the CD group, the cut-off value was ≤ 23.43 (m/kg²); the area under the curve was 0.73 (95%CI: 0.59–0.84); the sensitivity was 77%, and the specificity was 63% (Figure 3A). In the UC group, the cut-off value was ≤ 23.5 (m/kg²); the area under the curve was 0.65 (95%CI: 0.43–0.83); the sensitivity was 50%, and the specificity was 81% (Figure 3B).

There was no significant difference in the lowest *t*-score between the CD and UC patients receiving anti-TNF- α therapy and those who did not receive it (Table 4).

DISCUSSION

The main finding in our study is the relatively high percentage of undiagnosed reduced BMD: 56% among CD patients (37% osteopenia and 19% osteoporosis) and 32% among UC (25% osteopenia and 7% osteoporosis). Such high percentages of reduced BMD should alert us to an anticipated increase in fracture risk among Saudi patients with IBD. Hence, there is a need for proper screening programs to better control BMD loss and to ensure better quality of life for those patients.

To the best of our knowledge, our study is the first study to investigate this health problem in Al-Qassim province, Saudi Arabia. Moreover, it is the only study to provide updated data regarding BMD status among adult Saudi patients with IBD.

Based on our results, the burden of reduced BMD among adult Saudi patients with IBD is still high but is showing a decreasing trend compared to the results of a retrospective study conducted between 2001 and 2008 by Ismail *et al*^[16] on 95 Saudi patients with IBD; osteopenia burden was 48.6% and 32.6%, and osteoporosis burden was 55.8% and 27.5% among CD and UC patients, respectively.

Table 2 Comparison of laboratory investigations of patients in the Crohn's disease and ulcerative colitis groups

Parameters	CD (62 pts)	UC (28 pts)	P value
Hemoglobin (g/dL)	12.41 ± 2.4	12.54 ± 2.58	NS
WBC (× 10 ⁹ /L)	6.7 ± 1.1	7.302 ± 3.6	NS
Platelets (× 10 ⁹ /L)	333 ± 101	318 ± 121	NS
ALT (U/L)	13.61 ± 10.6	22.55 ± 28.48	NS
AST (U/L)	16.62 ± 8.38	20.69 ± 14.2	NS
ALP (U/L)	72.125 ± 29.02	84.434 ± 38.99	< 0.05
Albumin (g/L)	36.335 ± 6.44	38.13 ± 6.98	NS
Serum creatinine (μmol/L)	60.81 ± 16.15	62.96 ± 16.6	NS
Serum calcium (mmol/L)	2.25 ± 0.17	2.23 ± 0.13	NS
Phosphorus (μmol/L)	1.17 ± 0.34	1.19 ± 0.18	NS
PTT (s)	29.53 ± 0.65	32.09 ± 7.58	NS
PT (s)	12.457 ± 2.65	12.71 ± 1.73	NS
INR	1.32 ± 74.48	1.11 ± 0.23	NS
ESR (mm/h)	22.67 ± 19.33	29.256 ± 31.87	NS
CRP (> 3 mg/L) (%)	21	17	NS
Serum iron (μmol/L)	8.16 ± 6.24	9.423 ± 7.39	NS
TIBC (μg/dL)	46.985 ± 13.52	58.19 ± 20.12	NS
Ferritin (ng/mL)	30.25 ± 12.03	32.34 ± 9.25	NS
Serum vitamin D (ng/mL)	12.09 ± 10.8	12.85 ± 4.21	NS
Serum vitamin B12 (ng/mL)	231.32 ± 182.34	314.67 ± 62.43	< 0.05
Fecal calprotectin (μg/mg)	653 ± 265.13	1688.43 ± 426.79	< 0.05

CD: Crohn's disease; UC: Ulcerative colitis; pts: Patients; WBC: White blood count; ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; ALP: Alkaline phosphatase; PTT: Partial thromboplastin time; PT: Prothrombin time; INR: International normalized ratio; ESR: Erythrocyte sedimentation rate; CRP: C-reactive protein; TIBC: Total iron-binding capacity; NS: Not significant.

Table 3 Comparison of dual x-ray energy absorptiometry-scan parameters in the Crohn's disease and ulcerative colitis groups

Parameters	CD (62 pts)	UC (28 pts)	P value
Mean <i>t</i> -score femur	-0.94 ± 1.27	-0.51 ± 0.9	NS
Mean <i>z</i> -score femur	-0.67 ± 1.06	-0.33 ± 0.82	NS
Mean <i>t</i> -score lumbar	-0.97 ± 1.46	-0.49 ± 1.27	< 0.05
Mean <i>z</i> -score lumbar	-0.45 ± 1.32	-0.29 ± 1.26	NS
Mean lowest <i>t</i> -score	-1.35 ± 0.91	-0.84 ± 0.03	< 0.05
Osteopenia (%) ¹	37	25	< 0.05
Osteoporosis (%) ¹	19	7	< 0.05

¹Bone mineral density measurement is based on the lowest *t*-score. CD: Crohn's disease; UC: Ulcerative colitis; pts: Patients; NS: Not significant.

The relative improvement in BMD status in our study could be due to the improved standard of care, including increased use of biological therapies in our patients (53%), compared to the previously mentioned study, where the percentage of biological therapy use was 28%.

On the other hand, our results are still generally higher than those found in other Asian counties. In a study conducted by Wada *et al.*^[17] on 388 Japanese patients with IBD, they reported a prevalence of 40.4% osteopenia and 6.4% osteoporosis among CD

Table 4 The lowest t-score in relation to anti-tumor necrosis factor- α therapy in both study groups

Groups	mean \pm SD	95%CI	P value
CD group			
No anti-TNF- α	-1.10 \pm 1.04	-1.56 to -0.63	0.98
Anti-TNF- α	-1.48 \pm 1.23	-1.88 to -1.09	
UC group			
No anti-TNF- α	-0.74 \pm 1.11	-1.25 to -0.22	0.185
Anti-TNF- α	-1.10 \pm 0.87	-1.83 to -0.37	

CD: Crohn's disease; UC: Ulcerative colitis; TNF: Tumor necrosis factor.

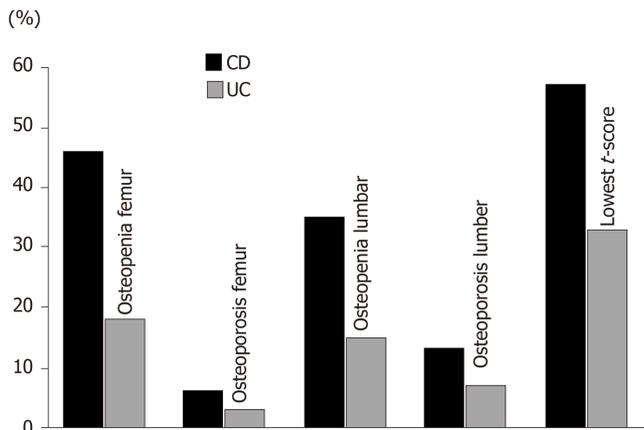


Figure 1 The percentages of patients with reduced bone mineral density in Crohn's disease compared to ulcerative colitis. CD: Crohn's disease; UC: Ulcerative colitis.

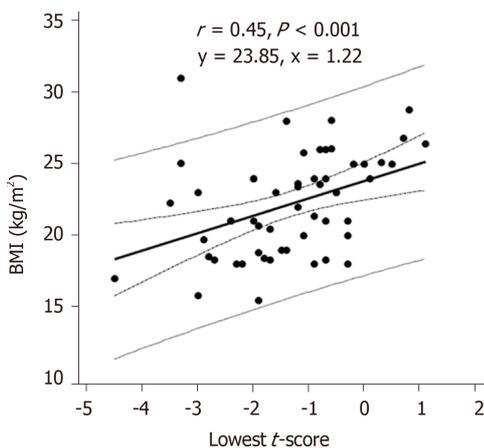


Figure 2 Scatterplot showing the correlation between lowest t-score and body mass index. BMI: Body mass index.

patients, and 31.0% osteopenia and 4.3% osteoporosis among UC patients.

In a larger cohort study by Tsai *et al*^[18] on the Asian population in Taiwan Province, the incidence of reduced BMD in IBD patients was 40% more than that in non-IBD participants. Moreover, the study showed an osteoporosis incidence rate of 7.3% in CD patients and 6.3% in UC patients, which is comparable to the above-mentioned Japanese study but is much lower than that found in our study. On the other hand, the prevalence among Western populations was initially investigated by Schulte *et al*^[19] on German participants and concluded the following ranges: 32% to 36% for osteopenia and 7% to 15% for osteoporosis. Similar findings were later mentioned by Sheth *et al*^[20]

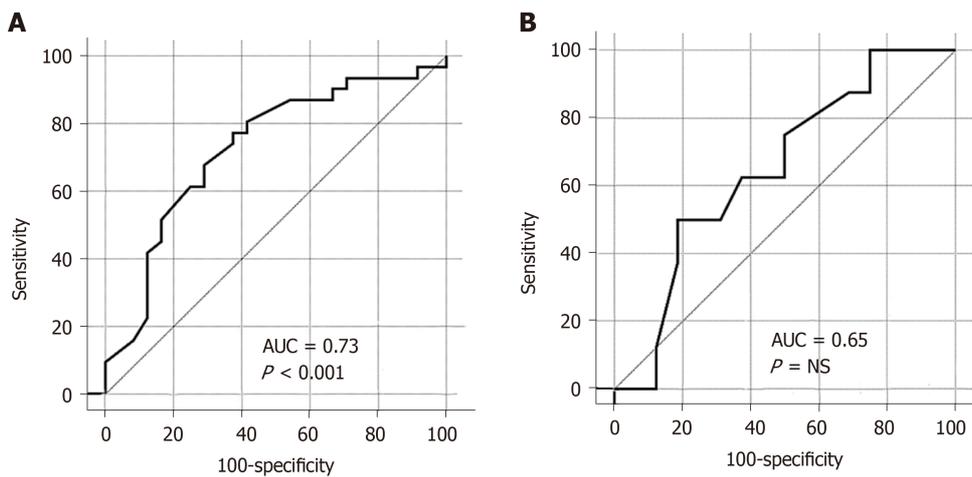


Figure 3 Receiver operating characteristic-curves showing prediction of low body mass index for low *t*-score in Crohn's disease group (A) and in ulcerative colitis group (B). AUC: Area under curve.

Most of the reports that estimated the fracture risk among IBD patients were based on Western populations as highlighted by Szafors *et al*^[21] in their systematic review, with an overall 38% higher fracture risk in IBD patients compared to the controls.

The different findings among IBD studies regarding BMD prevalence (including those related to IBD subtypes CD and UC) could be attributed to either variability in research methodology (study design and sample size) or variability in patients' characteristics, including ethnicity, age, gender, IBD severity, nutritional status and quality of health care settings. For example, we conducted our study in the largest central tertiary care hospital in the region, which usually manages advanced cases of complicated disease that need a high level of care. Accordingly, there is a possibility that this setting could partly explain the high prevalence of both osteopenia and osteoporosis in our sample as compared to other studies.

Another important finding in our study is that CD patients were at higher risk of developing both osteoporosis and osteopenia than UC patients, a finding that mirrors previously published data^[18,22,23]. This risk could be explained by more chronic inflammation (indicated by higher hospital admissions and biological therapy use and lower BMI) in CD patients than in UC patients. On the other hand, there are other studies that did not show any epidemiological BMD difference between CD and UC patients^[24].

The prevalence of CD (69%) was higher than UC (31%) in our sample, a finding that is consistent with previous epidemiological studies in Saudi Arabia^[25,26]. Taking into consideration the increasing trend of CD patients in Saudi Arabia, who are at higher risk for reduced BMD than UC patients, health care providers should anticipate more burden of osteoporosis and osteopenia among those patients and take the necessary preventive and screening actions.

It is speculated that the cornerstone pathogenic factor of reduced BMD among IBD patients is chronic inflammation that is induced by pro-inflammatory mediators and cytokines, including interleukin-1 (IL-1), IL-6 and TNF- α . These pro-inflammatory mediators disturb the physiologic bone remodeling process through an imbalance of osteoprotegerin, receptor activator of nuclear factor kappa-B (RANK), and the RANK ligand (RANKL) pathway. When there is a decrease in osteoprotegerin, a decoy receptor that limits RANKL-RANK interaction, it activates osteoclast, which is responsible for bone resorption^[27,28].

The third main finding in our study is that low BMI was a risk factor for reduced BMD, which matches data from previous studies^[17,29,30]. This finding was more evident in CD patients than in UC patients; BMI could predict the severity of reduced BMD with a sensitivity of 77% and a specificity of 63%, AUC 0.73 (95%CI: 0.59–0.84) in the CD group.

An unexpected finding in our study and in previous studies is the lack of correlation between steroid use and BMD^[6,22,31,32]. For our study, this result may be due to the lack of a registry to precisely record our patients' steroid therapy details. Intake of prednisolone > 7.5 mg/d for 3 mo is an established risk for developing osteoporosis^[33], as shown in previous studies^[17,27,30].

It is known that patients with IBD requiring biological therapy have the most severe

inflammation and a greater anticipated decrease in their BMD than other IBD patients^[34]. Our study, in contrast, did not find any significant difference in BMD between the CD and UC patients receiving anti-TNF- α therapy and those not receiving it (P value = 0.980 and 0.185, respectively). This finding could spotlight the beneficial role of biological therapy for BMD in IBD patients, but it needs further clarification in future studies.

Study limitation

The cross-sectional nature of the study precluded us from conducting a follow-up of reduced BMD risk factors in our patients. Moreover, our study is a single-center study, and it may be better to conduct a study in all health care centers in the province in order to enroll a diverse spectrum of IBD patients and increase the sample size.

CONCLUSION

Adult Saudi patients with IBD, although better than before, still have higher reduced BMD than Eastern Asian countries, with a significantly higher risk among CD patients compared to UC patients. Low BMI was a significant risk factor for reduced BMD in the CD group. We recommend further prospective multicenter studies among adult Saudi patients with IBD for a better assessment of reduced BMD risk factors and to investigate the current DXA screening practices among those patients.

ARTICLE HIGHLIGHTS

Research background

Inflammatory bowel disease (IBD) is showing an increasing trend in newly industrialized countries worldwide, including Saudi Arabia. Reduced bone mineral density (BMD) is a major documented extraintestinal complication in patients with IBD. As with other IBD patients, Saudi patients with IBD will have increased fracture risk and lower quality of life if not properly screened for reduced BMD.

Research motivation

Little is known about how much reduced BMD occurs among Saudi patients with IBD or about the predisposing factors in that population. Our study gives an update about reduced BMD among adult Saudi patients with IBD. We hope it will help health care providers curb the anticipated complications through proper preventive and screening measures.

Research objectives

We aimed to assess the current burden of reduced BMD and its possible risk factors among adult Saudi patients with IBD. Moreover, we investigated any possible variations between Crohn's disease (CD) and ulcerative colitis (UC) patients, either in the disease burden or its related risk factors.

Research methods

Ninety adult patients with IBD - 62 CD and 28 UC - were recruited from King Fahad Specialist Hospital gastroenterology clinics in the city of Buraidah, Saudi Arabia. Demographics, clinical workups and dual x-ray energy absorptiometry (DXA) scan data were obtained. Patients were divided into two groups (CD and UC) to explore their clinical characteristics and possible risk factors for reduced BMD. Appropriate statistical tests were used according to the variables. A $P < 0.05$ was considered significant.

Research results

Patients with CD were at higher risk for reduced BMD than those with UC; 19% of CD patients had osteopenia, and 37% had osteoporosis, while among the UC patients, 7% had osteopenia, and 25% had osteoporosis (P value < 0.05). In the CD group, the lowest t -score showed a statistically significant correlation with body mass index (BMI) ($r = 0.45$, $P < 0.001$), best cut-off value at ≤ 23.43 (m/kg²); area under the curve was 0.73 (95%CI: 0.59–0.84). In the UC group, the lowest t -score showed only statistically significant correlation with the lumbar z -score ($r = 0.82$, $P < 0.05$) and

femur z-score ($r = 0.80$, $P < 0.05$).

Research conclusions

There is still an increased risk of reduced BMD for Saudi patients with IBD, more so in CD patients. Low BMI is a significant risk factor for reduced BMD in CD patients.

Research perspectives

We recommend further prospective multicenter studies among adult Saudi patients with IBD for a better assessment of reduced BMD risk factors and to investigate the current DXA screening practices among those patients.

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Observational Study

Clinical features of cardiac nodularity-like appearance induced by *Helicobacter pylori* infection

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Institutional review board

statement: This retrospective study was approved by the Ethical Review Committee of Hattori Clinic on September 6, 2019 (approval no. S1909-U06).

Informed consent statement:

Patients were not required to give informed consent to the study because the analysis used anonymous clinical data that were

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Abstract**BACKGROUND**

We have previously reported that *Helicobacter pylori* (*H. pylori*)-associated nodular gastritis could occur in both the antrum and the cardia. Cardiac nodularity-like appearance (hereafter, called as cardiac nodularity) had a high predictive accuracy for the diagnosis of *H. pylori* infection. In the previous study, we included only the patients who were evaluated for *H. pylori* infection for the first time, and excluded patients with a history of eradication. Therefore, the prevalence and clinical features of cardiac nodularity remains unknown.

AIM

To perform this cross-sectional study to explore the characteristics of cardiac nodularity.

METHODS

Consecutive patients who underwent esophagogastroduodenoscopy between

obtained after each patient agreed to treatment by written consent.

Conflict-of-interest statement:

There are no conflicts of interest to report.

Data sharing statement: No additional data are available.

STROBE statement: The authors have read the STROBE Statement – checklist of items, and the manuscript was prepared and revised according to the STROBE Statement – checklist of items.

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May, 2017 and August, 2019 in the Toyoshima Endoscopy Clinic were enrolled in this study. We included *H. pylori*-negative, *H. pylori*-positive, and *H. pylori*-eradicated patients, and excluded patients with unclear *H. pylori* status and eradication failure. *H. pylori* infection was diagnosed according to serum anti-*H. pylori* antibody and the urea breath test or histology. Cardiac nodularity was defined as a miliary nodular appearance or the presence of scattered whitish circular small colorations within 2 cm of the esophagogastric junction. Nodularity was visualized as whitish in the narrow-band imaging mode. We collected data on the patients' baseline characteristics.

RESULTS

A total of 1078 patients were finally included. Among *H. pylori*-negative patients, cardiac nodularity and antral nodularity were recognized in 0.14% each. Among *H. pylori*-positive patients, cardiac nodularity and antral nodularity were recognized in 54.5% and 29.5%, respectively. Among *H. pylori*-eradicated patients, cardiac nodularity and antral nodularity were recognized in 4.5% and 0.6%, respectively. The frequency of cardiac nodularity was significantly higher than that of antral nodularity in *H. pylori*-positive and -eradicated patients. The frequencies of cardiac nodularity and antral nodularity in *H. pylori*-eradicated patients were significantly lower than those in *H. pylori*-positive patients ($P < 0.001$). The patients with cardiac nodularity were significantly younger than those without cardiac nodularity ($P = 0.0013$). Intestinal metaplasia score of the patients with cardiac nodularity were significantly lower than those without cardiac nodularity ($P = 0.0216$). Among *H. pylori*-eradicated patients, the patients with cardiac nodularity underwent eradication significantly more recently compared with those without cardiac nodularity ($P < 0.0001$).

CONCLUSION

This report outlines the prevalence and clinical features of cardiac nodularity, and confirm its close association with active *H. pylori* infection.

Key Words: Cardia; Nodularity; *Helicobacter pylori*; Diagnosis; Gastritis

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Core Tip: The prevalence of cardiac and antral nodularity in *Helicobacter pylori* (*H. pylori*) -negative, -positive, and -eradicated patients were 0.14% and 0.14%, 54.5% and 29.5%, and 4.5% and 0.6%, respectively. Cardiac nodularity was more frequent than antral nodularity in *H. pylori*-positive and -eradicated patients. Cardiac nodularity was often found in younger patients and patients with less intestinal metaplasia. Cardiac nodularity decreased after eradication, especially in patients who underwent eradication a long time ago.

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INTRODUCTION

Helicobacter pylori (*H. pylori*) infection leads to the development of gastric atrophy, peptic ulcer, and gastric cancer^[1-5]. Eradication of *H. pylori* infection has been reported as an effective strategy for treating atrophic gastritis and peptic ulcer, and preventing gastric cancer^[6-9]. Therefore, it is important to evaluate *H. pylori* infection status^[10-12].

Nodular gastritis is a form of chronic gastritis that has a unique miliary pattern on endoscopy, with "gooseflesh-like" appearance. Many studies have shown a strong association between nodular gastritis and *H. pylori* infection^[13-15]. Children and young women are reported to be predisposed to nodular gastritis. Nodular gastritis improves

gradually with age^[16]. Several reports have suggested an association between nodular gastritis and diffuse type gastric cancer^[13,15,17].

We have previously reported that nodularity could occur in both the antrum and the cardia^[18]. Cardiac nodularity-like appearance is found more frequently than antral nodularity. Cardiac nodularity-like appearance (hereafter, called as cardiac nodularity) had a high predictive accuracy for the diagnosis of *H. pylori* infection. Our previous report also showed excellent interobserver agreement on cardiac nodularity. Furthermore, histological examination of cardiac nodularity often revealed lymphoid follicles displaying lymphocyte infiltration in the cardiac gland^[18].

However, the prevalence and clinical features of cardiac nodularity remains unknown. Therefore, we performed this cross-sectional study to explore the characteristics of cardiac nodularity.

MATERIALS AND METHODS

Ethics

This study was approved by the ethical review committee of Hattori Clinic on September 6, 2019 (approval no. S1909-U06)^[12,19]. All clinical investigations were conducted according to the ethical guidelines of the Declaration of Helsinki.

Patients

Consecutive patients who underwent esophagogastroduodenoscopy (EGD) between May, 2017 and August, 2019 in the Toyoshima Endoscopy Clinic were enrolled in this study. Inclusion criteria included defined *H. pylori* status (*H. pylori*-negative patients, *H. pylori*-positive patients, and *H. pylori*-eradicated patients). The patients with unclear *H. pylori* status and eradication failure were excluded from the study. EGD was conducted for the examination of symptoms and screening. We collected data on the patients' baseline characteristics, including age and sex, and period since eradication for eradicated patients.

Endoscopic procedures

EGD was performed using the Olympus Evis Lucera Elite system with a GIF-H290Z or GIF-HQ290 endoscope (Olympus Corporation, Tokyo, Japan)^[20]. An expert physician (Toyoshima O) performed endoscopic procedures. Furthermore, EGD images were retrospectively reviewed by other expert physicians. Discrepancies in diagnosis between the two sets of physicians were resolved through discussion. Sedation with midazolam and/or pethidine was performed at the patient's discretion^[21-23]. Antral nodularity was defined as a miliary nodular appearance consisting of whitish circular micronodules measuring ≤ 1 mm in both height and diameter. Cardiac nodularity was defined as a miliary nodular appearance or the presence of scattered whitish circular small colorations within 2 cm of the esophagogastric junction. Nodularity was visualized as whitish in the narrow-band imaging (NBI) mode. The representative endoscopic images are shown in [Figure 1](#).

We scored atrophy, intestinal metaplasia, diffuse redness, and enlarged folds, according to the Kyoto classification^[24].

Endoscopic atrophy was diagnosed based on the Kimura and Takemoto classification^[25]. Non-atrophy and C1 were scored as Atrophy score 0, C2, and C3 as Atrophy score 1, and O1 to O3 as Atrophy score 2.

The absence of intestinal metaplasia was scored as Intestinal metaplasia score 0, the presence of intestinal metaplasia within the antrum as Intestinal metaplasia score 1, and intestinal metaplasia extending into the corpus as Intestinal metaplasia score 2. The Intestinal metaplasia score was diagnosed using white light imaging.

The absence of diffuse redness was scored as Diffuse redness score 0, mild diffuse redness or diffuse redness with regular arrangement of collecting venules (RAC) as Diffuse redness score 1, and severe diffuse redness or diffuse redness without RAC as Diffuse redness score 2.

The absence and presence of enlarged folds was scored as Enlarged folds score 0 and 1, respectively.

Diagnosis of *H. pylori* infection

Serum anti-*H. pylori* antibody was measured on the day of EGD. The antibody titer was measured using an enzyme immunoassay kit with antigens derived from Japanese individuals (E-plate Eiken *H. pylori* antibody II; Eiken Chemical, Tokyo,

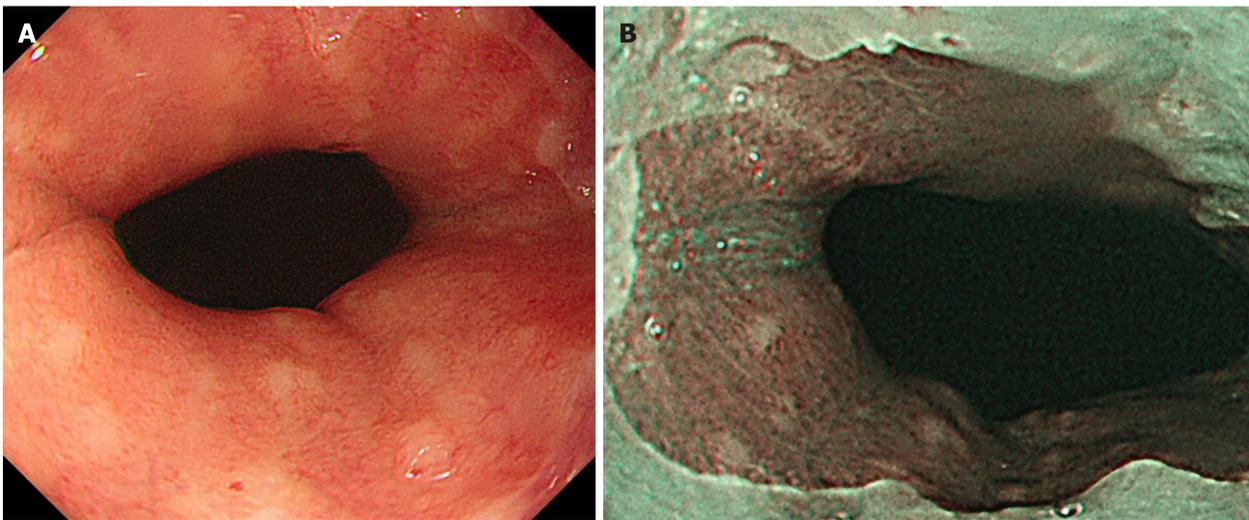


Figure 1 Endoscopic images of cardiac nodularity-like appearance. A: White light observation. A miliary pattern with a “gooseflesh-like” appearance was found in the cardia. Whitish circular micronodules measuring ≤ 1 mm in both diameter and height were observed; B: Narrow-band imaging observation. Whitish coloration denoted nodularity.

Japan). An antibody titer ≥ 10 U/mL (the cut-off value recommended by the manufacturer) was considered positive for *H. pylori*^[26]. When the serum anti-*H. pylori* antibody titer was 3.0-9.9 U/mL, the findings of urea breath test or histological assessment was added. If either the urea breath test or histology was positive, patients were considered positive for *H. pylori*^[27,28]. An antibody titer < 3.0 U/mL or negative urea breath test was considered to indicate *H. pylori* negativity. Eradication was confirmed by urea breath test.

Statistical analysis

Categorical data were compared using the chi-square test. Continuous data were compared using Student's or Welch's *t*-test, as appropriate. A two-sided *P* value of < 0.05 was considered as statistically significant. Calculations were carried out by the Stat Mate IV software (ATOMS, Tokyo, Japan).

RESULTS

The endoscopist performed 1215 EGDs during the study period. We excluded 137 patients (135 patients with unclear *H. pylori* infection status and two with eradication failure). A total of 1078 patients were finally included.

The characteristics of the participants in the present study are shown in Table 1. Among *H. pylori*-negative patients, cardiac nodularity and antral nodularity were recognized in one patient each (0.14% each). Among *H. pylori*-positive patients, cardiac nodularity and antral nodularity were recognized in 24 (54.5%) and 13 (29.5%) patients, respectively. The frequency of cardiac nodularity was significantly higher than that of antral nodularity ($P < 0.05$). Among *H. pylori*-eradicated patients, cardiac nodularity and antral nodularity were recognized in 15 (4.5%) and 2 (0.6%) patients, respectively. The frequency of cardiac nodularity was significantly higher than that of antral nodularity ($P < 0.01$). The frequencies of cardiac nodularity and antral nodularity in *H. pylori*-eradicated patients were significantly lower than those in *H. pylori*-positive patients ($P < 0.001$).

Clinical characteristics of cardiac nodularity in *H. pylori*-positive patients are shown in Table 2. The patients with cardiac nodularity were significantly younger than those without cardiac nodularity ($P = 0.0013$). Intestinal metaplasia score of the patients with cardiac nodularity were significantly lower than those without cardiac nodularity ($P = 0.0216$).

Among *H. pylori*-eradicated patients, the patients with cardiac nodularity were also significantly younger than those without cardiac nodularity ($P = 0.0003$, Table 3). Furthermore, the patients with cardiac nodularity underwent eradication significantly more recently compared with those without cardiac nodularity ($P < 0.0001$).

Table 1 Characteristics of enrolled subjects

	<i>H. pylori</i> negative	<i>H. pylori</i> positive	<i>H. pylori</i> eradicated
Patient number	704	44	330
Mean age (standard deviation)	54.2 ± 11.1	51.0 ± 13.4	60.3 ± 12.3
Male:female	358:346	19:25	185:145
Cardiac nodularity	1 (0.14%)	24 (54.5%) ^a	15 (4.5%) ^{bf}
Antral nodularity	1 (0.14%)	13 (29.5%)	2 (0.6%) ^f

^a*P* < 0.05,^b*P* < 0.01 vs antral nodularity;^f*P* < 0.001 vs *Helicobacter pylori* positive. *H. pylori*: *Helicobacter pylori*.**Table 2 Clinical characteristics of cardiac nodularity in *Helicobacter pylori* positive patients**

	Cardiac nodularity (+)	Cardiac nodularity (-)	<i>P</i> value
Patient number	24	20	
Mean age (standard deviation)	44.9 ± 7.8	58.3 ± 15.1	0.0013
Male:female	9:15	10:10	0.598
Atrophy score	1.46 ± 0.59	1.55 ± 0.51	0.588
Intestinal metaplasia score	0.21 ± 0.59	0.80 ± 0.95	0.0216
Enlarged fold score	0.54 ± 0.51	0.60 ± 0.50	0.705
Diffuse redness score	1.75 ± 0.55	1.67 ± 0.64	0.648

Table 3 Clinical characteristics of cardiac nodularity in *Helicobacter pylori* eradicated patients

	Cardiac nodularity (+)	Cardiac nodularity (-)	<i>P</i> value
Patient number	15	315	
Mean age (standard deviation)	49.2 ± 12.3	60.8 ± 12.1	0.0003
Male:female	5:10	180:135	0.121
Months after eradication	41.5 ± 30.1	91.6 ± 100.0	< 0.0001

DISCUSSION

The prevalence of cardiac nodularity was 0.14%, 54.5%, and 4.5% in *H. pylori*-negative, -positive, and -eradicated patients, respectively. Cardiac nodularity was more frequent than antral nodularity in *H. pylori*-positive and -eradicated patients. Cardiac nodularity was often found in younger patients and patients with less intestinal metaplasia. Cardiac nodularity decreased after eradication, especially in patients who underwent eradication a long time ago.

Our previous study showed excellent prediction accuracy of cardiac nodularity due to *H. pylori* infection, with 0.928 of accuracy, 0.996 of specificity, 0.571 of sensitivity, 0.960 of positive predictive value, and 0.925 of negative predictive value^[18]. In our previous study, we included only the patients who were evaluated for *H. pylori* infection for the first time, and excluded patients with a history of eradication. However, the present cross-sectional study included the patients with a history of eradication also. The frequency of cardiac nodularity in *H. pylori*-positive patients was remarkably higher than that in *H. pylori*-negative patients and *H. pylori*-eradicated patients. Cardiac nodularity may serve as one of the predictive markers for active *H. pylori* infection.

Nodular gastritis is more frequent in children than in adults^[29]. The prevalence of nodular gastritis has been reported to be 32.9%-85% in *H. pylori*-positive children^[30-34]. The prevalence of nodular gastritis gradually decreased with age^[13]. Our study also

showed that the patients with cardiac nodularity were significantly younger than those without cardiac nodularity. Age dependence of cardiac nodularity is in line with that of antral nodularity.

Miyamoto *et al*^[3] demonstrated that atrophy scores were lower in patients with nodular gastritis than in *H. pylori*-positive controls. Nakashima *et al*^[35] also reported that atrophy and intestinal metaplasia were rare in nodular gastritis. Our study also showed that compared with patients without cardiac nodularity, Intestinal metaplasia score of the patients with cardiac nodularity was significantly lower. Cardiac nodularity seemed to disappear with the progression of intestinal metaplasia.

Dwivedi *et al*^[36] reported that 87.5% of nodular gastritis patients showed complete normalization of the gastric mucosa after *H. pylori* eradication therapy. Our study also showed significantly low prevalence of cardiac nodularity in *H. pylori*-eradicated patients, especially in patients who underwent eradication a long time ago. Cardiac nodularity seemed to disappear with improvement in gastric inflammation after *H. pylori* eradication.

This study had some limitations. First, this study employed only a single experienced endoscopist. Second, the study was a retrospective review at a single institution. Our results should be validated in diverse settings for generalizability.

CONCLUSION

This report outlined the prevalence and clinical features of cardiac nodularity, and confirmed its close association with active *H. pylori* infection.

ARTICLE HIGHLIGHTS

Research background

Helicobacter pylori (*H. pylori*)-associated nodular gastritis could occur in both the antrum and the cardia. Cardiac nodularity-like appearance is found more frequently than antral nodularity.

Research motivation

Previous study included only the patients who were evaluated for *H. pylori* infection for the first time. There still remains a lack of the prevalence and clinical features of cardiac nodularity-like appearance.

Research objectives

We aimed to evaluate the characteristics of cardiac nodularity-like appearance.

Research methods

We enrolled consecutive patients who underwent esophagogastroduodenoscopy between May, 2017 and August, 2019 in the Toyoshima Endoscopy Clinic. We included *H. pylori*-negative, *H. pylori*-positive, and *H. pylori*-eradicated patients, and excluded patients with unclear *H. pylori* status and eradication failure. Cardiac nodularity was defined as a miliary nodular appearance or the presence of scattered whitish circular small colorations within 2 cm of the esophagogastric junction.

Research results

A total of 1078 patients were finally included. The prevalence of cardiac and antral nodularity in *H. pylori*-negative, -positive, and -eradicated patients were 0.14% and 0.14%, 54.5% and 29.5%, and 4.5% and 0.6%, respectively. Cardiac nodularity-like appearance was more frequent than antral nodularity in *H. pylori*-positive and -eradicated patients. Cardiac nodularity-like appearance was often found in younger patients and patients with less intestinal metaplasia. Cardiac nodularity-like appearance decreased after eradication, especially in patients who underwent eradication a long time ago.

Research conclusions

This report outlines the prevalence and clinical features of cardiac nodularity-like appearance, and confirm its close association with active *H. pylori* infection.

Research perspectives

Our results should be validated in diverse settings for generalizability.

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Systematic review of the prevalence and development of osteoporosis or low bone mineral density and its risk factors in patients with inflammatory bowel disease

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Abstract

BACKGROUND

The inflammatory bowel diseases (IBD), Crohn's disease (CD) and ulcerative colitis (UC) are chronic, immune-mediated disorders of the digestive tract. IBD is considered to be a risk factor for developing osteoporosis; however current literature on this matter is inconsistent.

AIM

To assess prevalence and development of osteoporosis and low bone mineral density (BMD), and its risk factors, in IBD patients.

METHODS

Systematic review of population-based studies. Studies were identified by electronic (January 2018) and manual searches (May 2018). Databases searched included EMBASE and PubMed and abstracts from 2014-2018 presented at the United European Gastroenterology Week, the European Crohn's and Colitis Organisation congress, and Digestive Disease Week were screened. Studies were eligible for inclusion if they investigated either the prevalence of osteoporosis or osteopenia and/or risk factors for osteoporosis or low BMD in IBD patients. Studies on children under the age of 18 were excluded. Only population-based studies were included. All risk factors for osteoporosis and low BMD investigated in any included article were considered. Study quality and the possibility of bias were analysed using the Newcastle-Ottawa scale.

RESULTS

Twelve studies including 3661 IBD patients and 12789 healthy controls were included. Prevalence of osteoporosis varied between 4%-9% in studies including

investigator in studies by Amgen and MSD and received payment for lectures sponsored by Amgen and LEO Pharma. Kärnsund S, Lo B and Bendtsen F have nothing to declare.

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both CD and UC patients; 2%-9% in studies including UC patients, and 7%-15% in studies including CD patients. Among healthy controls, prevalence of osteoporosis was 3% and 10% in two studies. CD diagnosis, lower body mass index (BMI), and lower body weight were risk factors associated with osteoporosis or low BMD. Findings regarding gender showed inconsistent results. CD patients had an increased risk for osteoporosis or low BMD over time, while UC patients did not. Increased age was associated with decreased BMD, and there was a positive association between weight and BMI and BMD over time. Great heterogeneity was found in the included studies in terms of study methodologies, definitions and the assessment of osteoporosis, and only a small number of population-based studies was available.

CONCLUSION

This systematic review found a possible increase of prevalence of osteoporosis in CD cohorts when compared to UC and cohorts including both disease types. Lower weight and lower BMI were predictors of osteoporosis or low BMD in IBD patients. The results varied considerably between studies.

Key Words: Inflammatory bowel disease; Osteoporosis; Systematic review; Epidemiology; Bone mineral density

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Core Tip: Being diagnosed with inflammatory bowel disease (IBD) is considered a risk factor for development of osteoporosis, which leads to an increased risk of pathological fractures. This makes osteoporosis associated with great economic and psychological burden. Research made on the relationship between IBD and osteoporosis differs in study design and study populations, and results are inconsistent. The aims with this research are to assess the prevalence of osteoporosis among IBD patients compared to healthy individuals, assess the disease course of osteoporosis or low bone mineral density (BMD) in IBD patients and assess risk factors associated with osteoporosis and low BMD in IBD patients.

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INTRODUCTION

The inflammatory bowel diseases (IBD), encompassing Crohn's disease (CD) and ulcerative colitis (UC) are chronic, immune-mediated disorders of the digestive tract of unknown aetiology. Being diagnosed with IBD is considered a risk factor for the development of osteoporosis, which leads to an increased risk of pathological fractures^[1]. It is hypothesized that the severity and extent of gut inflammation and intestinal malabsorption leading to calcium and vitamin D deficiency in IBD patients might have a detrimental effect on bone^[2-4]. Other known risk factors for osteoporosis, that also apply to the population without IBD are female gender, older age, low BMI and smoking^[2-5]. As bone-protecting factors, physical activity has been found to have beneficial effects on both bone and cartilage in patients with osteoporosis, whether it's glucocorticoid-induced or not^[6-8].

While osteoporosis is asymptomatic before fractures occur, the development of osteoporotic fractures as a consequence makes osteoporosis associated with great economic and psychological burden^[9,10]. Several studies have investigated the relationship between inflammatory bowel diseases and osteoporosis but differences in study design and study populations, as well as inconsistent results and diverging interpretations of them, make it difficult to draw firm conclusions.

With this systematic review, we aimed to assess the prevalence of osteoporosis among IBD patients compared to healthy individuals, as well as the disease course of

osteoporosis or low BMD in IBD patients. We also aimed to assess risk factors associated with osteoporosis and low BMD in IBD patients with the intention to find more substantial evidence as to the cause of osteoporosis or low BMD in this patient group.

MATERIALS AND METHODS

Protocol and registration

This systematic review was conducted in accordance with the MOOSE (Meta-analyses Of Observational Studies in Epidemiology) guidelines. Prior to data extraction and analysis, a protocol was registered with PROSPERO (ID CRD42018084259) that has been updated regularly.

Sources

Studies were identified through electronic searches and by manually reviewing the reference lists of these studies, as well as relevant review articles. Electronic searches were conducted on January 30, 2018. Databases searched included EMBASE and PubMed. Searches were adjusted where needed for each database. Terms related to “inflammatory bowel disease”, “osteoporosis”, “osteopenia” and “study design” were used. The detailed search strategy is presented in [Supplementary Table 1](#). Prior to title and abstract screening, duplicates and articles written in a language other than English were excluded. Titles and abstracts were screened independently by two of the review’s authors (SK/BL). Disagreement was resolved by consensus. Potentially eligible studies were read in full by the same two authors (SK/BL). Disagreements that could not be resolved by consensus were discussed with a third author (JB) until an agreement was reached. Screening and study selection were made using the review management tool Covidence (www.covidence.org).

The search for unpublished articles occurred between May 14-16, 2018, where abstracts from 2014-2018 presented at the United European Gastroenterology Week, the European Crohn’s and Colitis Organisation congress, and Digestive Disease Week were screened. Only the European Crohn’s and Colitis Organisation congress had published abstracts from 2018. The screening was made by searching for the terms “osteoporosis”, “osteopenia”, “bone mineral density” and “inflammatory bowel disease”.

Study selection, eligibility criteria and quality assessment

Studies were eligible for inclusion if they investigated either the prevalence of osteoporosis or osteopenia and/or risk factors for osteoporosis or low BMD in IBD patients. Studies on children under the age of 18 were excluded. Only population-based studies were included. All risk factors for osteoporosis and low BMD investigated in any included article were considered.

Quality assessment and risk of bias assessment were performed using the Newcastle-Ottawa scale (NOS), a scale developed for assessment of nonrandomized studies including cohort studies^[11]. Stars were given to each article based on criteria in the categories of “selection”, “comparability” and “outcome”. A maximum of nine stars could be allocated to any one study.

Data extraction

From each included study the following information was extracted: (1) Author, year of publication, study period, number of patients included, country of study; (2) Prevalence of osteoporosis in patient groups and, if included in the study, healthy control groups; (3) T, Z and BMD (g/cm²) scores in patient groups and, if included in the study, healthy control groups; (4) Prevalence of osteoporosis and T, Z and BMD (g/cm²) scores in subgroups including gender, type of IBD, age (>/< 50 years), treatment (steroid/non-steroid), previous surgery, and Montreal disease classification; (5) Information regarding changes in rates of osteoporosis over a period of time; and (6) All clinical and socio-demographic risk factors that are investigated to be associated with osteoporosis or lowering of BMD in IBD patients.

Dual-energy X-ray absorptiometry (DXA) is performed on several bone areas and studies were therefore expected to present both overall measurements and/or information on each specific area. Examining risk factors for osteoporosis or low BMD in IBD patients, we considered it an association if at least one measured bone area showed significant association to an investigated risk factor, or if at least one measured

bone area showed significantly lower BMD than that same area in a comparison group. If a study only presented the proportion of patients with osteoporosis in each individual bone area, the overall prevalence was defined as that in the bone area in which most patients had osteoporosis. Prevalence of osteopenia was not considered.

If several studies analyzed the same cohort, prevalence estimates and risk factors were only registered once for each cohort. Authors were contacted for possible unpublished data. Studies analyzing CD and UC patients combined are referred to as “IBD studies”, while studies analyzing CD or UC exclusively are described as “CD studies” or “UC studies”, respectively.

RESULTS

Study characteristics

The search identified 449 records. After removing duplicates, non-English language studies and screening abstracts, 84 full-text articles were assessed for eligibility. A total of 12 papers were included in our study, one^[12] of which was found *via* screening of references. An overview of the number of titles, abstracts and full-text articles that were excluded, with justification for their exclusion, can be found in the PRISMA flow diagram, [Figure 1](#). No conference abstracts matched our criteria for inclusion. Authors either declined to provide data or did not respond to our queries in eight cases.

A detailed overview of the characteristics of each study is presented in [Table 1](#). The 12 studies were based on a total of seven cohorts. All twelve studies contributed with unique information despite the fact that some included the same cohort. Information was only registered once for each cohort. Six studies investigated only CD patients^[12-17], while the remainder investigated both CD and UC patients. No studies investigated only UC patients. Four studies included a healthy control group^[12,15,17,18]. Five were follow up studies^[3,12,18-20]. Two studies investigated only premenopausal women^[21,22]. Two studies presented only the number of patients that had osteoporosis in each measured bone area but no overall number^[13,17]. The total population across all studies was 3661 IBD patients, of which 1833 (50%) were women and 1828 (50%) men. A total of 1546 (42%) patients had UC and 2115 (58%) had CD. The control groups consisted of 12789 healthy individuals.

Quality assessment

[Table 2](#) provides detailed quality assessments of the studies according to the NOS. All included studies were allocated stars for the representativeness of the exposed cohort – the average IBD patient – since they are all population based. Osteoporosis was either diagnosed by DXA scan or from ICD-10 codes and hence all studies received at least two stars with regards to selection. With regards to comparability, gender and age were identified to be the most relevant confounding variables. With reference to outcome, 2 years were set as long enough follow-up time for outcomes (osteoporosis or change in BMD) to occur. A maximum of 25% of patients could be lost to follow up in order to receive a star for adequacy of follow up of cohorts.

Prevalence of osteoporosis (diagnosis based on T- and Z-scores or ICD-10 codes)

The prevalence of osteoporosis in IBD patients ranged from 2%^[18] to 15%^[16]. In patients with UC, this range was 2%-9%^[18,19], while it was 7%-15%^[16,18,19] in CD patients. Two studies provided age- and sex matched controls and in these the prevalence of osteoporosis was 3%^[18] and 10%^[17], respectively.

Risk factors for low bone mineral density

Nine studies based on six study cohorts investigated risk factors for osteoporosis or low BMD of which four, based on two study cohorts, investigated both UC and CD patients^[19-22] and of which five, based on four study cohorts, investigated only CD patients^[12-15,17]. An overview of the most relevant risk factors associated with osteoporosis or low BMD can be found in [Table 3](#), while a detailed list can be found in [Supplementary Table 2](#). Overall, a CD diagnosis, lower body mass index (BMI) and lower body weight were associated with osteoporosis or low BMD. Female gender was found to be associated with lower BMD in a study of both CD and UC patients^[20]. In CD cohorts, one study found males to have lower BMD than women^[12], one study found no significance^[13] and one study found female gender to be predictive for decreased BMD^[17]. Use of corticosteroids in any form and with any duration was found to be associated with osteoporosis or low BMD only in studies investigating CD

Table 1 Study characteristics

Ref.	Publication year	Country of study	Type of study	DXA scan ¹	No. of patients	Average age of patients	Cohort	Control group	Follow-up	Comments
Andreassen <i>et al</i> ^[1]	1998	Denmark	Cross-sectional study inviting all IBD patients from a well-defined area	Yes	115	37 (16-75); median (range)	CD only	No	No	
Andreassen <i>et al</i> ^[2]	1999	Denmark	Cross-sectional case-control study inviting all IBD patients from a well-defined area	Yes	113	37 (16-75); median (range)	CD only	Yes; <i>n</i> = 113	No	Same cohort used as in Andreassen <i>et al</i> ^[14] (1998)
Bernstein <i>et al</i> ^[3]	2003 ²	United States	Cross-sectional data extracted from population-based Manitoba IBD research registry	Yes	70; UC: <i>n</i> = 12; CD: <i>n</i> = 58	33.0 (7.4); mean (SD)	UC and CD	No	No	Includes only premenopausal women
Bernstein <i>et al</i> ^[4]	2003 ³	United States	Cross-sectional data extracted from population-based Manitoba IBD research registry	Yes	66 (DXA results: <i>n</i> = 70); UC: <i>n</i> = 11; CD: <i>n</i> = 55	33.3 (18-44); mean (range)	UC and CD	No	No	Includes only premenopausal women. Same cohort used as in Bernstein (2002)
Haugeberg <i>et al</i> ^[5]	2001	Norway	Cross-sectional data from a population-based study. Case control study	Yes	55	38.5 (12.7); mean (SD)	CD only	Yes; <i>n</i> = 52	No	
Jahnsen <i>et al</i> ^[6]	1997	Norway	Cross-sectional case control study	Yes	60	36 (21-75); median (range)	CD only	Yes; <i>n</i> = 60	No	Includes a cohort of UC patients that is not population-based which was therefore not included
Jahnsen <i>et al</i> ^[7]	2004	Norway	Follow-up study	Yes	60	36 (21-75); median (range)	CD only	No	Yes	Includes a cohort of UC patients that is not population-based which was therefore not included
									2 yr	Same cohort used as in Jahnsen (1997)
Leslie <i>et al</i> ^[8]	2008	Canada	Follow-up study with cohort extracted from population-based Manitoba IBD research registry	Yes	101; UC: <i>n</i> = 45; CD: <i>n</i> = 56	46.9 (15.5); mean (SD)	UC and CD	No	Yes; 2.3 ± 0.3 yr	
Leslie <i>et al</i> ^[9]	2009	Canada	Follow-up study with cohort extracted from population-based Manitoba IBD research registry	Yes	101 UC: <i>n</i> = 45 CD: <i>n</i> = 56	47 (15); mean (SD)	UC and CD	No	Yes; 2.3 ± 0.3 yr	Same cohort used as in Leslie <i>et al</i> ^[19] (2008)
Schoon <i>et al</i> ^[10]	2000	The Netherlands	Cross-sectional cohort	Yes	119	42 (14); mean (SD)	CD only	No	No	
Targownik <i>et al</i> ^[11]	2012	Canada	Follow-up study with data extracted from population-based Manitoba IBD research registry	Yes	86; UC: <i>n</i> = 32; CD: <i>n</i> = 50; Unclass: <i>n</i> = 4	46.7 (14.9); mean (SD); 46 (35-57) median (IQR)	UC and CD	No	Yes; 4.3 ± 0.3 yr	Same cohort used as in Leslie <i>et al</i> ^[19] (2008)
Tsai <i>et al</i> ^[12]	2015	Taiwan	Follow-up case control study with data extracted from population-based registry	No	3141; UC: <i>n</i> = 1489; CD: <i>n</i> = 1652	46.7 (35.6-61.0); median (IQR)	UC and CD	Yes; <i>n</i> = 12564	Yes; 6.49 ± 3.09 yr	Diagnosis of osteoporosis based on ICD-10 codes

¹BMD scores derived from DXA scan.²published in May.

³published in November. CD: Crohn's disease; UC: Ulcerative colitis; IQR: interquartile range; Unclass.: unclassified; IBD: inflammatory bowel diseases.

Table 2 Quality assessment according to the Newcastle–Ottawa Scale

	Schoon <i>et al</i> ^[13] (2000)	Jahnsen <i>et al</i> ^[12] (1997)	Jahnsen <i>et al</i> ^[16] (2004)	Tsai <i>et al</i> ^[18] (2015)	Targownik <i>et al</i> ^[3] (2012)	Leslie <i>et al</i> ^[20] (2009)	Leslie <i>et al</i> ^[19] (2008)	Andreassen <i>et al</i> ^[14] (1998)	Andreassen <i>et al</i> ^[15] (1999)	Bernstein <i>et al</i> ^[21] (2003, May)	Bernstein <i>et al</i> ^[22] (2003, November)	Haugeberg <i>et al</i> ^[17] (2001)
Selection	**	***	**	****	**	**	**	**	***	**	**	***
Comparability		**		**					**			**
Outcome	*	*	**	**	***	**	**	*	*	*	*	*
Total number of stars allocated	3	6	4	7	5	4	4	3	6	3	3	6

exclusively. Age was associated with osteoporosis or low BMD in studies including only CD patients, where one study found increased age to be a risk factor^[15], and one study found patients with reduced BMD to be significantly younger than the patient group without reduced BMD^[17].

Risk factors for change in bone mineral density over time

Five studies based on three cohorts analysed risk factors for a change in BMD over a period of time^[3,16,18-20]. Follow-up for the studies varied between 2 years^[16] and 6.49 ± 3.09 years^[18]. One study included only CD patients^[16]. An overview of the most relevant risk factors for change in BMD can be found in [Table 4](#), while a detailed list of all risk factors can be found in [Supplementary Table 3](#). CD patients appeared to have an increased risk of developing lower BMD or osteoporosis over time, while UC patients had no such increased risk. Gender analyses showed contradicting results. An increase in age was found to be associated with a decrease in BMD, whereas an increase (or decrease) in weight and BMI was associated with an increase (or decrease) in BMD.

DISCUSSION

This systematic review summarises the prevalence and development of, and risk factors for, osteoporosis or low BMD among patients with IBD. Though not statistically proven to be significant, it seems that CD cohorts have a higher prevalence of osteoporosis as compared to the UC cohorts. We found an association between

Table 3 Overview of most relevant risk factors for low bone mineral density or osteoporosis

Risk factors for reduced BMD	CD	CD + UC	Comments
General risk factors			
Gender ^[5,6,9,10]	+/-	+	Female gender was found to be significantly correlated by Leslie <i>et al</i> ^[20] (2009) investigating both CD and UC patients. In CD studies, Haugeberg <i>et al</i> ^[5] found female gender to be a predictive factor for osteoporosis. Jahnsen <i>et al</i> ^[6] found men to have lower Z-scores than women, whereas Schoon <i>et al</i> ^[10] found no significant association.
Age ^[2,3,5,9]	+	+/-	Age was significantly associated in the CD studies. However, Haugeberg <i>et al</i> ^[5] found patients with reduced BMD to be significantly younger than those without reduced BMD.
Weight ^[2,3,5,9]	+, ¹ -	+	Low weight was found to be a risk factor for low BMD in both CD + UC cohorts. In CD cohorts, Andreassen <i>et al</i> ^[15] (1999) found a significant positive correlation only in males. Haugeberg <i>et al</i> ^[17] found a positive correlation between weight and BMD for both genders.
BMI ^[2,5,6,9]	+/-	+	Leslie <i>et al</i> ^[20] (2009), the only study investigating BMI in CD + UC, found a positive correlation between BMI and BMD. Haugeberg <i>et al</i> ^[17] found a significant association for CD patients in a bivariate analysis, but not in a multiple linear regression analysis.
Steroid treatment ^[2,3,5,6,9]	+/- ²	-	Multiple risk factors related to steroid usage were investigated. No correlation was found in CD + UC. However, most CD studies did find a correlation.
Height ^[3,5,9]	+/-	+/-	
Smoking ^[3,5,6]	-	-	
Vitamin D supplement ^[3-5]	-	-	
Calcium supplement ^[3-5]	-	-	
Serum 25(OH)D ^[1,5,8]	+/-	+/-	
Serum calcium ^[1,5,8]	-	-	
Serum parathyroid hormone ^[1,3,8]	+/-	+	
Disease-specific risk factors			
UC diagnosis ^[3,9]	Not relevant	-	
CD diagnosis ^[3,6,9]	Not relevant	+/-	
Disease location ^[1,3,5]	-	-	
Disease duration ^[2,3,5,6]	+ ³ , -	-	
Surgery ^[2,3,5,6]	+/-	-	

¹Only in females.

²Only in males.

³Postmenopausal females. A plus sign means that a significant association was found and a minus sign means that no association was found. If studies found different results, both signs are present. CD: Crohn's disease; UC: Ulcerative colitis; BMI: Body mass index; BMD: Bone mineral density; +: Positive association; -: No association; +/-: Significant association and no association were found, depending on the study and/or statistical analysis carried out.

osteoporosis or low BMD and lower weight and lower BMI in both CD cohorts and cohorts including both CD and UC patients. Two out of four studies investigating gender found female gender to be associated with lower BMD. Age and steroid usage were found to be associated only among CD cohorts. In cohorts that analysed change in BMD over time, increased age was associated with a decrease in BMD and increased weight and BMI were associated with increased BMD. Furthermore, and unlike UC patients, CD patients had an increased risk of osteoporosis or low BMD over time.

Prevalence of osteoporosis

The prevalence of osteoporosis among IBD patients ranged from 2%^[18] to 15%^[16], with a range of 2%^[18] to 9%^[19] in UC patients and 7%^[18,19] to 15%^[16] in CD patients. The prevalence among healthy controls was investigated in two studies and was found to be 3%^[18] and 10% respectively^[17]. Since the data for osteoporosis prevalence in some studies were extracted from measurements of only one bone area, these numbers

Table 4 Overview of the most relevant risk factors for change in bone mineral density over time

Risk factors for change in BMD	CD	CD + UC	Comments
General risk factors			
Gender ^[8,9,11,12]	No data	+/-	No difference was found between genders in one study cohort ^[8,9,12] , whilst another cohort ^[11] found a greater incidence of osteoporosis in women than in men.
Age ^[8,9,11,12]	No data	+/-	
Weight ^[9,11]	No data	+	
BMI ^[7,9,11]	+	+	
Steroid treatment ^[7-9,11]	-	+/-	
Smoking ^[7]	-	No data	
Serum 25-OH D ^[7,8,11]	+	+/-	
Disease-specific risk factors			
Diagnosis ^[9,11,12]	Not relevant	+ ¹ , -	One ^[13] out of three studies found CD to be associated with an increased risk of osteoporosis. The others found no associations.
Disease location ^[7]	-	No data	
Disease activity ^[11]	No data	-	

¹Only in Crohn's disease. CD: Crohn's disease; UC: Ulcerative colitis; +: Positive association; -: No association; +/-: Significant association and no association were found, depending on the study and/or statistical analysis carried out. A plus sign means that a significant association was found and a minus sign means that no association was found. If studies found different results, both signs are present. Follow-up time for the respective studies was as follows: Jahnsen *et al*^[16]: 2 yr; Leslie *et al*^[19]: 2.3 ± 0.3 yr; Leslie *et al*^[20]: 2.3 ± 0.3 yr; Targownik *et al*^[5]: 4.3 ± 0.3 yr; Tsai *et al*^[18]: 6.49 ± 3.09 yr.

could be underestimations. The available data did not allow for a meaningful comparison of IBD patients and healthy controls.

When looking at osteoporosis prevalence worldwide in people without IBD, the numbers vary. Approximately 172400 people (around 3%) had osteoporosis in Denmark in 2017 according to the Danish Health Authority^[23] and The International Osteoporosis Foundation relies on the estimate that over 200 million people worldwide (around 3%) suffer from it^[9]. However, it has been estimated that the actual number of people aged 50 years or older with osteoporosis in Denmark, including undiagnosed inhabitants, is between 146481 and 518272, depending of the calculation method^[23]. A nationwide register based Danish study showed that the estimated prevalence of osteoporosis was 40.8% in women and 17.7% in men, all ≥ 50 years^[24]. Due to the wide range of estimates for the prevalence of osteoporosis and the small number of papers included in our study, it is not possible for us to conclude whether its overall prevalence is higher among IBD patients.

General risk factors for osteoporosis and low BMD

The included studies investigated many different risk factors using a variety of methodologies, making it difficult to draw firm, generalized conclusions. We found lower BMI and lower body weight to be associated with lower BMD. Female gender was found to be associated in two out of four studies investigating this risk factor. These are well-documented risk factors for osteoporosis in the background population as well^[5].

Surprisingly, use of prednisolone in any dose and duration was found to be associated with decreased BMD in cross-sectional analyses only in CD patients. Steroids are well-recognized bone-resorbing agents^[25,26]. Our finding might be explained by the fact that we have considered all forms of prednisolone use with any duration and hence the bones of some patients included in the analyses might have not been exposed enough to prednisolone to be affected^[27].

Older age is a well-known risk factor for osteoporosis^[5]. Remarkably, age showed significant association with BMD in studies including CD patients only, and one study found the patient group with reduced BMD to be younger than the patients with normal BMD. These studies were small and one of them only included premenopausal women. Hence the analysed population might not be fully representative.

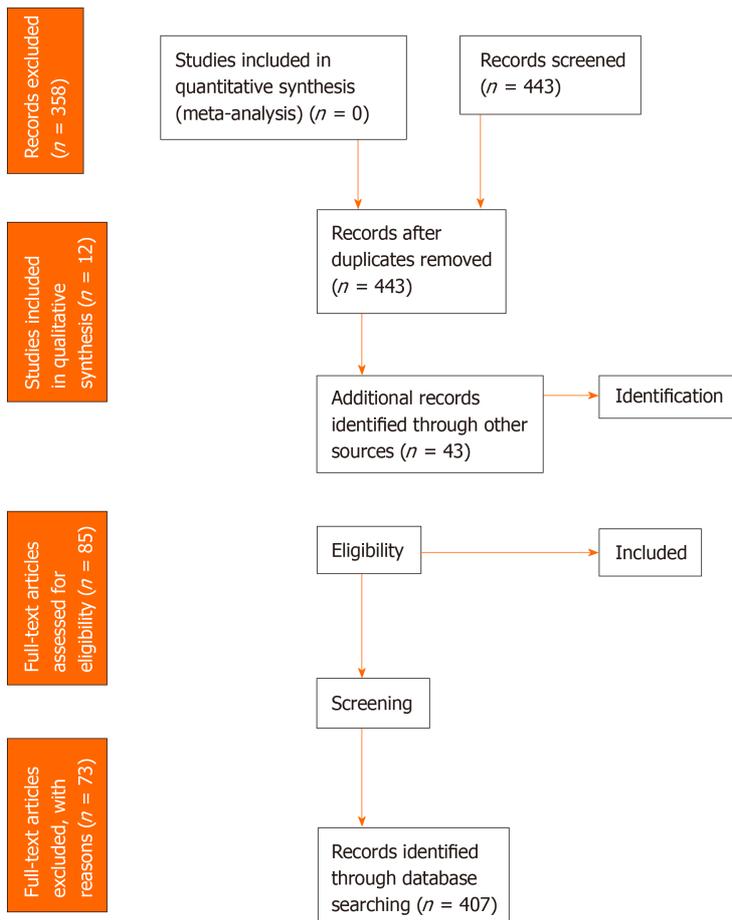


Figure 1 PRISMA flow diagram for the systematic review of the literature.

General risk factors for development of osteoporosis or low BMD over time

We found that increased age was associated with a decrease in BMD and that increased weight and BMI were associated with an increase in BMD over time. The results of analyses of gender and use of steroids showed no uniformity. These discrepant results are additionally surprising since females are known to be at higher risk of developing osteoporosis^[5]. This might again be explained by the lack of large-scale studies and that one study only includes premenopausal women. The only register-based study included in our review concluded that female gender was a risk factor for osteoporosis^[18].

Disease-specific risk factors

The CD cohorts presented the highest range in the prevalence of osteoporosis, though the numbers overlapped. CD, and not UC, appeared to be associated with osteoporosis or low BMD. Only CD patients seemed to have an increased risk for osteoporosis or low BMD over time. Suggested risk factors for developing osteoporosis are small-bowel disease or resection, smoking and corticosteroid treatment^[26]. Small-bowel disease and resection are specific to CD and as such could partly explain why the risk of osteoporosis appears to be greater among CD patients. Moreover, CD patients have been shown to have a higher prevalence of smoking than UC patients^[29]. Two population-based studies of CD and UC patients, respectively, have shown that on average around 2% of UC patients take corticosteroids at any given time, whereas almost 10% of CD patients do^[30,31]. Future analyses ought to be made of UC and CD separately.

Gut inflammation is a disease-specific risk factor that few of the studies included here chose to analyse. According to a synopsis on research evaluating bone disease in patients with IBD from 2014, increased systemic inflammation increases bone resorption^[1]. Inflammation serum markers and their role in IBD is an interesting subject that should be researched further.

Screening and treatment of osteoporosis

Current guidelines recommend that high risk IBD patients should be screened for osteoporosis^[32,33]. A Danish study found in a cohort of 513 unselected IBD patients with ten years of follow-up that the incidence of osteoporosis was twice as high for IBD patients compared to a control population^[34]. This indicates that adequate screening of osteoporosis could benefit IBD patients.

Strengths and limitations

There are several limitations to this systematic review. A systematic review is evidently dependent on the quality of the studies under review. The number of available studies was small, as was the number of patients in most cohorts. Furthermore, the quality of the studies reviewed varied considerably, as did the statistical analyses and use of covariates. This has precluded the possibility of performing a meta-analysis. Also, as all but one study originated in Europe, United States or Canada, their data might not be representative of other parts of the world. Half of the studies investigated only CD patients, while studies analysing both UC and CD patients did not provide stratified information on IBD subtype. Therefore, no data on UC patients exclusively were available. The risk factors discussed above were considered to be associated with osteoporosis if only one measurement (*e.g.*, total hip, femoral neck, *etc.*) was significant. Therefore, the association between BMD and some risk factors may vary in strength. The follow up time for the included studies varied between two and 6,5 years and hence may have been too short in some studies to identify any change in BMD. One study^[18] excluded patients diagnosed with osteoporosis before their IBD diagnosis; to compare this study with other studies that did not exclude this patient group might have affected our results. Finally, analyses conducted during each study were based on different measurements, *i.e.*, T, Z, and BMD scores, and this may also have distorted our analyses.

CONCLUSION

In conclusion, there seems to be an increased prevalence of osteoporosis among CD, as compared to UC, patients. We found an association between osteoporosis or low BMD and lower weight and lower BMI for CD and UC patients while findings regarding gender were inconsistent across studies. Steroid usage was found to be associated with an increased risk of osteoporosis or low BMD only in patients with CD. Increase in age, decrease in weight and BMI, and diagnosis of CD seem to be associated with a decrease in BMD over time. Firm conclusions are difficult to draw due to considerable heterogeneity in terms of study methodologies, definitions and the assessment of osteoporosis, and the small number of population-based studies. Osteoporosis is a common disease that is associated with great economic and psychological burden worldwide due to the consequences of the disease in terms of osteoporotic fractures, and physicians treating patients with IBD should be aware of the risk for osteoporosis in this patient group. Given the importance of adequate screening and treatment of osteoporosis, there is a need for more prospective population-based research on the relationship between osteoporosis and IBD-patients and subgroups in this population. Any such future studies should assess CD and UC separately, should include healthy subjects as controls, and should assess disease specific risk factors such as gut inflammation markers.

ARTICLE HIGHLIGHTS

Research background

The inflammatory bowel diseases (IBD), encompassing Crohn's disease (CD) and ulcerative colitis (UC) are chronic, immune-mediated disorders of the digestive tract. Being diagnosed with IBD is considered a risk factor for the development of osteoporosis. The consequence of development of osteoporosis is the increased risk of pathological fractures that in turn are associated with great economic and psychological burden. Several studies have investigated the relationship between inflammatory bowel diseases and osteoporosis but differences in study design and study populations, as well as inconsistent results and diverging interpretations of them, make it difficult to draw firm conclusions.

Research motivation

Considering the severe consequences of osteoporosis, research on risk factors and prevalence of the disease in IBD patients is of great importance in order to conclude how prevailing the disease is in this patient group and its subgroups. It may give clues on how guidelines for screening and treatment of osteoporosis in IBD-patients should be developed, as well pinpointing what areas need more research.

Research objectives

The objectives with this research was to assess the prevalence of osteoporosis among IBD patients compared to healthy individuals, as well as the disease course of osteoporosis or low BMD in IBD patients. We also aimed to assess risk factors associated with osteoporosis and low BMD in IBD patients with the intention to find more substantial evidence as to the cause of osteoporosis or low BMD in this patient group.

Research methods

For this systematic review, we searched databases including EMBASE and PubMed as well as abstracts from 2014-2018 presented at the United European Gastroenterology Week, the European Crohn's and Colitis Organisation congress, and Digestive Disease Week were screened. Studies were eligible for inclusion if they investigated either the prevalence of osteoporosis or osteopenia and/or risk factors for osteoporosis or low bone mineral density (BMD) in IBD patients. Studies on children under the age of 18 were excluded. Only population-based studies were included. All risk factors for osteoporosis and low BMD investigated in any included article were considered. Study quality and the possibility of bias were analysed using the Newcastle-Ottawa scale.

Research results

Twelve studies including 3661 IBD patients and 12789 healthy controls were included. Prevalence of osteoporosis varied between 4%-9% in studies including both CD and UC patients; 2%-9% in studies including UC patients, and 7%-15% in studies including CD patients. Among healthy controls, prevalence of osteoporosis was 3% and 10% in two studies. CD diagnosis, low body mass index (BMI) and low body weight were risk factors associated with osteoporosis or low BMD. Two out of four studies investigating gender found an association between female gender and lower BMD. CD patients had an increased risk for osteoporosis or low BMD over time, while UC patients did not. Increased age was associated with decreased BMD, and there was a positive association between weight and BMI and BMD over time. Great heterogeneity was found in the included studies in terms of study methodologies, definitions and the assessment of osteoporosis, and only a small number of population-based studies was available.

Research conclusions

This systematic review found a possible increase of prevalence of osteoporosis in CD cohorts when compared to UC and cohorts including both disease types. Lower weight and lower BMI were predictors of osteoporosis or low BMD in IBD patients. The results varied considerably between studies. Firm conclusions are difficult to draw due to considerable heterogeneity in terms of study methodologies, definitions and the assessment of osteoporosis, and the small number of population-based studies.

Research perspectives

Osteoporosis is a common disease that is associated with great economic and psychological burden worldwide due to the consequences of the disease in terms of osteoporotic fractures. Given the importance of adequate screening and treatment of osteoporosis, there is a need for more prospective population-based research on the relationship between osteoporosis and IBD-patients and subgroups in this population. Any such future studies should assess CD and UC separately, should include healthy subjects as controls, and should assess disease specific risk factors such as gut inflammation markers.

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Gastrointestinal tract injuries after thermal ablative therapies for hepatocellular carcinoma: A case report and review of the literature

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Abstract

BACKGROUND

Radiofrequency ablation (RFA) and microwave ablation (MWA) represent the standard of care for patients with early hepatocellular carcinoma (HCC) who are unfit for surgery. The incidence of reported adverse events is low, ranging from 2.4% to 13.1% for RFA and from 2.6% to 7.5% for MWA. Gastrointestinal tract (GIT) injury is even more infrequent (0.11%), but usually requires surgery with an unfavourable prognosis. Due to its low incidence and the retrospective nature of the studies, the literature reporting this feared complication is heterogeneous and in many cases lacks information on tumour characteristics, comorbidities and treatment approaches.

CASE SUMMARY

A 77-year-old man who had undergone extended right hepatectomy for HCC was diagnosed with early disease recurrence with a small nodule compatible with HCC in the Sg4b segment of the liver with a subcapsular location. He was treated with percutaneous RFA and a few week later he was urgently admitted to the Surgery ward for abdominal pain and fever. A subcutaneous abscess was diagnosed and treated by percutaneous drainage. A fistulous tract was then documented by the passage of contrast material from the gastric antrum to the abdominal wall. The oesophagogastroduodenoscopy confirmed a circular wall

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defect at the lesser curvature of gastric antrum, leading directly to the purulent abdominal collection. An over-the-scope clip (OTSC) was used to successfully close the defect

CONCLUSION

This is the first reported case of RFA-related GIT injury to have been successfully treated with an OTSC, which highlights the role of this endoscopic treatment for the management of this complication.

Key Words: Gastrointestinal tract; Radiofrequency ablation; Hepatocellular carcinoma; Complications; Endoscopy; Over-the-scope clip; Case report

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Core Tip: Thermal ablative therapies have a key role in the treatment algorithm for hepatocellular carcinoma, and besides their efficacy and tolerability, several studies have proven their overall safety. Nevertheless, albeit rarely, a number of complications have been reported and awareness is crucial to proposing the best treatment for each patient. We report the unusual case of a gastric perforation that was treated in our division and how it was managed with an endoscopic over-the-scope clip for the first time. The literature review aims to discuss the most relevant published data on gastrointestinal tract injuries after thermal ablation therapies.

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INTRODUCTION

Hepatocellular carcinoma (HCC) represents about 90% of primary liver cancers and, with an ever-greater incidence, is the seventh most common malignant tumour and the fourth major cause of cancer death worldwide^[1]. Approximately 70%-90% of HCC cases occur in cirrhotic liver and the choice of the most appropriate treatment must take into account not only cancer staging, but also liver function assessment, evaluation of extrahepatic disease, patient comorbidities and performance status^[2-4]. All the available therapeutic options have drawbacks that can affect both safety and health-related quality of life. Clinicians have to choose those interventional procedures whose benefits outweigh the risks for each individual patient^[5,6].

Although liver transplantation and surgical resection remain the gold standard for HCC, only a small proportion of patients are eligible, making locoregional therapies valuable options with a good survival benefit and safety profile^[7,8]. Of these, according to the most widely accepted staging and treatment algorithm for HCC, the Barcelona Clinic Liver Cancer algorithm^[9,10], ablative modalities have earned a pivotal role, representing the first-line option with curative intent for unresectable Stage 0 (very early) or Stage A (early) HCC. In addition, they can represent an alternative to resection in single tumours with favourable locations or for those tumours < 3 cm in size^[11]. They can also be included in a multimodal approach for intermediate and advanced cases, or play a role as a bridging therapy prior to transplantation^[12,13]. Radiofrequency ablation (RFA) and microwave ablation (MWA) are the most extensively clinically-validated thermal ablative therapies^[14,15]. Using one or more electrodes that generate electrical current and electromagnetic energy respectively, they induce heat in the tumour tissue above a lethal threshold, leading to coagulative necrosis^[15,16]. Although they are less invasive than surgical resection, the complication rate ranges from 2.4% to 13.1% for RFA and from 2.6% to 7.5% for MWA^[8], with no significant difference between the two techniques^[14]. Direct mechanical injury caused by the passage of the electrode through the vessels or biliary tree may lead to bleeding or bile leakage^[17,18]. Heat damage represents the other mechanism that can complicate

these procedures causing gastrointestinal tract (GIT), diaphragm or gallbladder injury, pleural effusion, bile duct strictures, biloma, vascular injury with consequent liver infarction and grounding pad burns. Other possible adverse events include tumour seeding along the tract, septic complications with hepatic abscess or cholangitis, and vasovagal reflex^[12,19,20]. GIT haemorrhagic complications after thermal ablative therapies have also been reported and appear to be mostly associated with a worsening of pre-existing portal hypertension or portal vein thrombosis^[19,21,22].

Thermal damage with GIT injury is an uncommon yet severe complication. At the current time, there are a few reviews analysing the complications of thermal ablation treatments, none specifically investigating GIT injuries^[23-25].

We report the case of an RFA-related gastric perforation that was successfully managed using an over-the-scope clip (OTSC). To the best of our knowledge, this is the first reported endoscopic treatment for an RFA-related GIT complication. We also briefly review and discuss the most relevant published data on GIT injuries after thermal ablation therapies, with regard to their prevalence, risk factors and proposed treatment.

CASE PRESENTATION

Chief complaints

In March 2020, a 77-year-old man was urgently admitted to the Surgery ward for abdominal pain and fever.

History of present illness

In June 2019, he was diagnosed with a bulky hepatic mass with a maximum diameter of 28 cm involving the whole right lobe, with no evidence of pre-existing liver disease. The condition was diagnosed at another hospital and the patient was subsequently treated with combined extended right hepatectomy, hepatic pedicle lymphadenectomy and cholecystectomy. The histopathological study showed a moderately differentiated hepatocellular carcinoma and confirmed a healthy liver parenchyma. No lymph nodes were involved and the tumour resection margins were clear (staging pT3N0G2 - R0). The 6-mo follow-up total-body computed tomography scan showed early disease recurrence and progression with a small 27 mm nodule compatible with HCC in the Sg4b segment of the liver with a subcapsular location, on the edge of the previous partial resection site, and a 5 cm adrenal metastasis. A subsequent contrast-enhanced ultrasound (US) scan of the liver confirmed the diagnosis (Figure 1). In January 2020, the patient had a multidisciplinary consultation at our hospital and was deemed fit for locoregional treatments. In February 2020, he was admitted in our Surgery ward and, once written informed consent had been obtained, he was treated with chemoembolisation of the adrenal metastasis and percutaneous RFA of the small HCC in Sg4b. The ablation was performed with anaesthesiological support, and under real-time US guidance. The device used to apply the radiofrequency current was a 20 cm long, 17-Gauge electrode with an uninsulated 3 cm tip (RF-AMICA probe, HS Hospital Service, Aprilia, Italy). No immediate complications were reported after the procedure.

History of past illness

The patient's medical history included arterial hypertension, surgical resection of a parathyroid adenoma and radioactive iodine therapy for Plummer's disease.

Physical examination

The clinical abdominal examination revealed epigastric tenderness. The patient's temperature was 38.5 °C, blood pressure was 140/90 mmHg, heart rate was 100 bpm, respiratory rate was 15 breaths per min, and oxygen saturation in room air was 99%.

Laboratory examinations

The patient's biochemistry tests showed no clear evidence of systemic inflammation. White blood cells and serum C-reactive protein were at the upper limit of the normal range. Serum transaminases, liver function tests and routine blood biochemistry were normal.

Imaging examinations

A subcutaneous abscess was diagnosed by abdominal ultrasound and treated with

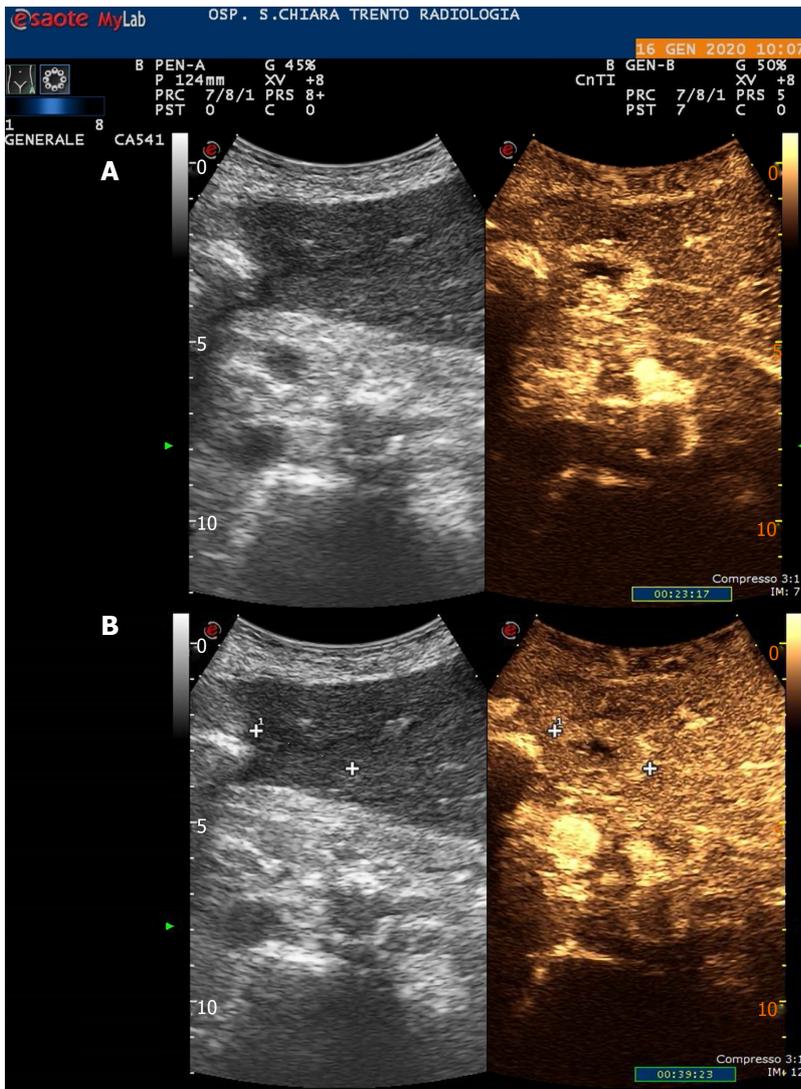


Figure 1 Contrast-enhanced ultrasonography showing the subcapsular 20 mm hepatocellular carcinoma at the 4th liver segment. A: During wash-in phase; B: During wash-out phase.

percutaneous drainage, observing necrotic and purulent secretion, together with air leak. Since no decrease in drain output was observed over the following d, an abdominal film with oral water-soluble contrast agent was performed. A fistulous tract was documented by the passage of contrast material from the gastric antrum to the abdominal wall (Figure 2).

FINAL DIAGNOSIS

The final diagnosis of the presented case was RFA-related gastric perforation.

TREATMENT

The patient was treated conservatively with fasting and broad-spectrum antibiotics; a prompt endoscopic assessment was planned. The oesophagogastroduodenoscopy confirmed a circular wall defect, approximately 15 mm in size, at the lesser curvature of gastric antrum, leading directly to the purulent abdominal collection (Figure 3). An OTSC was used to successfully close the defect (Figure 4) and there were no immediate complications. Technical success was confirmed after one week by an abdominal film with oral water-soluble contrast agent (Figure 5). The patient gradually resumed oral feeding and was finally discharged in good conditions.



Figure 2 Abdominal film with oral water-soluble contrast agent showing a gastric perforation with a gastro-cutaneous fistulous tract (surgical drain in place).



Figure 3 Endoscopic finding of the gastric perforation in communication with a purulent collection. Pylorus can be seen in the lower part of the picture.

OUTCOME AND FOLLOW-UP

A short time after the complete closure of the external fistula, recurrence of a mild cutaneous leakage (less than 40 mL/d) was observed for 40 d, followed by spontaneous closure. In June 2020, no signs of perforation recurrence were detected and the HCC was in remission in the remaining liver, according to mRECIST criteria^[26]. The case report timeline is showed in Supplementary Figure 1.

DISCUSSION

We performed a review of the literature reporting the largest series of GIT complications published to date, highlighting the features that may help clinicians in the detection and management of these feared events (Table 1). Published studies are mainly retrospective and extremely heterogeneous as regards information on tumour size and location, comorbidities and treatment approach, which are often missing, or otherwise include lesions other than HCC.

Epidemiology and outcome

The reported prevalence of GIT injuries ranges from 0.04% to 2.5%, particularly when

Table 1 Studies reporting gastrointestinal tract injuries after thermal ablation therapies for hepatocellular carcinoma

Ref.	Study design	Number of patients	Overall complication rate(%)	GIT injury rate (%)	Type of GIT injury	Thermoablative treatment	Timing of GIT injury	Management of GIT injury	Outcome	Associated conditions
Livraghi <i>et al</i> ^[29] , 2003	Multicentre, retrospective, questionnaire-based ¹	2320	7.1 (2.4 ²)	0.7 ²	5 colonic perforations; 1 jejunal perforation; 1 gastric perforation	Percutaneous RFA	2 d-4 d	Surgery (7/7)	2 deaths after colonic perforation	Gut wall distance < 1 cm (7/7); adherence due to previous abdominal surgery or inflammatory chronic cholecystitis (6/7); large superficial HCC in left lobe + aggressive treatment (1/7)
De Baere <i>et al</i> ^[31] , 2003	Multicentre, prospective ¹	312	12 (5.7 ²)	0.3 ²	1 colonic perforation	RFA ³	4 d	Surgery	Death	NA
Curley <i>et al</i> ^[57] , 2004	Multicentre, prospective ¹	608	9.5	0.16 ²	1 stomach wall necrosis	Open RFA	Immediate	Surgery	Recovery	Left lobe
Jansen <i>et al</i> ^[58] , 2005	Multicentre, prospective ¹	122	9.8 (6.3 ²)	2.5 (0 ²)	2 transient paralytic ileus	RFA ³	NA	Spontaneous resolution (2/2)	Recovery	NA
Casariil <i>et al</i> ^[32] , 2007	Single-centre, retrospective ¹	83	25 (7.2 ²)	0.7 ²	1 colonic perforation	Percutaneous RFA	36 d	NA	Death	Superficial HCC in Sg4; Child-Pugh B
Kasugai <i>et al</i> ^[22] , 2007	Multicentre, retrospective, questionnaire-based	2614	7.9 ²	0.2 ²	1 duodenum injury; 1 stomach injury; 1 colonic perforation	RFA ³	NA	External drainage (1/3)	Recovery	NA
Chen <i>et al</i> ^[34] , 2008	Single-centre, retrospective ¹	104	5.2 ²	0.6 ²	1 colonic perforation with fistula and abscess	Percutaneous RFA	3 wk	External drainage	Recovery	Superficial HCC in Sg4; previous surgery for Denver shunt
Liang <i>et al</i> ^[30] , 2009	Single-centre, retrospective ¹	1136	2.6 ²	0.2 ²	2 colonic perforations	Percutaneous MWA	3 d-5 d	Surgery (2/2)	Recovery	HCC located < 1 cm from colonic wall + prior right partial hepatectomy (2/2)
Livraghi <i>et al</i> ^[35] , 2012	Multicentre, retrospective, questionnaire-based ¹	736	10.2 (2.9 ²)	0.2 ²	1 ileal perforation; 1 colonic perforation	Percutaneous MWA	NA	Surgery (2/2)	Recovery	Superficial HCC in Sg4 + abdominal adhesions (2/2)
Koda <i>et al</i> ^[53] , 2012	Multicentre, retrospective, questionnaire-based	13283	3.5 ²	0.05 (0.04 ²)	1 colonic perforation; 3 stomach injuries; 2 duodenum injuries	RFA ³	NA	Surgery (3/6)	1 Death after colonic perforation	NA
Ding <i>et al</i> ^[19] , 2013	Single-centre, retrospective ¹	879	8.8-9.4 (3.1-3.5 ²)	0.3 ²	1 bowel perforation	Percutaneous RFA	Immediate	External drainage	Recovery	Previous Whipple procedure

Park <i>et al</i> ^[54] , 2017	Single-centre, retrospective	1211	6.8 (2 ²)	0.2 ²	1 colonic perforation	Percutaneous RFA	NA	NA	Recovery	NA
Jeong <i>et al</i> ^[28] , 2017	Single-centre, retrospective ¹	3933	NA	1.32 (0.05 ²)	28 stomach injuries; 16 colonic injuries; 6 small bowel injuries; 1 small bowel perforation; 1 colonic perforation	Percutaneous RFA	2 d-13 d (perforations)	Surgery (2/2 perforations)	Recovery	Subcapsular HCC (47/52); previous percutaneous treatments (7/52) or abdominal surgery (19/52)
Maeda <i>et al</i> ^[59] , 2020	Multicentre, retrospective, questionnaire based	9411	3.5 ²	0.04 ²	2 colonic perforations	NA	NA	NA	1 Death	NA

¹HCC and other liver tumors included;

²Major complications;

³Route approach not specified. GIT: Gastrointestinal tract; HCC: Hepatocellular carcinoma; RFA: Radiofrequency ablation; MWA: Microwave ablation; NA: Not available.

thermal ablative therapies were administered percutaneously.

The great variability in the GIT injury rate depends on whether minor injuries were included in the studies. Most literature concerns only major complications, strictly defined as those that increase the level of care, leading to significant morbidity and disability^[27]. This probably plays down the effect that thermal ablation may have on GIT. Two previous reviews on the complications of thermoablative treatments found an extremely low prevalence of GIT injuries (0.11%-0.5%)^[23,24]. However, a subsequent study on radiological predictors of major GIT injury reported a rate of 1.32%^[28] and in a review that included also minor injuries, this rate rose to 3.2%^[25].

Outcome is often unfavourable, as confirmed by previous studies. After sepsis and liver failure, GIT injuries were more frequently associated with death than other more commonly-observed complications^[24,29,30]. GIT complications accounted for two in six fatal adverse events in one Italian multicentre study^[29], one in five in the series from De Baère *et al*^[31], and the only lethal event observed by Casaril *et al*^[32].

Predisposing conditions

Associated conditions that may represent precipitating factors for GIT injury are HCC nodules or gut wall close to liver capsule (< 1 cm), previous abdominal surgery or percutaneous treatments.

It is well known that structures located within 0.5 cm-1 cm from the tumour margin are at-risk of heat-induced damage, since ablative treatment usually includes an area of healthy peritumoral tissue, in order to eradicate any microscopic satellites and prevent local recurrence^[12]. However, this is not the only factor involved, as stressed by Liang *et al*^[30] in their retrospective analysis, which did not identify any significant difference in tumour location between patients with *vs* without major complications^[30]. The association of an unfavourable location and a predisposing history is clearly shown by the data reported in the literature. In two studies analysing

cases^[39].

Imaging

Some authors advocate using of imaging techniques soon after RFA. Gastrointestinal wall thickening, fat stranding and free fluid can be found around the injured area as a result of minimal insult^[39,40]. Similarly, the presence of free air does not always indicate a major perforation, as it is found in more than half of all patients with minor complications and usually subsides within one month^[41]. On the other hand, immediate post-treatment computed tomography, may show concentric bowel wall thickening with mucosal disruption, which significantly correlates with the risk of major GIT injury requiring surgery^[26]. However, immediate imaging is not routinely performed in all centres, as it is not always possible to make a distinction between transient hyperaemia and the residual unablated tumour, which hampers the evaluation of treatment efficacy^[41]. Nevertheless, in selected cases, when dealing with tumours with a high-risk location in high-risk patients, close imaging parallel to clinical follow-up could be advised.

Management

Few studies focused on the detailed course of these complications and their management, although the impact on patient morbidity and quality of life is non-negligible. Whenever possible, patients were treated minimally-invasively with fasting and percutaneous drain placement, but most required surgical intervention to repair the injured GIT^[39]. To the best of our knowledge, the case reported here is the first case of gastric perforation after thermal ablation therapies to be managed endoscopically with an OTSC.

OTSCs differ from traditional through-the-scope clips in several characteristics, namely higher compression force, larger diameter and grasping accessories that allow the closure of wall defects of up to 30 mm, including the muscle layer^[42-44]. They have been successfully used and validated in literature in different settings, *i.e.*, haemostasis in acute GI bleeding, closure of GI perforations, leaks and fistulas or as anchor to prevent stent migration^[45]. While clinical success is nearly 100% for haemostasis, it decreases to 40%-75% for GI defect closure, with best outcomes in acute perforations, which have fresh edges with less fibrosis^[44,46,47]. Nevertheless, their use has been increasingly reported in postoperative leakages or fistulas as well, owing to the attractive possibility of avoiding complex surgery^[48-50]. Clinicians must take into account that a multidisciplinary approach should always be taken, since surgical or radiological placement of a drain is often advisable to prevent abscess formation after defect closure.

Preventive measures

An interesting issue is whether preventive measures may reduce the incidence of GIT injuries caused by thermal ablation therapies. These lesions are mainly associated with the percutaneous route and surgical management showed the presence of fibrotic adhesions that affixed the GI wall to the liver. Thus, a laparoscopic or intraoperative thermal ablation approach may allow the mechanical separation of the GIT from the surface of the liver and protect it from subsequent thermal damage^[32,51]. Nevertheless, the rate of other complications of these invasive routes is higher than for the percutaneous route^[21].

One well-established, easy and safe procedure is the use of artificial ascites. This technique allows the displacement of the liver, with its considered high-risk ablation area, from the adjacent organs^[52]. Authors who routinely perform this procedure reported a lower incidence of GIT complications despite dealing with high-risk tumours^[53,54]. Nevertheless, the presence of perihepatic adhesions due to previous abdominal surgery, other locoregional treatments such as transarterial chemoembolization or intra-abdominal inflammation, represent a limit for technical success. Moreover, this technique may be of limited efficacy in tumours located in left liver, since the nearby stomach is not easy to displace^[55]. Two other tips to help minimise adjacent organ injury are the interposition of thermocouples that ensure controlled temperature increase^[30] and the use of straight needle electrodes, which are more appropriate for monitoring the distance from GIT than expandable devices^[56].

CONCLUSION

This is the first reported case of RFA-related GIT injury endoscopically treated with OTSC. OTSCs have become part of the endoscopist's armamentarium and are now widely used to treat GI defects. This application may help reduce the need for complex surgery for this rare yet severe complication.

Our review raises awareness on an overlooked but severe complication of thermal ablative treatments. Nowadays, following the expansion of ablation criteria for HCC, these therapeutic modalities are gaining wider application. Therefore, clinicians must consider possible complications and accurately weigh up the risks and benefits, choosing the best treatment option not only according to fixed algorithms for HCC, but also tailored to the specific patient.

Since GIT injuries are rare but have an unfavourable prognosis and outcome, careful patient evaluation may help detect the tumour-related (location < 1 cm from the GI tract) or patient-related (previous surgery or locoregional treatments) risk factors that may trigger this event. These features do not represent an absolute contraindication to thermal ablation therapies, since these treatments remain safe and have an acceptable complication rate. However, according to local expertise, a non-percutaneous (laparoscopic or intraoperative) route should be chosen or preventive measures such as artificial ascites should be used. Otherwise, other ablative methods for HCC should be preferred.

In the case of GIT injury occurrence, the initial subtle clinical presentation warrants a low threshold for GI imaging. Finally, prompt identification of the injury is mandatory to avoid diagnostic delay and provide timely management.

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