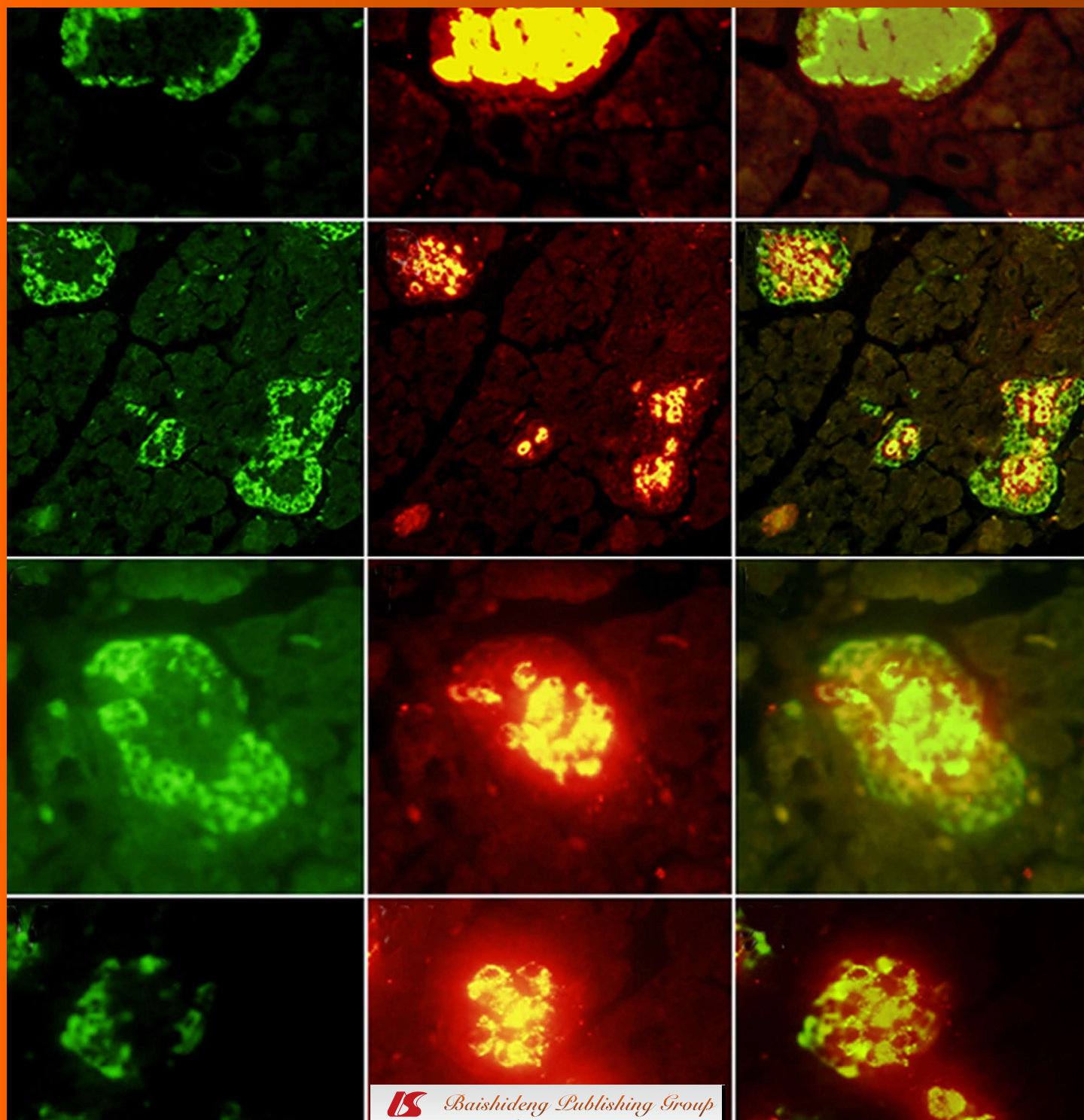


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Targeting key signalling pathways in oesophageal adenocarcinoma: A reality for personalised medicine?

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adenocarcinomas. This may be achievable in the future with the advent of gene signatures and a combinatorial approach.

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Abstract

Cancer treatments are rapidly changing. Curative treatment for oesophageal adenocarcinoma currently involves surgery and cytotoxic chemotherapy or chemoradiotherapy. Outcomes for both regimes are generally poor as a result of tumor recurrence. We have reviewed the key signalling pathways associated with oesophageal adenocarcinomas and discussed the recent trials of novel agents that attempt to target these pathways. There are many trials underway with the aim of improving survival in oesophageal cancer. Currently, phase 2 and 3 trials are focused on MAP kinase inhibition, either through inhibition of growth factor receptors or signal transducer proteins. In order to avoid tumor resistance, it appears to be clear that targeted therapy will be needed to combat the multiple signalling pathways that are in operation in oesophageal

INTRODUCTION

Oesophageal adenocarcinoma is the 10th commonest malignancy in the UK yet it is the 5th commonest cause of cancer death^[1]. This poor prognosis is partly attributable to a disease afflicting an elderly population. All too often the disease presents with symptoms of dysphagia which usually heralds advanced disease, typically with lymph node or distant metastases^[2]. The 5 year survival, despite recent advances in neo-adjuvant chemotherapy, radiotherapy and surgery is approximately 25%. The incidence has been steadily increasing over the past 30 years^[3-5]; this is thought to be due to the trend of an aging and increasingly obese population in combination with *Helicobacter pylori* eradication^[1,6,7]. Barrett's oesophagus has been established

as a clear risk factor for oesophageal adenocarcinoma^[8]. It has been demonstrated that surveillance of patients with Barrett's oesophagus can identify early stage adenocarcinomas^[9,10]. If diagnosed at an early stage, with the disease confined to the submucosa, 5 year survival rates are as high as 90%^[11]. Unfortunately current strategies for surveillance of Barrett's oesophagus are insufficient to reduce the incidence of oesophageal adenocarcinoma and most cases are diagnosed in patients that are not on Barrett's surveillance programs^[10]. This may be accounted for by the fact that a significant proportion of patients with Barrett's oesophagus are asymptomatic. Currently, it is not economically viable to screen the whole population for Barrett's oesophagus^[12]. Until this is addressed, there does not seem to be a solution to providing an early diagnosis of oesophageal adenocarcinoma for the majority of patients. This indicates the importance of developing improved treatments for advanced disease.

CURRENT MEDICAL TREATMENTS

The medical therapies in mainstream use for the treatment of oesophageal and junctional adenocarcinomas are cytotoxic and antimetabolite agents. They target rapidly dividing cells in a non cancer cell specific manner^[13]. 5-Fluorouracil (5-FU) inhibits DNA synthesis through inhibition of thymidylate synthetase^[14]. The platinum agents cisplatin and oxaliplatin form DNA adducts and cross-links which prevents DNA transcription and replication^[15]. The anthracyclines epirubicin and doxorubicin induce DNA damage and inhibit DNA transcription through inhibition of topoisomerase II and DNA helicase activity^[16]. The cytotoxic action of taxanes are predominantly due to disruption of microtubules^[17].

Cytotoxic chemotherapy is generally not very effective and side effects are common. The agents are usually contraindicated in severe cardiac and liver disease, a common occurrence in the affected elderly population. Recent advances have been made with the route of administration. A tablet form is now available, capecitabine, which is an effective alternative to infusing 5-FU. This reduces the morbidity associated with central venous catheterisation. Furthermore, oxaliplatin appears to be less toxic and more potent than cisplatin, and it can be infused over a shorter period of time^[18,19]. Approximately 30% of patients with oesophageal adenocarcinoma are offered palliative chemotherapy and radiotherapy^[1,20]. Prognosis is only 6-11 mo^[21,22], with a 5 year survival of 4%^[22]. Surgery is beneficial in patients that present with disease localised to the oesophagus or with localised lymph node metastases. Neo-adjuvant chemotherapy modestly improves survival compared to surgery alone; 5 year survival is 23% compared to 36% with neo-adjuvant chemotherapy^[23]. On subgroup analysis, patients with tumors at the gastro-oesophageal junction seemed to benefit the most and this regimen is offered in the UK^[24]. In the USA, the protocol of neo-adjuvant chemo-radiotherapy is favoured^[25]. 5 year survival is 8%-20% in selected patients. Curative chemo-radiation is an alternative strategy to surgery and prognosis is similar^[2].

This may be due to the avoidance of postoperative mortality and morbidity. Whatever regimen is used, the poor prognosis for oesophageal adenocarcinoma is largely a result of disease recurrence and the morbidity surrounding major surgery^[2]. Treatment failure is thought to be a consequence of the blanket therapy approach due to the nature of the non-specific or non-targeted mechanism of action of the medical agents described earlier. Recent evidence suggests that standard chemotherapy and radiotherapy activate signalling pathways that stimulate growth and resistance of cancer cells^[26]. Prognosis may improve with agents that specifically target mitogenic signalling pathways and intense research is currently underway.

The aim of this review is to explore the key signalling pathways that are associated with oesophageal adenocarcinoma and review the clinical trials of novel therapeutic agents that are in progress. We will draw parallels from breast and colon cancer. We will address the question: by targeting key signalling pathways is personalised medicine a reality in oesophageal adenocarcinoma?

DEFINING SIGNALLING PATHWAYS

Signalling pathways are essential components in all cells; they are important to stimulate cell growth, proliferation, differentiation, invasion and apoptosis. Certain pathways are specifically important in embryonic development, inflammation and carcinogenesis. Signalling pathways have common mechanisms of action. They convey extra-cellular stimuli, usually *via* cell surface receptors, onto a chain of signal transducer proteins which subsequently enter the nucleus. In the nucleus the signalling proteins activate transcriptional machinery on gene promoters. Gene expression and cell phenotype are altered. In the context of cancer cells, phenotypic change may include cell growth, cell division, increased cell motility, evasion of apoptosis and sustained angiogenesis. These changes constitute the hallmarks of cancer^[27]. Signalling pathways in cancer cells are usually unregulated and resistant to feedback inhibition, and this usually occurs as a consequence of sustained activation from their components. The components are commonly known as oncogenes or tumor suppressor genes^[28]. Oncogenes and tumor suppressor genes are usually expressed as a result of genetic mutations. In oesophageal cancer, mutations occur as a consequence of DNA damage from bile or acid reflux, nitric oxide, alcohol and cigarette smoking. Mutations usually involve chromosomal translocations of oncogenes or tumor suppressor genes onto housekeeping genes or other genes undergoing active transcription^[29,30]. This culminates in persistent activation or inhibition of specific signalling pathways. Components of signalling pathways can be potentially inhibited at a variety of levels. Inhibitors can target the cell surface receptor, signal transducer proteins or even transcription factors. Unfortunately multiple pathways and receptors are associated with oesophageal cancer and the complexity that exists between different pathways is likened to a computer circuit (Figure 1). Blockade of one pathway or component may not be sufficient.

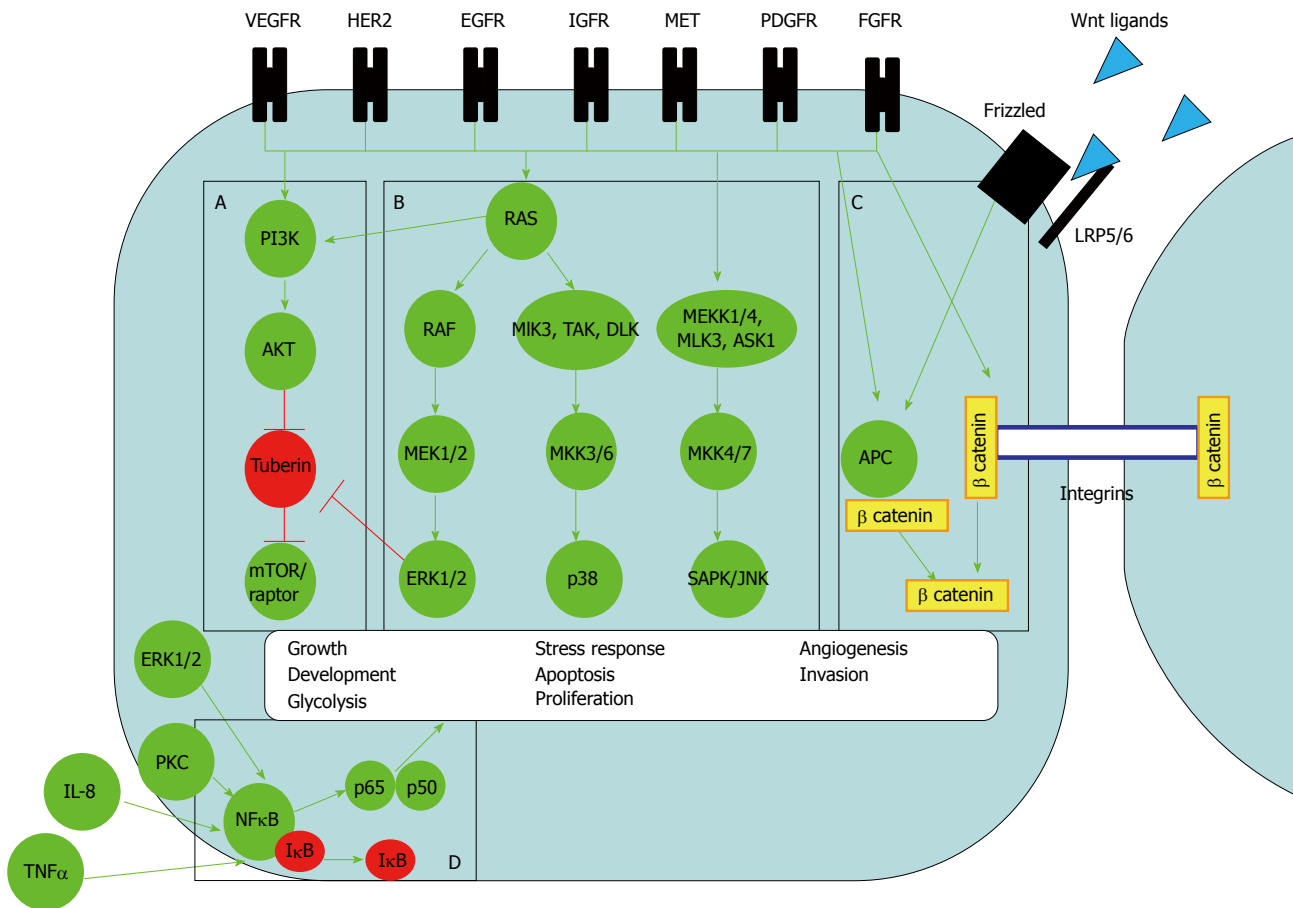


Figure 1 Signalling pathways in oesophageal adenocarcinoma. The pathways known to be operative in oesophageal adenocarcinoma are A: PI3-Kinase, B: Mitogen activated protein (MAP) Kinase, C: Wnt signalling and D: Nuclear factor- κ B (NF- κ B). The green arrows indicate activation, the red arrows indicate inhibition. Vascular epidermal growth factor (VEGF), human epidermal growth factor receptor 2 (HER2), epidermal growth factor receptor 1 (EGFR), insulin growth factor receptor (IGFR), hepatocyte growth factor receptor (MET), platelet derived growth factor receptor (PDGFR) and fibroblast growth factor receptor (FGFR) are the known receptor tyrosine kinase (RTK) associated with oesophageal adenocarcinomas. The pathways are complex and inter-connected. For example RTKs can activate all 4 known pathways. The ultimate biological response varies from cell proliferation, development, apoptosis, differentiation, inflammatory response, angiogenesis and invasion depending on which specific pathway or receptor is activated. A: PI3-Kinase pathway. RTK activates PI3-Kinase directly or through RAS. As a consequence of phosphorylation, PI3K recruits AKT. AKT inhibits tuberlin, this allows activation of the Raptor/mTOR complex to activate transcriptional machinery. mTOR/raptor activates transcription factors and co-activator proteins cMyc and hypoxia inducible factor (HIF)-1 α that drive the biological response of growth, proliferation, glycolysis, angiogenesis and invasion; B: MAP Kinase pathways. The 3 main MAP Kinase pathways are extracellular related kinase (ERK), p38 and JUN kinase (JNK). They are all activated by similar RTKs. The signalling pathways have a common feature of a cascade of phospho-proteins. A MAPKK Kinase (e.g. RAF), a MAPK Kinase [e.g. MAP ERK kinase (MEK)1/2] and a MAP Kinase (eg. ERK) transfer the signal onto multiple transcription factors on gene promoters^[31]. ERK signalling for example can alter the gene expression of over 200 genes^[32]. The subsequent biological response varies from cell proliferation, development, apoptosis, differentiation and inflammatory response, depending on the specific pathway activated; C: Wnt signalling. Wnt signalling exerts a biological response through release of β catenin into the nucleus with subsequent action on gene promoters. β catenin is released directly from RTK phosphorylation of Axin. Alternatively Wnt ligands bind to Frizzled receptors and form a complex with the LRP5/6 membrane receptor. The membrane receptor complex recruits dishevelled and axin from a cytoplasmic complex of dishevelled, Axin, adenomatous polyposis coli protein (APC) and β catenin. This allows release of β catenin; D: NF- κ B pathway. NF- κ B (p65/p50) activates gene promoters only when released from I κ B. Interleukin-8 (IL-8), tumour necrosis factor (TNF) α and radiation activate the pathway. Adding to complexity, ERK MAP Kinase and Wnt, through protein Kinase C, can also potentially activate NF- κ B although this link has not been investigated in oesophageal adenocarcinoma.

KEY SIGNALLING PATHWAYS IN OESOPHAGEAL ADENOCARCINOMA

MAP-Kinase and PI3 kinase pathways

MAP-Kinase (MAPK) pathways are the most well described pathways in carcinogenesis. They are made up of three distinct pathways: ERK, SAP/JNK and p38^[31] (Figure 1^[31,32]). The pathways are normally activated by growth factors, temperature changes, cytokines and hypoxia *via* a variety of cell surface receptors^[33]. In oesophageal cancer cells, gastric and bile acid^[34,35] and the cytotoxic agent etoposide^[36] are known to activate MAPK pathways. Cell surface receptors known to activate MAPK include receptor tyrosine kinase (RTK), G protein linked receptors and integrins^[33]. Following activation of cell

surface receptors a cascade of phospho-proteins is initiated *via* GTPase signal transducer proteins. RAS and RAF are examples of GTPase signal transducer proteins which act as a hub, receiving signals from many different cell surface receptors^[28] (Figure 1). GTPase signal transducer proteins also amplify signals onward through multiple signalling pathways (Figure 1). MAPK pathways are often up-regulated in breast^[37,38], ovarian^[39] and prostate cancer^[40]; however the impact on prognosis of MAPK signalling is sometimes conflicting. ERK MAPK is active in 60% of ERK MAPK oesophageal adenocarcinomas^[36]. Tumors with active ERK MAPK signalling frequently have metastases and a worse prognosis. This suggests that blockade of ERK MAPK in oesophageal adenocarcinomas may have an important therapeutic role.

The PI3-Kinase (PI3K) pathway is activated by RTKs and RAS (Figure 1). Following RAS and/or RTK activation, AKT is phosphorylated by PI3K. Activation of the PI3K pathway stimulates cell growth, glycolysis, and proliferation^[41] mainly through cMyc and hypoxia inducible factor 1 α (HIF-1 α) stimulation. Components of the PI3K pathway are up-regulated in oesophageal adenocarcinoma. The expression of phosphorylated AKT is increased in oesophageal adenocarcinoma tissue compared to normal epithelial and Barrett's tissue^[34]. PI3K pathway mutations are thought to occur in 6% of oesophageal adenocarcinomas^[42]. Crosstalk exists between the MAPK and PI3K pathways at the levels of RAS and ERK (Figure 1). This is likely to play a role in drug resistance seen in therapies that target signal transducer proteins. Crosstalk indicates that inhibition of multiple pathways may be needed for effective anti-cancer therapy.

Mechanisms of sustained MAPK and PI3K activation

RTKs on the cell surface are key activators of MAPK and PI3K pathways. RTKs can be activated constitutively by dimerisation, by ligand activation or by receptor over-expression^[43]. Alternatively RAS mutations can render the GTPase in its active form so that the signal is permanently switched on, resistant to the activity of cell surface receptors. RAS mutations occur in only 10% of oesophageal adenocarcinomas. Aberrant expressions of RTK are frequently associated with oesophageal adenocarcinoma and there are many different family members (Figure 1). Receptor over-expression is usually associated with disease recurrence and a poor prognosis. Human epidermal growth factor receptor 1 (EGFR) and human epidermal growth factor receptor 2 (HER2) are over-expressed in 50% of oesophageal adenocarcinomas and positive expression is associated with a poor prognosis and cytotoxic drug resistance^[30,44]. High expression of the hepatocyte growth factor receptor (Met) predicts metastases and recurrence in resectable oesophageal adenocarcinoma^[45]. Vascular endothelial growth factor receptors (VEGF) are commonly associated with oesophageal adenocarcinoma, VEGF is thought to be important in angiogenesis and correlates with tumor microvessel density, crucial for tumor growth. VEGF A and C expression indicates a poor prognosis^[46]. The significance of insulin like growth factor receptors (IGFR) has not been studied in oesophageal adenocarcinoma^[47,48], however low IFGR expression correlates with an improved survival in metastatic gastric adenocarcinoma. The platelet derived growth factor receptor (PDGF) has also been shown to be expressed in oesophageal adenocarcinoma^[49]. In oesophageal squamous cell carcinoma, fibroblast growth factor receptors^[50] and tropomyosin-related kinase receptors^[51] are indicators of tissue invasion and chemo-resistance respectively. Each member of an RTK family may have up to 20 subtypes^[52] and it has been demonstrated that oesophageal adenocarcinoma cells often co-express the different subtypes of RTKs^[49]. Therefore a therapy that targets only one receptor may not be effective. Furthermore cancers are known to be heterogeneous, made up of a population

of genetically different cells. Gene expression at the invasive site of a tumor is different from the centre^[53] and the gene expression of primary tumors is different to those at metastatic sites^[54]. The variety of RTKs and downstream MAPK signalling pathways indicates that complete blockade of such a complex and diverse system may be impossible. Growth inhibition is more pronounced in oesophageal adenocarcinoma cells treated with combined inhibition of the EGFR and IGFR compared to inhibition of either receptor in isolation^[55]. Furthermore patients with co-expression of HER-2 and EGFR also have a worse outcome^[56]. Even if drug inhibition of both IGFR and EGFR is successful, resistance will prevail if alternative receptors or signal transducer proteins are active. Tumor heterogeneity may explain the modest improvement in response and survival seen with agents directed towards a solitary receptor, discussed in more detail below.

Targeting the epidermal growth factor receptor 1

Gefitinib and Erlotinib: Gefitinib and Erlotinib are small molecular inhibitors of tyrosine kinase phosphorylation of EGFR (Figure 2). Gefitinib therapy has been investigated in metastatic oesophageal adenocarcinoma^[57]. Two thirds of patients had prior standard cytotoxic chemotherapy of which half had received surgery. Partial response and stable disease (according to Response Evaluation Criteria of Solid Tumors) was achieved in 37% and the median survival was 4.5 mo^[57]. It is difficult to compare small phase 2 clinical trials but results were not significantly different compared to treatment with combined cytotoxic chemotherapy in a similar cohort of patients. Partial response was 12.5% and a median survival of 5 mo was seen in patients treated with irinotecan with docetaxel^[58]. Partial response was 29% and median survival was 6.4 mo in patients treated with irinotecan with 5-FU/leucovorin^[59]. To understand the poor results seen with gefitinib, ERK MAPK and PI3K pathway activation was determined by immunohistochemistry. Staining for phospho-ERK and phospho-AKT was assessed before and after treatment in 7 patients. No differences in staining patterns were seen in tumors treated with gefitinib, suggesting that the two pathways were not inhibited by the drug. This result is mirrored in a larger study of 70 gastric adenocarcinomas treated with gefitinib^[60]. This indicates ERK MAPK and PI3K pathway resistance to EGFR blockade. A further study conducted in 43 metastatic adenocarcinomas at the gastro-oesophageal junction treated with gefitinib^[61] also had similar survival and response rates to the study by Ferry *et al*^[57]. Trends for favourable outcome were more likely in tumors with expression of EGFR, ERK MAPK and PI3K signalling activation. This was assessed by immunohistochemistry prior to treatment although assessment was not made post treatment. The differences in outcome did not meet statistical significance, but this is likely due to the small sample size. Of the poor responders, 2 (9%) had k-RAS mutations. This study indicates the importance of patient selection with targeted therapy. On the contrary in gastric and oesophageal adenocarcinomas treated with a similar EGFR inhibitor, erlotinib (Figure 2), EGFR expression

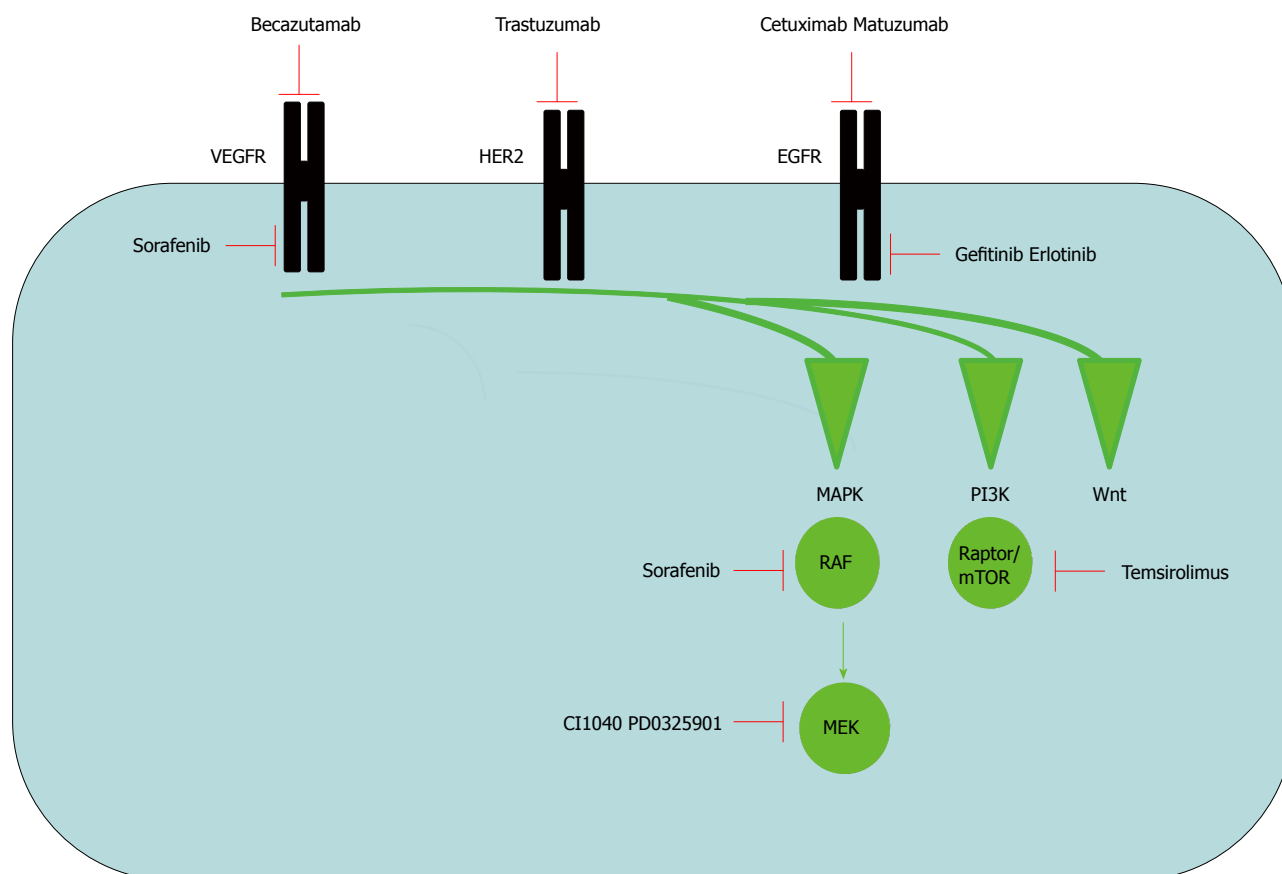


Figure 2 Drug inhibition of signalling pathways. Drugs that target signalling pathways can be divided into two groups. Antibodies [Becazutumab, trastuzumab, cetuximab and matuzumab] are antibodies that target the receptor tyrosine kinase (RTK), vascular epidermal growth factor receptor (VEGFR), human epidermal growth factor receptor 2 (HER2) and epidermal growth factor receptor 1 (EGFR) respectively] and small molecular inhibitors [The small molecular inhibitors gefitinib and erlotinib target EGFR. Temsirolimus specifically inhibits the PI3-kinase pathway at the level of Raptor/mTOR. CI1040 and PD0325901 inhibits ERK MAP kinase pathway at the level of MEK. Sorafenib is a dual inhibitor of the VEGF receptor and ERK MAP kinase at the level of RAF].

and PI3K signalling activation was not found to influence drug response^[62]. The difference may be explained by different receptor specificity between gefitinib and erlotinib or it may indicate the activity of additional RTKs or other cell surface receptors

Matuzumab: Matuzumab is a humanised monoclonal antibody that binds with the EGFR (Figure 2). Phase 1 trials have been conducted in metastatic oesophageal adenocarcinoma treated with conventional therapy with matuzumab^[63]. EGFR was evident in 80%-100% of tumor specimens; however MAPK activity was not measured post treatment. This makes it difficult to assess the efficacy of the medication in the absence of survival data from this phase 1 study.

Cetuximab: Cetuximab is a monoclonal antibody directed against the EGFR (Figure 2), utilised in the treatment of advanced colorectal adenocarcinoma^[64]. Trials have shown an improvement in average survival to 9 mo. RAS mutations occur commonly in colon cancer and account for resistance seen with cetuximab. When taken into account, colorectal carcinoma patients without k-RAS mutations have a significantly improved response to cetuximab compared to patient with k-RAS mutations which have survival

times comparative to that of supportive care alone^[65]. RAS mutations are less commonly seen in oesophageal adenocarcinomas and occur in less than 10% of cases so this is unlikely to account for the poor response seen with tyrosine kinase receptor inhibition^[66]. Phase 2 clinical trials with cetuximab in advanced oesophageal adenocarcinoma have shown modest results similar to that seen with gefitinib^[67].

Targeting the epidermal growth factor receptor 2

A Phase II trial has been conducted with trastuzumab, a monoclonal antibody targeted to targeting the epidermal growth factor receptor 2 (HER2) (Figure 2). Trastuzumab was tested in combination with cisplatin, paclitaxel and radiotherapy in locally advanced oesophageal adenocarcinoma^[68]. Patients were selected and included those with HER2 expression on immunohistochemistry. 74% of patients had positive HER2 expression. Median survival was 24 mo and 50% survived for 2 years. The patient population was different to the patients treated with gefitinib and cetuximab. None of the patients had organ metastases and distant lymph node metastases were present in only 37%, which makes it difficult to make direct comparisons.

Targeting the vascular epidermal growth factor receptor

Becazutumab is a monoclonal antibody directed against

the targeting of vascular epidermal growth factor receptor (VEGFR) (Figure 2). A phase 2 trial in metastatic gastric adenocarcinomas with 23 oesophageal junctional adenocarcinomas showed a response rate of 65% and median survival time of 12.3 mo^[69]. Most patients were inoperable and the results were an improvement on standard cytotoxic therapies. Although VEGFR is frequently over-expressed in oesophageal adenocarcinomas^[49], an assessment of VEGFR expression was not made prior to treatment. This may suggest that an improved outcome could be achieved by selecting tumors with high VEGFR expression.

Taken together, this may indicate that tailored RTK inhibition has a role in the treatment of selected patients with oesophageal adenocarcinomas. Initial trials have yet to make a significant impact and this may be down to poor patient selection and the use of growth factor receptor inhibitors in isolation.

Wnt signalling

Wnt signalling is important in cell growth, motility, angiogenesis, differentiation and other important phenotypic characteristics of cancer cells. Wnt ligands activate the Frizzled cell membrane receptor; Wnt is under feedback control from Wnt ligand inhibitors. Once activated, Frizzled forms a complex with another receptor LRP5/6 and recruits Dishevelled and Axin. The complex of APC, Axin and GSK and β -catenin is disrupted releasing unphosphorylated β -catenin (Figure 1). β -catenin can then enter the nucleus, and activate genes that stimulate growth, angiogenesis, invasion and cell cycle progression (*c-Myc*, *COX2*, *MMP7* and *Cyclin D1*). Alternatively β -catenin can also be released by RTK phosphorylation of E-cadherin or Axin (Figure 1). Furthermore Wnt ligands can also directly activate calmodulin kinase II and protein kinase C in turn releasing intracellular calcium or increasing JNK. Components of the pathway are altered in oesophageal adenocarcinoma. APC, Axin and Wnt ligand inhibitors are silenced by loss of heterozygosity or DNA methylation and collectively these events increase β -catenin activity. Although APC mutations are less commonly seen than in colorectal cancer, β -catenin or Wnt ligands are over-expressed in up to 77% of oesophageal adenocarcinomas^[70,71]. This makes components of this pathway a potential target for drug inhibition.

Transforming growth factor- β pathway

Transforming growth factor- β (TGF- β) is a tumor suppressor gene and a potent inhibitor of cell growth. TGF- β binds to serine/threonine kinase type 1 and type 2 receptors. Upon binding to receptors, TGF- β forms a complex and phosphorylates intracellular signalling mediators called SMAD2/3. SMAD2/3 dissociates from the receptors and forms a complex with SMAD4 allowing it to enter the nucleus and regulate a large number of target genes. One target is *SMAD7* which targets ubiquitin to the membrane receptor complex resulting in feedback inhibition of the pathway. Down regulation of SMAD4 has been shown in the progression of Barrett's oesophagus to adenocarcinoma. TGF- β is anti-proliferative in some oesophageal

cancer cell lines^[72]. In contrast TGF- β expression has been demonstrated at the invasive margin of oesophageal adenocarcinomas and promotes cell invasion^[73]. This may be explained by cross talk between the TGF- β pathway with PI3K, Wnt, PKC and the MAP-Kinase pathways. One potential mechanism is *via* SMAD7 inhibition leading to loss/diminished feedback inhibition of the pathway.

Nuclear factor- κ B pathways

Nuclear factor- κ B (NF- κ B) is a proinflammatory transcription factor. It exists as a heterodimer p50/p65, situated in the cytoplasm under inhibitory control by I κ B (Figure 1). Numerous activators have been identified including ERK MAPK signalling, cytokines (IL-8, TNF- α) and radiation. Specifically for oesophageal adenocarcinoma, bile salts and gastric acid have been shown to activate NF- κ B. Gastrin has been shown to activate NF- κ B through PKC signalling in gastric cancer cells^[74]. Once activated, NF- κ B enters the nucleus and through chromatin re-modelling it becomes a central regulator of many genes including cell cycle regulators (*cyclin D1*, *cMyc*, *p53*), inhibitors of apoptosis (*Bcl-2*), cytokines (*interleukins*, *TNF- α*), angiogenic mediators (*COX2*) and the growth factor receptor *EGFR*. Increased NF- κ B expression is seen in Barrett's oesophagus and adenocarcinoma. In oesophageal adenocarcinoma the expression correlates with chemo-radiation resistance^[75].

Wnt signalling, TGF- β pathway and NF- κ B pathways all activate important mediators in oesophageal adenocarcinoma. However there are no trials investigating the impact of specific inhibitors of these pathways outside the laboratory setting. RTK inhibitors have been investigated in oesophageal adenocarcinoma; however their role in Wnt signalling inhibition of β catenin has not been evaluated. The development of agents that inhibit alternative components of the Wnt, TGF- β and NF- κ B signalling pathways are needed to avoid resistance and improve the modest responses seen with current therapies in clinical trials in oesophageal adenocarcinoma that focus on RTKs and MAPK.

POTENTIAL FUTURE TREATMENT TARGETS IN OESOPHAGEAL ADENOCARCINOMA

ERK MAPK inhibition by targeting MEK

An alternative approach is to target signal transducer proteins which may be downstream of many different RTKs. Theoretically this may reduce resistance of RTK co-expression. MEK is a downstream signal transducer protein of the ERK MAP Kinase pathway (Figure 1). No clinical trials have explored the role of MEK inhibition in oesophageal adenocarcinoma but lessons may be learned from trials in other cancers. Phase 2 clinical trials of the MEK inhibitor CI1040 (Figure 2) in advanced pancreatic, breast and non small cell lung cancer failed to make an impact on tumor progression^[76]. Parallels can be drawn from colon cancer where RAS mutations reduced the efficacy of ce-

tuximab. Patients treated with MEK inhibition were tested for ERK MAPK and PI3K signalling activation in archived samples, sometimes many months preceding treatment. This did not influence recruitment into the study and patients were enrolled if ERK or PI3K activation was judged to be low. Better patient selection may have resulted in a better response to treatment. ERK MAPK signalling activity was not assessed post treatment which may mean that the dosage was insufficient. More potent MEK inhibitors, such as PD0325901, have been evaluated in hepatocellular carcinomas^[77]. Alternatively the poor responses with MEK inhibition may be explained by “cross talk” between different signalling pathways (Figure 2). Resistance to MEK inhibition may be explained by PI3-Kinase activation. The combination of MEK inhibition and PI3-Kinase inhibition is superior to treatments in isolation for inhibiting the growth of breast cancer cells^[78]. This suggest that dual therapy is needed to combat both pathways.

ERK MAPK inhibition by targeting RAF and VEGF

A combined targeted approach may be beneficial in oesophageal adenocarcinoma. Sorafenib, a multifunctional kinase inhibitor, which acts on several growth regulatory pathways including VEGF and RAF (Figure 2), has been shown to be of benefit in renal cell carcinoma and hepatocellular carcinomas^[78,79]. Sorafenib has been shown to inhibit key signalling pathways in SEG-1 lung adenocarcinoma cells^[80]. This method of inhibition of both receptor and signalling protein such as RAF may prove beneficial due the diversity of growth factor receptors displayed by tumors and this approach may have a future role in the treatment of oesophageal adenocarcinoma.

PI3 kinase by targeting mTOR

No inhibitors of the PI3 kinase have been evaluated in oesophageal adenocarcinoma. Cell line studies in oesophageal adenocarcinoma have identified that the PI3 kinase pathway is important for cell growth. Mutations of the PI3 kinase pathway occur infrequently in oesophageal adenocarcinoma. However, activation of the pathway is known to occur from RTK, a common occurrence in oesophageal adenocarcinomas. Indeed in breast cancer, the PI3 kinase pathway has been proposed as a mechanism of drug resistance to MEK inhibition^[55]. Inhibition of the PI3 kinase pathway has been used with success in metastatic renal cell carcinoma. Analogues of rapamycin have been developed to target mTOR (Figure 2). The agent temsirolimus has been evaluated in stage 3 clinical trials^[81] (Figure 2). In this trial, 626 patients were divided into 3 groups; temsirolimus alone, interferon alone, and interferon in combination with temsirolimus. Overall survival was 10.9, 7.3 and 8.4 mo respectively in favour of temsirolimus. In view of this, a strategy of mTOR inhibition may have a future role in oesophageal adenocarcinoma.

Targeting transcription factors

Targeting an activated transcription factor or central regulator such as NF- κ B would theoretically reduce the

chance of the development of drug resistance from the activity of multiple surface receptors and multiple signalling pathways. This is not without problems. Firstly transcription factors are difficult to target. Interference RNA technology involves the insertion of an oligonucleotide into the nucleus of a cancer cell, usually using a viral vector. Oligonucleotides can be manufactured to complement the sequence and therefore dimerize with any RNA of interest such as NF- κ B. This allows the targeting of transcription factor RNA with the prevention of protein translation. Interference RNA technology may be the answer to transcription factor inhibition but the technology remains in its infancy. The major hurdle appears to be the development of an efficient delivery system of oligonucleotides into cancer cells. Phase 1 trials are currently underway targeting VEGF in macular degeneration using direct ocular injection^[82,83]. If this technology is developed in oesophageal cancer then gene expression profiling of tumors would be required to ensure that specific targeted therapy is delivered. The identification of more central regulators of carcinogenesis, such as HIF-1 α and PEA3/ETV4 transcription factors, is likely to increase treatment options. The advent of gene expression profiling will certainly increase the number of potential targets.

CONCLUSION

An international effort is underway with the aim of improving survival in oesophageal adenocarcinoma by targeting key signalling pathways. Clinical trials using receptor tyrosine kinase inhibitors in oesophageal adenocarcinomas have so far only recruited patients with advanced or metastatic cancer. Studies utilised agents that inhibit solitary receptor tyrosine kinase, sometimes in an unselected manner. This strategy is problematic. At an advanced stage the heterogeneity within the tumor is extensive, which increases the likelihood of alternative signalling pathways resistant to receptor blockade. Secondly the pathway or receptor of interest may not be active or expressed, culminating in ineffective treatment. Tumor growth is immensely complex and this is emphasised in a study of 75 oesophageal adenocarcinoma specimens. Micro array studies identified 4 genes important in disease progression^[84]. The genes independently predicted prognosis independent from traditional radiological methods. Unfortunately a further 115 genes were also indicators of survival. It is not clear what role the genes play in carcinogenesis; however this study indicates the complexity and diversity of the factors implicated in oesophageal adenocarcinoma development. Taken together, this suggests that a tailored combinatorial approach for treatment that inhibits multiple genes may be useful; therapies targeting either receptors, hub signalling proteins or even transcription factors, is likely to be necessary to deliver effective responses. By tailoring therapy to tumors that express specific gene and protein signatures and prescribing a regimen of treatments that act in fundamentally different

mechanisms, then further improvements in survival are likely to be possible in oesophageal adenocarcinoma.

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Need for a comprehensive medical approach to the neuro-immuno-gastroenterology of irritable bowel syndrome

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Abstract

Irritable bowel syndrome (IBS) is defined by the Rome III criteria as symptoms of recurrent abdominal pain or discomfort with the onset of a marked change in bowel habits with no evidence of an inflammatory, anatomic, metabolic, or neoplastic process. As such, many clinicians regard IBS as a central nervous system problem of altered pain perception. Here, we review the recent literature and discuss the evidence that supports an organic based model, which views IBS as a complex, heterogeneous, inter-dependent, and multi-variable inflammatory process along the neuronal-gut axis. We delineate the organic pathophysiology of IBS, demonstrate the role of inflammation in IBS, review the possible differences between adult and pediatric IBS, discuss the merits of a comprehensive treatment model as taught by the Institute of Functional Medicine, and describe the potential for future research for this syndrome.

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INTRODUCTION

Functional abdominal pain (FAP) and irritable bowel syndrome (IBS) are debilitating and common conditions. IBS is defined by the Rome III criteria as, "symptoms of recurrent abdominal pain or discomfort and a marked change in bowel habit for at least six months, with symptoms experienced on at least three days of at least three months, with two of the three following findings: (1) Pain is relieved by a bowel movement; (2) Onset of pain is related to a change in frequency of stool; and (3) Onset of pain is related to a change in the appearance of stool"^[1].

FAP occurs in 10%-15% of school-aged children, of which 17%-24% have pain significant enough to disrupt their activity, and 13%-15% awaken from their sleep due to the pain^[2,3]. Up to 53% of children with abdominal pain continue to have abdominal pain as adults, and 18% are ultimately diagnosed with IBS^[4].

Chronic abdominal pain is associated with significant morbidity, including depression^[2], decreased quality of life measures^[5], and disability leading to inability to work^[6]. Adults with abdominal pain have higher rates of potentially unnecessary surgeries^[7-10]. Patients with IBS and FAP are costly to the medical system^[11,12]. Both children and adults with IBS frequently visit the offices of primary care physicians and gastroenterologists^[13]. Adults with IBS

have significantly more hospitalizations, outpatient visits, diagnostic testing, and overall medication use than well patients^[14]. A large percentage of the medical costs associated with IBS are related to hospitalizations and inpatient diagnostic testing, such as endoscopies^[15]. Antidepressants and other neuropsychopharmacological agents help the symptoms of IBS^[16], but these treatments have their own limitations and potential adverse effects.

IBS is thought to be just a functional problem that is “without demonstrable evidence of a pathological condition such as an anatomic, metabolic, infectious, inflammatory, or neoplastic disorder”^[17]. IBS is seen as a non-organic syndrome, primarily involving altered perception and processing of pain. As a result, the majority of current therapies for IBS revolve around stress reduction, alteration of pain pathways, and alleviation of symptoms^[16].

In this literature review, we delineate the gastrointestinal-neuro-immune pathophysiology of IBS and discuss the link between inflammation and pain. We believe that more effective treatment models are possible through a patient-centered approach that simultaneously treats the multiple variables that lead to IBS, as addressed in this review. The integration of this IBS treatment model may improve patient outcomes while reducing the medical cost burden of IBS. This paper will also discuss the possible differences between adult and pediatric IBS and present potential areas of future research.

STRESS AND THE GASTROINTESTINAL-NEURO-IMMUNE AXIS

Stress in various forms predisposes individuals to developing IBS^[18-20] and increases IBS symptoms in children^[21]. Abuse or other significant stressors change the neurobiology of stress and alters the levels of corticotropin-releasing factor (CRF) or hormone (CRH)^[22], a hypothalamic stress hormone. CRF activates the pituitary-adrenal axis and mediates behavioral, autonomic, immune, and visceral responses to stress^[23]. Patients with IBS have enhanced stress responses and release higher amounts of CRF in response to stress^[24].

Stress changes the physiology of the gastrointestinal tract. Maternal separation of rat pups causes CRF-mediated mucosal barrier dysfunction with macromolecular permeability and increased bacterial adherence/penetration of the gastrointestinal mucosa with translocation to the spleen^[25]. These animals also have mitochondrial swelling of the gut epithelial cells, immune cell infiltration, mucus depletion, and mast cell degranulation^[23,26-29]. Stressed human beings show similar findings^[30].

Stress compromises the integrity of the gut and induces inflammation through numerous pathways, as demonstrated by several published papers^[22,28,31]. CRF released from the hypothalamus can directly influence human colonic mast cells^[32,33], which then induce intestinal epithelial pathophysiology and mucosal barrier defects^[34-37]. Substance P (SP) and calcitonin gene-related peptide (CGRP)-containing gastrointestinal efferent neurons can also influence mast

cells^[38-41] and result in degranulation^[42] and release of TNF- α ^[43]. These compounds, in turn, result in gut inflammation and intestinal permeability^[44].

These stress-induced changes in the gastrointestinal tract “persist after the stressor is removed from the animal”^[37]. This is likely to be due to the ability of mast cells to influence their environment. In rats, inflammation results in increased mast cell-neuronal contacts and mucosal nerve cell density that last well beyond the initial insult^[43,45]. Gastrointestinal inflammation in humans also results in neuron proliferation^[46-48]. Stress and inflammation modulate nerve growth factor (NGF), which then affects mucosal nerve remodeling^[49,50], sprouting, and synaptogenesis^[51]. Mast cells, in close contact with neurons, synthesize and release NGF, and thus, can alter neuronal density and synaptogenesis^[49,52].

Furthermore, inflammation preceding a psychological stress can alter the epithelial response to stress signals and make the gut more susceptible to stress^[53]. In addition, inflammation can change the morphology of mast cells and their intracellular contents, further changing the susceptibility of the gut to various future stressors^[54-57].

Inflammation can play an important part in the manifestation of IBS symptoms^[58]. Once the inflammatory cascade is activated, this immune response can create a vicious cycle of self-perpetuating inflammation. Activated mast cells can directly release CRF^[59]. Patients with inflammatory bowel disease (IBD) and IBS have CRF-immunoreactive macrophages, enterochromaffin cells, lymphocytes, neutrophils, and eosinophils, which are present in higher concentrations than in healthy controls^[60-63]. CRF induces lymphocyte proliferation^[64] and macrophage release of pro-inflammatory cytokines (TNF- α , IL-1, and IL-6)^[65]. These activated immune cells, in turn, locally release CRF and other immune peptides^[61,66], which then activate mast cells^[22]. Mast cell-derived tryptase is another compound that recruits lymphocytes, eosinophils, and macrophages^[67], and can further perpetuate inflammation.

INFLAMMATION INDUCED NEUROLOGICAL TONE

Patients with IBS have central processing abnormalities associated with the perception of pain^[68-71]. Colonic irritation can lead to visceral hypersensitivity^[72]. Patients with IBS have inflammatory changes in their gut mucosa, which can only be identified by quantitative histopathology, immunohistochemistry, and electron microscopy^[73]. These patients have increased numbers of mast cells in the mucosa of the colon^[30,74,75]. Mast cell concentrations and their distance from mucosal nerve cells are positively associated with various IBS symptoms^[75]. The tryptase released from these mast cells can directly activate gastrointestinal neurons in animals and humans, and can cause visceral hypersensitivity^[76-78]. Tryptase cleaves and activates transmembrane proteins called proteinase-activated receptor-2 (PAR2), which are found on the primary afferent neurons of the gastrointestinal tract^[79]. Activation of PAR2 receptors leads to neuronal activation, which then creates the experience of

chronic pain.

In addition to central nervous system activation, patients with IBS also have sensitization and upregulation of the dorsal horn^[70,71,80], which explains the cutaneous hyperalgesia found in the lower extremities, rather than upper extremities, due to viscerosomatic convergence of nociceptive afferent neurons from the colon/rectum and lower extremities^[81]. Seybold *et al.*^[82] review the mechanisms by which gastrointestinal inflammation leads to gastrointestinal primary afferent neuronal activation and spinal cord activation/sensitization and inflammation.

If true, the perpetual mild mast-cell mediated inflammation can trigger the “excessive or prolonged stimulation of extrinsic afferents (that) may also result in the development of neuronal sensitization, at peripheral, spinal, or higher CNS levels, such that perception of sensations from the bowel is heightened, resulting in symptoms of urgency, bloating, and pain”^[83]. This sub-clinical inflammation may also influence gastrointestinal serotonin pathways.

IBS, NEUROLOGICAL TONE, AND SEROTONIN

Serotonin (5-HT) can influence the motor function and sensitivity of the gastrointestinal tract^[84-89]. Serotonin exerts a range of effects *via* its seven receptor subtypes (5-HT₁ to 5-HT₇). Serotonin receptor 5HT₅, 5HT₆, 5HT₇ are found in the brain, whereas 5HT₁, 5HT₂, 5HT₃, 5HT₄, and 5HT₇ are the gastrointestinal serotonin receptors^[90]. A large majority of the body's serotonin is stored in gastrointestinal enterochromaffin cells (EC)^[85]. Patients with diarrhea predominant IBS have increased EC cells^[91-93], which are activated by inflammation to release serotonin and may result in the elevated serotonin levels found in patients with IBS^[94,95]. Tegaserod, a partial 5HT₄ agonist has been used for constipation dominant IBS and Alosetron, a 5HT₃ antagonist, in diarrhea dominant IBS.

Serotonin reuptake transporters (SERT) in the gut epithelial cells terminate the effects of serotonin^[96,97] and influence serotonin concentrations and symptoms of IBS^[85]. Patients with IBS have genetic polymorphisms that lead to lower expression of transport proteins and less serotonin reuptake^[83,98,99]. The noted inflammation may also alter SERT expression and decrease its function in patients with IBS^[100]. Further studies on the modulation of the gastrointestinal tract serotonin pathways may help further define and treat IBS.

INTESTINAL PERMEABILITY, CHRONIC INFLAMMATION, AND ANTIGENS

The presence and activity of mast cells, along with other inflammatory cells, alone are not likely result in chronic inflammation. Other intestinal antigens, such as food, bacteria, and fungi, are likely to be needed to perpetuate the inflammation in the presence of an impaired gastrointestinal epithelial barrier.

Healthy individuals have tight junctions that help to form the gastrointestinal epithelial barrier along with mucous, SigA, and other peptides. This epithelial barrier controls the interaction between luminal bacteria and antigens and the mucosal immune system^[22,101]. It also allows immune tolerance of food antigens and bacteria. Activation of PAR2 not only leads to neuronal activation, but also to epithelial barrier defects in patients with IBS^[102,103].

Low level PAR2 activation of the myosin light chain kinase (MLCK), causes phosphorylation of the myosin light chain, which then leads to contraction of the actin-myosin ring. Tight junction protein zona occludens-1 (ZO-1) relocalizes into the cytoplasm and disrupts the tight junctions, which increases paracellular permeability. High level PAR2 activation in the rat colon results in localized inflammation and increased production of TNF- α and IFN- γ . INF- γ decreases ZO-1 expression and alters the actin cytoskeleton organization^[104]. TNF- α activates MLCK and results in tight junction protein relocation^[105,106]. A more detailed discussion of these pathways can be found in articles by Gareau *et al.*^[23] and Cenac *et al.*^[103].

Children and adults with IBS have increased intestinal permeability^[107,108]. Increased intestinal permeability results in “mucosal barrier defects (that) allow the passage of an increased load of luminal antigens of dietary and bacterial origin which, in turn, elicit the activation of mucosal immune responses”^[109].

Various triggers can activate mast cells. Bacteria are powerful antigens for the gastrointestinal immune system^[110-115]. Stress can result in increased bacterial adherence and penetration into the gastrointestinal mucosa^[23,25-27], which may increase the interaction between the luminal bacteria and local immune response. This may explain why patients with IBS have higher antibody titers to specific bacterial flagella than healthy controls^[116]. The DNA of these bacteria can interact with toll-like receptors^[117], which then influence the immune system through regulation of tumor necrosis factor alpha and interferon gamma^[118].

Escherichia coli, *Campylobacter*, and other bacteria can negatively influence the GI immune system and result in gastrointestinal inflammation and intestinal permeability^[46,91,119-121]. Conversely, commercially available beneficial bacteria, in the form of probiotics, can reduce gastrointestinal inflammation^[122-125], reverse or prevent intestinal permeability^[120], and stop bacterial adhesion^[126] and translocation^[27,127]. Probiotics can also reverse visceral hypersensitivity from various causes^[128,129], including stress^[130]. Probiotics attenuate the upregulation of pain pathways at the spinal and supraspinal levels^[131], and induce epithelial cells to express micro-opiate receptor 1 (MOR1) and cannabinoid 2 (CB2) opioid receptors^[132]. Probiotics can reduce the symptoms of IBS^[133,134].

Adults with IBS have gastrointestinal microflora that are significantly different than those of healthy populations^[135]. Children with IBS are also likely to have significant alterations in their gastrointestinal microflora. We speculate that there may be a subset of children who are predisposed to developing IBS through repeated or

prolonged exposure to antibiotics for various reasons (recurrent otitis media, sepsis, meningitis, osteomyelitis, vesicoureteral reflux, acne, *etc*). Various antibiotics, including Augmentin, the macrolides, and amoxicillin significantly alter the composition of the bacteria in the GI tract^[136-138]. Antibiotic use has been related to increased rates of IBS and functional abdominal pain^[139,140].

Gastrointestinal bacteria are also influenced by the diet. Dietary soluble fiber encourages the growth of beneficial species like lactobacilli and bifidobacteria^[141-143]. In mice, a white bread diet significantly prolonged antibiotic induced bacterial perturbations^[136]. It is common knowledge that the standard American diet lacks fiber, and thus may predispose human beings to have prolonged antibiotic induced bacterial perturbations.

Prebiotics are short chain carbohydrates that help some of the beneficial bacteria or probiotics in the intestines to grow more effectively^[142,143]. Prebiotics may decrease IBS symptoms^[144-146]. Prebiotics are fermented by probiotics and metabolized into short chain fatty acids (SCFA). SCFAs can decrease inflammation and are used in maintaining the intestinal epithelial lining^[147]. While breast milk naturally contains prebiotics^[148], up until a few years ago, most infant formulas did not contain prebiotics. Thus, there may be a population of children who were formula fed and required several courses of antibiotics that now have perturbed gastrointestinal flora, as well as intestinal epithelial barriers. We believe that these children may be at risk of developing IBS.

Food proteins are other significant antigens for the gut immune system. Food antigens induce mast cell activation^[149] and degranulation, which can lead to visceral hypersensitivity. In children, certain foods may exacerbate intestinal permeability and the elimination of the foods help resolve the IBS symptoms^[150]. Elimination of certain foods may decrease immune activation by removing the allergic antigenic load to the local immune system. In patients with IBS, sodium cromoglycate can eliminate IBS symptoms^[151-153] by preventing the degranulation of mast cells and inhibiting the release of inflammatory mediators, following contact with an allergen^[154].

Over 60% of patients believe that certain foods worsen their IBS symptoms and that elimination of these foods can reduce their symptoms^[155-157]. Some believe that these food reactions are psychological in origin^[158-160]. Blinded food challenges have raised many questions about the validity of elimination diets for IBS treatment^[161-163]. There is also a growing body of evidence to support the use of elimination diets as part of a treatment protocol for IBS^[164-167]. Milk, wheat, and eggs are the most commonly identified food triggers^[163].

Another potential antigen for the gastrointestinal immune system is *Candida albicans*. Adult studies have shown that *Candida* does not play a significant role in patients with IBS^[168,169]. To our knowledge, the role of candida in pediatric IBS has not been determined. Some children who have received numerous courses of antibiotics, such as amoxicillin, can have disruption of the bacterial balance and have overgrowth of the commensal *Candida*^[137,170-173]. *Candida* induces inflammation. It produces alcohols and

glycoproteins that stimulate mast cells to produce histamine and prostaglandins^[174,175]. *Candida* also produces inflammatory prostaglandins that affect mammalian cells^[176], as well as proteases that degrade the gastrointestinal IgA and, thus, allow candida to overcome the local immune defense mechanisms^[177]. Candidal proteases can induce a B-cell response and result in increased inflammation^[174]. In animals and humans, *Candida* perpetuates intestinal inflammation^[169].

SMALL INTESTINAL BACTERIAL OVERGROWTH

Another possible contributing factor to IBS signs and symptoms is small intestinal bacterial overgrowth (SIBO), defined as bacterial counts greater than 10^5 cf/mL from small intestinal aspirates^[178]. Controversy exists over the ideal method of assessing SIBO^[178-181]. A significant number of patients with IBS complain of bloating and pain. SIBO may explain this bloating and pain, as well as other IBS-like-symptoms^[182-184]. Several studies have shown antibiotics to be helpful in reducing the symptoms of IBS^[185-188].

Patients with IBS who have delayed gastric emptying have a higher risk of developing SIBO^[189-192]. Stress is one cause of delayed gastric emptying^[193-196]. Once SIBO is present, it can trigger an inflammatory response. SIBO, through abnormal gastrointestinal flora fermentation, may be another cause of IBS symptoms and must be considered in the evaluation of the patient. Furthermore, proton pump inhibitors can also increase the risk of SIBO by decreasing gastric acidity and further perturbations of the gastrointestinal flora species^[170,197-200]. We speculate that SIBO may play a larger role in adults with IBS than in children. Further studies are required to elucidate the various differences between adult and pediatric IBS.

CONCLUSION

The evidence presented in our review suggests that IBS is an organic disease with a complex pathophysiology (Figure 1) that is difficult to identify by standard diagnostic tools. The pathophysiology of IBS varies from person to person and from children to adults. The underlying mast cell mediated inflammation of IBS, along with serotonin signaling, can drive the chronic nociceptive input from the periphery to dynamically maintain the altered central processing defects and perception of pain^[70,80,201].

In addition to the pathophysiology, clinicians must focus more attention on the well known and less well characterized risk factors that may predispose individuals to developing IBS (Table 1). It is our belief that clinicians should further use the field of neurogastroenterology to better understand the effects of stress on the gastrointestinal tract. Clinicians and researchers must work to develop and adopt models to help us better predict and prevent this condition in susceptible individuals. For chil-

Table 1 Risk factors for irritable bowel syndrome

Genetics/family history
Stress/high academic performance/parental psychiatric disorders
Recurrent or chronic antibiotic use
Bacterial or viral enteritis
Unrecognized food sensitivities
Low fiber diet/diet high in simple carbohydrates
Formula feeding
Chronic acid suppression

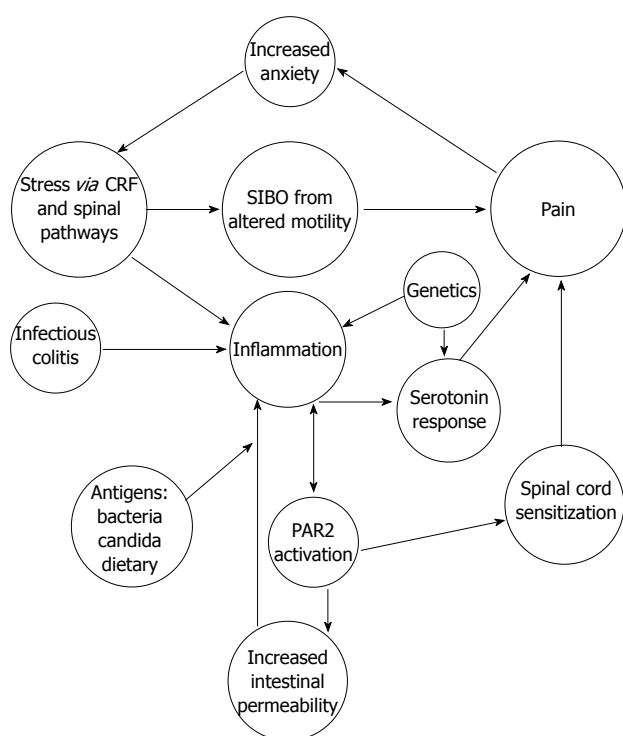


Figure 1 Proposed pathophysiology of irritable bowel syndrome. CRF: Corticotropin-releasing factor; SIBO: Small intestinal bacterial overgrowth; PAR2: Proteinase-activated receptor-2.

dren, these models will require additional studies to evaluate the impact of recurrent antibiotic use and resultant overgrowth of candida on the development of IBS.

Effective treatment models for IBS must reflect the complex physiology of IBS and simultaneously address multiple pathophysiological factors to break the vicious cycle of inflammation and ultimately allow for cessation of symptoms. The Institute of Functional Medicine (IFM)^[202] has created such a model of care for IBS. The IFM model has the potential to provide significant improvement in patient care, while reducing healthcare costs and deserves further consideration and evaluation. Please refer to the IFM website and various publications for a more detailed discussion on treatment options.

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Adiponectin, a key adipokine in obesity related liver diseases

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Abstract

Non-alcoholic fatty liver disease (NAFLD) comprising hepatic steatosis, non-alcoholic steatohepatitis (NASH), and progressive liver fibrosis is considered the most common liver disease in western countries. Fatty liver is more prevalent in overweight than normal-weight people and liver fat positively correlates with hepatic insulin resistance. Hepatic steatosis is regarded as a benign stage of NAFLD but may progress to NASH in a subgroup of patients. Besides liver biopsy no diagnostic tools to identify patients with NASH are available, and no effective treatment has been established. Visceral obesity is a main risk factor for NAFLD and inappropriate storage of triglycerides in adipocytes and higher concentrations of free fatty acids may add to increased hepatic lipid storage, insulin resistance, and progressive liver damage. Most of the adipose tissue-derived proteins are elevated in obesity and may contribute to systemic inflammation and liver damage. Adiponectin is highly abundant in human serum but its levels are reduced in obesity and are even lower in patients with hepatic steatosis or NASH. Adiponectin antagonizes excess lipid storage in the liver and protects from inflammation

and fibrosis. This review aims to give a short survey on NAFLD and the hepatoprotective effects of adiponectin.

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Key words: Hepatic steatosis; Non-alcoholic steatohepatitis; Adiponectin; Obesity; Adipose tissue

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INTRODUCTION

Obesity is associated with insulin resistance, a common risk factor for type 2 diabetes, cardiovascular disease, hepatic steatosis and non-alcoholic steatohepatitis (NASH)^[1,2]. Hypertrophied adipocytes in obesity fail to appropriately store excess triglycerides and excessive ectopic accumulation of lipids in skeletal muscle and liver disturbs insulin signalling^[3]. Body fat distribution appears to be even more important than the total amount of adipose tissue, and visceral fat mass is strongly linked to insulin resistance and non-alcoholic fatty liver disease (NAFLD)^[4]. Visceral fat released free fatty acids are transported to the liver by the portal vein and may contribute to hepatic steatosis, production of triglyceride rich very low density lipoproteins (VLDL) and elevated β -oxidation^[5,6] (Figure 1). Metabolically healthy but obese (MHO) individuals are insulin sensitive and hepatic fat accumulation is significantly lower compared to similarly overweight subjects that develop

insulin resistance^[7,8]. Despite comparable fatness between MHO and control cohorts that develop insulin resistance, MHO subjects have 49% less visceral fat which further emphasizes the unfavourable characteristics of this fat depot^[9]. Lean body mass may be associated with a higher insulin sensitivity and is significantly lower in MHO subjects^[9]. A recent study even describes an independent association of lean body mass with impaired glucose disposal and systemic C-reactive protein (CRP) levels in centrally obese postmenopausal women that may exacerbate the harmful effects of visceral fat mass^[10]. These studies further point to the highly complex interplay of various factors associated with metabolic diseases like the metabolic syndrome.

Various epidemiological studies have identified central obesity as an independent risk factor for metabolic diseases and highlight the crucial role of impaired production or activity of adipose tissue released proteins^[6,11]. Most of the adipokines identified so far are elevated in obesity and raised chemokine C-C motif ligand 2 (CCL2) contributes to the increasing number of adipose tissue resident macrophages^[11,12]. They produce inflammatory proteins like interleukin-6 (IL-6) and tumour necrosis factor (TNF) whose circulating levels are increased in obesity, a state of low-grade, chronic inflammation^[13]. TNF impairs insulin signalling and plays a crucial role in non-alcoholic steatohepatitis (NASH) progression^[14,15]. Visceral fat released proteins are directly transported to the liver by the portal vein and the anatomical feature of this fat depot may explain the harmful metabolic effects of visceral adiposity^[6]. IL-6 is preferentially released from visceral fat and upregulates suppressor of cytokine signalling 3 (SOCS3) in the liver that causes hepatic insulin resistance^[16-18]. Furthermore, IL-6 is a well known inducer of CRP, a marker protein for systemic inflammation^[19] (Figure 1). Leptin is mainly produced by adipocytes, and obesity is characterized by elevated systemic levels and central and peripheral leptin resistance^[6]. Leptin prevents lipid accumulation in non-adipose tissues like the liver. Leptin lowers stearoyl-CoA desaturase that catalyzes the rate-limiting reaction of monounsaturated fatty acid synthesis and thereby may ameliorate hepatic insulin sensitivity^[20]. Animal studies have proven that leptin directly promotes fibrogenesis. Leptin induces transforming growth factor β (TGF- β) and connective tissue growth factor (CTGF) production in hepatic stellate cells through indirect effects on Kupffer cells^[21]. In humans, a direct association of circulating leptin and liver fibrosis has not been confirmed yet and locally produced leptin and/or leptin resistance may have to be taken into account^[22].

The adipokine adiponectin is highly abundant in human serum and is secreted by adipose tissue in inverse proportion to the body mass index^[23]. Adiponectin circulates as trimer, hexamer and higher order multimer in serum and isoform-specific effects have been described^[24-26]. Adiponectin may also form hetero-oligomers with additional members of the C1q/TNF-related protein (CTRP) family like the recently described CTRP9^[27]. Early studies indicate

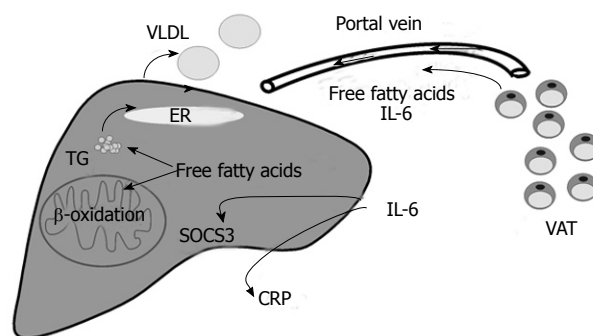


Figure 1 Crosstalk of visceral adipose tissue and the liver. Free fatty acids and Interleukin (IL)-6 released by visceral adipose tissue (VAT) are transported to the liver by the portal vein. Free fatty acids promote steatosis, enhance β -oxidation and the release of very low density lipoproteins (VLDL) contributing to dyslipidemia. IL-6 induces hepatic C-reactive protein (CRP) synthesis and suppressor of cytokine signalling 3 (SOCS3), and thereby is linked to systemic inflammation and hepatic insulin resistance, respectively (adapted from Schaffler A, Scholmerich J, Buchler C. Mechanisms of disease: adipocytokines and visceral adipose tissue—emerging role in nonalcoholic fatty liver disease. *Nat Clin Pract Gastroenterol Hepatol* 2005; 2: 273-280^[6]). ER: Endoplasmic reticulum; TG: Triglycerides.

that globular adiponectin, the globular C1q domain of this protein generated by proteolysis of the full-length protein, may also exist in serum^[28]. However, circulating levels seem to be rather low, questioning the biological significance of this protein^[29] that may nevertheless be of therapeutic relevance. Epidemiological studies revealed that low adiponectin levels are associated with NASH independent of insulin resistance and body mass index, and hepatoprotective effects of adiponectin have been identified in animal studies or with isolated liver cells^[30-32]. MHO individuals are insulin sensitive and have adiponectin levels similar to normal-weight controls despite excessive weight and body fat, and this association may further underline the protective effects of this adipokine^[33].

NAFLD not only compromises the hepatic manifestation of the metabolic syndrome but is linked to a higher risk of develop metabolic disorders like type 2 diabetes or cardiovascular disease^[34,35]. Fatty liver is even associated with dyslipidemia, metabolic syndrome and low adiponectin independent of body mass index (BMI), waist to hip ratio and visceral fat mass^[36]. NAFLD has been predicted to increase along with the growing epidemic of obesity^[37] and understanding of its pathophysiology is a prerequisite to develop non-invasive diagnostic tools and to establishing effective treatment regimes. Rising adiponectin levels may be beneficial in liver disease and its protective effects in hepatic steatosis and NASH^[38] are summarized in the current review article.

EPIDEMIOLOGY OF NAFLD

Diagnosis of NAFLD requires a careful anamnesis to exclude other liver diseases or drug-mediated liver damage. Moderate alcohol intake, defined by most physicians as 20 to 40 g/d in men and 20 g/d in women, has to be en-

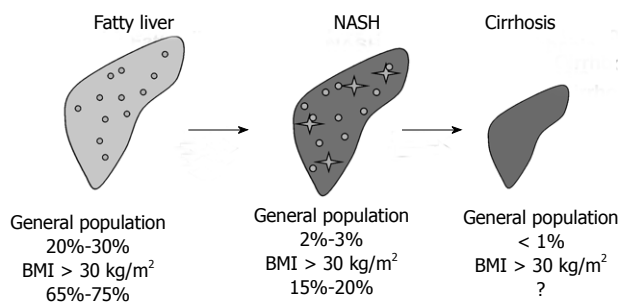


Figure 2 Epidemiology of non-alcoholic fatty liver disease. Current estimates of the prevalence of fatty liver, non-alcoholic steatohepatitis (NASH) and obesity-related liver cirrhosis in the general population and in obesity defined as body mass index (BMI) above 30 kg/m².

quired about^[39]. Liver biopsy is essential for diagnosis and staging but the use of this invasive method is limited to a subgroup of patients^[39].

When NAFLD is defined as elevation of aspartate aminotransferase (AST) or alanine aminotransferase (ALT) and transferrin saturation of less than 50% the frequency is 5.4% in the general population of the United States^[40]. When elevated gamma-glutamyltranspeptidase (GGT) is included and lower cut-off values are used the prevalence is 24%^[41]. Studies performed in gastroenterology units restricted cohorts identified 11% of the patients as having NAFLD^[42]. In bariatric surgery patients hepatic steatosis ranges from 65% to 90%^[43,44]; NASH has been diagnosed in 15 to 55% and fibrosis in 34% to 47%^[41,45].

Current estimates based on different studies in unselected and selected populations indicate that about 20% to 30% of adults in Western countries have excess fat accumulation in the liver, 2% to 3% of adults are thought to meet current diagnostic criteria for NASH and eventually up to one third of those with NASH suffer from progressive fibrosis or even cirrhosis^[41,45,46]. In obesity defined as BMI above 30 kg/m² and in morbidly obese patients these values are much higher and patients with NASH are over-represented in these populations^[41,45] (Figure 2).

GENETICS OF NAFLD

Visceral adiposity and insulin resistance are clearly related to NAFLD^[47] and genetic variations associated with obesity and disproportionate body fat distribution may predispose to development of steatotic liver. Chemerin is a recently identified adipokine and a common genetic variation is associated with increased visceral fat mass in non-obese subjects but epidemiological studies to link chemerin alleles with NAFLD are still lacking^[48]. The adiponectin 45T → G variant contributes to overall fatness and abdominal obesity but is not an important determinant of NAFLD at least in Chinese people^[49,50].

Gene variations may influence NAFLD stage, progression and even occurrence. NAFLD is much more likely in Hispanic Americans than among whites^[51] and African Americans have a lower degree of hepatic steatosis relative to whites^[52]. Familial clustering of NAFLD has been dem-

onstrated, and fatty liver is more common in siblings and parents of children with NAFLD indicating that NAFLD, similar to type 2 diabetes, is a multifactorial disease^[53]. Environmental and genetic factors define the individual risk of developing NAFLD and may also explain why only a subgroup of patients develop more progressive liver damage.

Studies in small cohorts have identified genetic associations of microsomal triglyceride transfer protein, an enzyme regulating hepatic VLDL release, the antioxidant mitochondrial enzyme superoxide dismutase 2, the inflammatory cytokine TNF and the main profibrotic cytokine TGF-β with NAFLD^[54,55]. Genome-wide association studies find that variations of patatin-like phospholipase domain containing 3 (PNPLA3, adiponectin), a protein with close homology to adipose triglyceride lipase but so far unknown function, contributes to ethnic and inter-individual differences in hepatic steatosis and susceptibility to NAFLD^[56,57].

This association has not been confirmed in a recent study in non-Hispanic, Caucasian, women with liver biopsy proven NAFLD, where an association between NASH activity score and single nucleotide polymorphisms (SNPs) within the squalene synthase (FDFIT1) gene, a key regulator of cholesterol biosynthesis, is described. Polymorphisms of the pregnancy zone protein, a proteinase involved in clearance of TGF-β, are linked to systemic AST levels, and variants of platelet-derived growth factor α are linked to liver fibrosis^[58].

Genetic variations of adiponectin are found to be associated with NAFLD^[50,59], and single nucleotide polymorphisms in adiponectin receptor 1 (AdipoR1) and AdipoR2 contribute to variations in hepatic fat accumulation in humans^[60,61].

SYSTEMIC ADIPONECTIN IN NAFLD

Systemic adiponectin concentrations are in the μg/mL-range indicating that adiponectin constitutes a substantial fraction of plasma proteins, and these high levels are remarkably constant. Despite its abundant presence in plasma, adiponectin is cleared rapidly by the liver with a half-life of about 75 min^[62].

Visceral adiposity is associated with elevated circulating free fatty acids and higher concentrations of most adipose tissue released proteins^[63]. Adiponectin differs from the adipokines described so far because its systemic levels are decreased in obesity^[23]. In high fat diet induced obese rodents and in ob/ob mice adiponectin levels are reduced in plasma and clearance is significantly prolonged, indicating markedly impaired adiponectin synthesis in obesity^[62,64,65]. Visceral fat accumulation is associated with hypoadiponectinemia and negative associations of visceral fat with systemic adiponectin have been identified^[66,67].

Besides adiponectin, circulating levels of omentin predominantly released from the stromovascular cells of visceral fat are found reduced in obesity and serum omentin levels are increased in patients with NAFLD and independently predict hepatocyte ballooning^[68].

In healthy Caucasians, BMI and adiponectin, but not insulin resistance, predict serum concentrations of both ALT and GGT^[69]. Low adiponectin levels are even found associated with NASH independent of insulin resistance and BMI^[30]. Multivariate regression analysis identifies decreased adiponectin as an independent predictor of liver steatosis and elevated ALT and GGT levels in healthy obese individuals^[32]. In NAFLD patients low adiponectin levels are closely associated with the degree of hepatic steatosis, necroinflammation and fibrosis^[30,32]. Shimada *et al*^[70] reported that 90% of patients with early-stage NASH can be predicted by a combined evaluation of the serum adiponectin level, homeostasis assessment model-insulin resistance (HOMA-IR) score, and serum type IV collagen 7S level.

Circulating adiponectin levels in the µg/mL range by far exceed concentrations commonly required for receptor-dependent signalling. This may indicate receptor independent functions of adiponectin and binding to growth factors like platelet derived growth factor (PDGF), extracellular matrix proteins, low density lipoprotein (LDL) and opsonization of apoptotic cells to stimulate phagocytosis have been described^[71-74].

Systemic adiponectin is about 20% to 60% lower in NAFLD than healthy controls^[75-77] but considering the high levels in the circulation and a half-maximal effective dose of 0.85 µg/mL full-length adiponectin for AdipoR2 stimulated fatty acid oxidation^[78] the question arises whether impaired receptor-mediated signalling due to reduced concentrations is a reasonable explanation for metabolic complications associated with hypoadiponectinemia. Therefore, it is likely that adiponectin receptor signal transduction pathways are also impaired in NAFLD.

ADIPONECTIN RECEPTORS IN NAFLD

Two 7-transmembrane proteins, AdipoR1 and AdipoR2, have been identified to function as adiponectin receptors^[78]. Although initial studies using rodent tissues reveal preferential expression of AdipoR2 in the liver, in human tissues AdipoR1 and AdipoR2 mRNAs are most abundant in skeletal muscle and both are moderately expressed in the liver^[78]. AdipoR1 protein is easily detected in human hepatocytes indicating that both receptors may play a role in liver physiology^[79].

Although there is a well documented relationship between low adiponectin and liver disease, an association of NAFLD and reduced expression of hepatic adiponectin receptors is not consistently reported. Furthermore, mainly mRNA expression has been analysed and this may not necessarily predict protein abundance^[80,81].

In animal models of obesity, hepatic adiponectin receptor mRNAs are found unchanged or even increased^[65,82,83]. In human biopsies, hepatic adiponectin receptor mRNAs are increased in biopsy-proven NASH compared to steatotic livers^[84]. Other studies, however, describe similar levels of adiponectin receptor mRNA in normal liver, steatotic liver and NASH^[85,86]. There are also reports on reduced AdipoR2 mRNA in NASH compared

to simple steatosis or lower AdipoR2 mRNA in fatty liver with no further reduction in NASH^[87,88].

Data on AdipoR2 proteins are sparse and one study demonstrates reduced AdipoR2 protein in human NASH compared to steatotic liver^[88]. Treatment of hepatocytes with palmitate is used as an in vitro model for hepatocyte steatosis and 200 µmol/L of this fatty acid reduce AdipoR2 protein in Huh7 cells^[89]. Activating transcription factor 3 (ATF3) is induced upon endoplasmic reticulum stress and in the liver of ob/ob mice, and suppresses AdipoR2 in HepG2 cells^[90]. Therefore, besides low circulating adiponectin, AdipoR2 may be reduced in hepatic steatosis and NASH indicating a possible adiponectin resistant state.

ANTISTEATOTIC EFFECTS OF ADIPONECTIN

Dyslipidemia is characterized by high circulating triglycerides^[91] and low high density lipoprotein (HDL) cholesterol levels, and is frequently accompanied by hepatic steatosis^[92]. Adiponectin negatively correlates with serum triglycerides and apolipoprotein B (ApoB), the main apolipoprotein of the triglyceride rich VLDL^[93,94]. Hepatocyte ApoB and triglycerides are reduced by adiponectin indicating lower hepatic VLDL release^[28,95,96]. Furthermore, VLDL catabolism is enhanced by an increased skeletal muscle lipoprotein lipase and VLDL receptor expression^[97]. This more favourable lipid profile may be linked to lower hepatic lipid storage.

A choline and L-amino acid deficient diet induces more severe hepatic steatosis in adiponectin deficient mice compared to wild type animals^[14]. Adenoviral expression of adiponectin ameliorates lipid deposition in the liver^[95]. SREBP-1c is a central regulator of fatty acid synthesis, and is suppressed by adiponectin in hepatocytes and in the liver of db/db mice^[95]. AMP-activated protein kinase (AMPK) is physiologically activated by low energy status, and switches on ATP-producing catabolic pathways (such as fatty acid oxidation and glycolysis), and switches off ATP-consuming anabolic pathways (such as lipogenesis)^[98]. Adiponectin activates AMPK by binding to AdipoR1^[78]. Suppression of SREBP-1c by adiponectin is mediated through AdipoR1/LKB1, an upstream kinase of AMPK, and AMPK pathway^[95]. AMPK in addition phosphorylates acetyl-CoA carboxylase (ACC) and this is subsequently associated with a higher activity of carnitine palmitoyl-transferase 1 (CPT-1), a rate limiting enzyme in fatty acid oxidation^[98].

Signalling *via* AdipoR2 enhances peroxisome-proliferator activated receptor α (PPAR α) activity^[78,99]. PPAR α up-regulates CPT-1, stimulates β -oxidation, reduces lipid synthesis and thereby prevents excess triglyceride storage^[100].

ANTIINFLAMMATORY AND ANTIAPOTOTIC EFFECTS OF ADIPONECTIN

Lipopolysaccharide (LPS) is involved in the pathogenesis

of NAFLD and elevated levels of circulating LPS are found in obesity^[101,102]. Increased gut permeability and a higher prevalence of small intestinal bacterial overgrowth correlates with the severity of steatosis but not with NASH^[103]. Besides age, inflammation was identified as an independent predictor of progression to advanced fibrosis in NASH patients^[104]. Hepatic steatosis may be accompanied by inflammatory cell infiltrates composed of neutrophils and mononuclear cells. In several mouse models of immune mediated hepatitis, adiponectin reduces TNF and induces interleukin-10 (IL-10) release from Kupffer cells^[105]. Adiponectin lowers CRP synthesis in cytokine stimulated rat hepatocytes, and an inverse correlation of systemic adiponectin and CRP has been identified in obese patients^[106,107]. Adiponectin may exert its anti-inflammatory activity by lowering nuclear factor kappa B (NFκB) action in preactivated cells or by inducing tolerance to inflammatory stimuli by a rapid and transient activation of NFκB that subsequently renders the cells inert to further activation^[108-111].

Nevertheless, in patients suffering from chronic inflammatory diseases like inflammatory bowel disease or type 1 diabetes that are not associated with adiposity elevated circulating adiponectin levels that even correlate with inflammatory markers are found^[112-114], and an induction of inflammatory proteins and activation of NFκB by recombinant adiponectin is described in several studies^[25,108,113,115]. Therefore, adiponectin seems to be regulated in the opposite direction in classic versus obesity-associated chronic inflammatory diseases and may even exert opposite activities in resting compared to activated cells^[116].

NFκB promotes cell survival and NEMO-mediated NFκB activation in hepatocytes has an essential physiological function to prevent the spontaneous development of steatohepatitis and hepatocellular carcinoma^[117]. Adiponectin activates NFκB in human hepatocytes, and thereby may prevent hepatocyte apoptosis. Adiponectin further upregulates the chemokine interleukin 8 (CXCL8) *via* AdipoR1 and NFκB dependent pathways in primary human hepatocytes^[118]. CXCL8 is an antiapoptotic protein^[119] and overexpression of the rodent CXCL8 homologous protein protects the liver from galactosamine and endotoxin induced damage^[120].

Adiponectin further antagonizes hepatocyte death by blocking fatty acid-induced activation of c-Jun NH2 terminal kinase^[121], by reducing TNF levels^[105] and by inhibiting fatty acid mediated upregulation of CD95^[122].

ANTIOXIDATIVE EFFECTS OF ADIPONECTIN

Fatty liver is thought to represent the first incident towards the subsequent development of liver fibrosis^[6]. Accelerated β-oxidation of fatty acids in hepatic steatosis is associated with excess reactive oxygen species (ROS), lipid peroxidation, the release of inflammatory cytokines, death of hepatocytes and activation of hepatic stellate cells^[1]. ROS and

lipid peroxidation are thought to contribute to the progression of liver injury partly by accelerating inflammation that in turn causes ROS production^[1]. Oxidative stress is enhanced in human hypoadiponectinemia and in adiponectin knock-out mice fed a choline-deficient L-amino acid deficient diet^[123,124]. Hepatic cytochrome P450 2E1 (CYP2E1) is elevated in these animals and in human NASH and may contribute to higher ROS levels^[125,126].

Aldehyde oxidase 1 (AOX1) is a xenobiotic metabolizing protein whose physiological role has not been evaluated in detail so far^[127]. AOX1 activity has been identified as an important source of ROS^[128] and is reduced in hepatocytes by adiponectin *via* activation of PPARα^[31]. Adiponectin also increases ROS detoxifying enzymes and AdipoR2 is involved in the induction of superoxide dismutase 1 and catalase^[129].

ANTIFIBROTIC EFFECTS OF ADIPONECTIN

Liver injury causes activation of otherwise “quiescent” hepatic stellate cells (HSC) and activated cells proliferate, synthesize CTGF and extracellular matrix proteins^[130]. TGF-β is the main profibrotic factor in fibrosis and induces CTGF synthesis. CTGF stimulates binding of TGF-β to its receptor and thereby enhances TGF-β activity^[130]. CTGF is induced by TGF-β indicating an autocrine or paracrine loop that mutually enhances synthesis of both proteins^[130]. Knock-down of AdipoR2 in mice fed a methionine-choline deficient diet to cause progressive fibrosing steatohepatitis is associated with higher levels of steatosis, inflammation and fibrosis^[131]. Overexpression of AdipoR2 is protective, and this mechanistically includes inhibition of TGF-β signaling and stimulation of PPARα activity^[131].

Expression of recombinant adiponectin in activated HSC reduces proliferation and lowers α-smooth muscle actin that is induced in activated HSC^[132]. Furthermore, apoptotic cell death of activated HSC is augmented^[132]. Exogenously added recombinant adiponectin suppresses PDGF-stimulated HSC proliferation by activation of AMPK^[133]. Adiponectin may also bind to growth factors like PDGF and thereby inhibits binding to their corresponding receptors^[71]. Leptin is a well described profibrotic adipokine and several studies have shown that adiponectin antagonizes leptin bioactivity^[134,135]. Adiponectin blocks leptin-induced STAT3 phosphorylation in activated HSC and leptin-mediated upregulation of TIMP-1 release and these in-vitro findings have been confirmed *in-vivo*^[134].

DIET, EXERCISE AND PHARMACOLOGICAL INTERVENTIONS

Studies analysing the impact of changes in life style and medications in NAFLD have been performed in small patient groups sometimes even lacking suitable controls. Currently weight loss and exercise are recommended as initial strategies to improve NASH^[136]. Diet and diet in conjunction with exercise for 6 mo cause a similar reduction in body weight and intrahepatic fat^[137]. In 19 sedentary obese

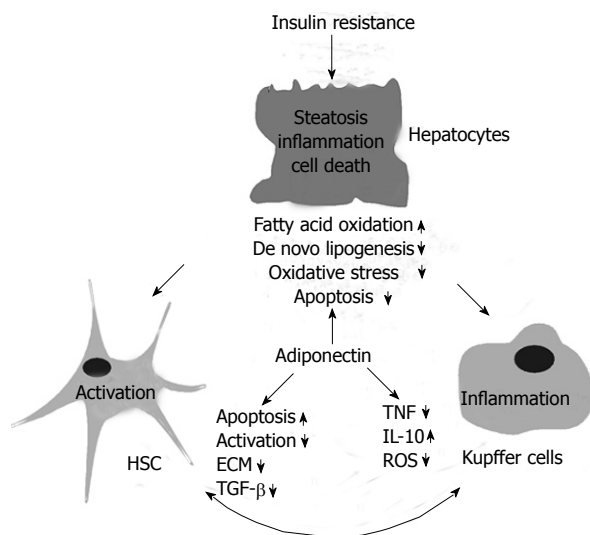


Figure 3 Hepatoprotective effects of adiponectin. Hepatic insulin resistance correlates with liver fat content, and is currently thought to represent the first incident in metabolic liver diseases. Insulin resistance and steatosis may also promote inflammation and fibrosis although the factors leading to advanced liver damage have not been identified so far. Major pathophysiological alterations of hepatocytes, hepatic stellate cells (HSC) and Kupffer cells in hepatic steatosis and/or non-alcoholic steatohepatitis are indicated. The protective activities of adiponectin are listed and arrows indicate an induction or repression of these pathways/proteins by adiponectin. IL: Interleukin; TGF: Transforming growth factor; TNF: Tumor necrosis factor; ECM: extracellular matrix; ROS: Reactive oxygen species.

men and women four weeks of aerobic exercise improved hepatic steatosis even in the absence of weight loss^[138]. In a randomized controlled trial enrolling 31 patients with biopsy-proven NASH intensive changes in life style with the objective of at least 7% weight loss and educational training without weight reduction have been compared^[139]. Weight loss significantly correlates with improvement in NASH histological activity score and weight loss of 7% or even more is recommended as a treatment strategy for these patients^[139]. Another study also reports improvements of histological and laboratory parameters when body weight is reduced by 10% in NASH patients^[140]. Adiponectin concentrations increase by about 36% in type 2 diabetic patients by 13% weight loss^[141], and this may partly contribute to the metabolic improvements observed in these patients.

Clinical trials using fibrates have revealed inconsistent results so far. Treatment of sixteen NASH patients with clofibrate did not ameliorate biochemical or histological parameters^[142], whereas a second study demonstrated biochemical and ultrasound improvements with fenofibrate^[143]. Emerging data on thiazolidinediones have demonstrated improvement in both liver enzymes and histology^[144,145]. These drugs activate PPAR γ and thereby inhibit growth of HSC and TGF- β mediated induction of CTGF, respectively^[146]. PPAR γ is the main adipogenic transcription factor and its agonists stimulate adipogenesis^[147]. Thiazolidinediones strongly stimulate adiponectin synthesis and elevate systemic adiponectin^[147]. Increase of adiponectin by pioglitazone is related to histological improvement of steatosis, inflammation and fibrosis confirming the crucial

role of adiponectin in NAFLD^[148]. The PPAR γ agonist rosiglitazone even induces AdipoR2 in hepatocytes^[146]. A recent study reports that pioglitazone therapy improves adipose tissue insulin sensitivity and this correlates with a reduction in hepatic fat and necroinflammation^[149]. Activation of PPAR γ primes human monocytes into alternative M2 macrophages with anti-inflammatory properties and patients may also benefit from reduced inflammation^[150]. In line with this hypothesis pentoxifylline with multiple pharmacological effects including antioxidant and anti-inflammatory activity^[151] has been tested in small clinical trials, and biochemical and histological improvements have been reported^[151,152]. Vitamin E therapy decreases AST and ALT levels and hepatic steatosis but does not improve necroinflammation and fibrosis^[153]. Antioxidants may even prevent health-promoting effects of physical exercise namely insulin sensitivity and rise of systemic adiponectin in untrained and pre-trained individuals, and therefore, may be more effective in patients with low physical activity^[154]. In summary to date no pharmacologic treatment has been reliably shown to be effective for the treatment of NASH patients.

CONCLUSION

Adiponectin has emerged as a protective adipokine in insulin resistance and obesity related liver diseases (Figure 3), and drugs that elevate systemic adiponectin may be useful as therapeutics for NAFLD. Adiponectin receptor signaling pathways and potential hepatic adiponectin resistance in NASH, however, have been poorly investigated so far. Identification of molecules downstream of AdipoR1/2 and strategies to enhance adiponectin receptor activity may constitute promising approaches towards treatment of NAFLD.

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Streptozotocin-induced expression of Ngn3 and Pax4 in neonatal rat pancreatic α -cells

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Abstract

AIM: To investigate the mechanism behind β -cell regeneration in neonatal rat pancreas treated with streptozotocin (STZ).

METHODS: Neonatal Sprague Dawley rats were intraperitoneally injected with 70 mg/kg STZ. Body weight, pancreas weight and blood glucose were recorded every two days after the treatment. To identify the expression and location of transcription factors in the rat pancreas, double immunofluorescent staining was performed using antibodies to specific cell markers and transcription factors.

RESULTS: Expression of Neurogenin 3 (Ngn3), a marker for endocrine precursor cells, was observed by immunofluorescence in a few β -cells and many α -cells. The expression reached a peak 12 d after treatment. Pax4, a transcription factor that lies downstream of Ngn3 and

plays an important role in β -cell differentiation, was also expressed in the α -cells of STZ-treated rats. We did not observe significant changes in Nkx6.1, which is essential for β -cell maturation in the treated rats.

CONCLUSION: α -cells dedifferentiated into endocrine precursor cells and acquired the ability to dedifferentiate in the neonatal rat pancreas after STZ treatment.

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Key words: Pancreatic remodeling; Dedifferentiation; Endocrine precursor cells; Streptozotocin; Transcription factors

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INTRODUCTION

The pancreas originates from gut endoderm. During development, the rat pancreas undergoes two transitions in embryonic days^[1]. After birth, many major developmental changes occur, including β -cell apoptosis, replication, and exogenesis^[2]. This stage is referred to as the remodeling of pancreas. In our previous work, we found alpha-fetoprotein and Mesothelin in embryonic rat pancreases but not in adult rat pancreases, nevertheless, we observed the expression of these two proteins during the remodeling of the rat pancreas^[3,4]. These studies indicate that during the remodeling phase, the neonatal pancreas is not fully matured. Furthermore, after treatment with Streptozotocin

(STZ) during this stage, the ontogeny of regeneration can be observed^[5]. Conversely, after treatment with STZ during adulthood, little regeneration of β -cells was found^[6]. Extensive studies have been reported on the model of STZ-induced depletion of β -cells in the neonatal rat pancreas, which showed that this model can be used to study β -cell replacement therapy for diabetes^[5,7,8].

The development of β -cells is regulated by a series of transcription factors^[9,10]. However, few studies have focused on the expression of these transcription factors during the regeneration of β -cells in STZ-treated neonatal rats. One of the most important upstream transcription factors is pancreas-duodenal homeobox 1 (Pdx1)^[11]. The initial expression of Pdx1 (E8.5-E9.0) marks the pre-pancreatic endoderm before it is visibly thickened^[12-14], and corresponds to the classically defined period of pancreatic specification^[15]. Following the expression of Pdx1 is the Neurogenin 3 (Ngn3), a basic helix-loop-helix transcription factor^[16] that marks endocrine pancreatic precursor cells. Among a series of transcription factors that differentiate endocrine precursors into β -cells, paired domain homeobox gene 4 (Pax4)^[17] and NK family member Nkx6.1^[18] lie downstream of Ngn3.

Although these factors are essential for the development and maturation of β -cells, it is unknown whether Ngn3, Pax4 and Nkx6.1 participate in the regeneration of β -cells after STZ treatment during the remodeling phase of the pancreas. Especially, there is little information on the differentiation factors that are involved in the remodeling of the rat pancreas. This study was designed to determine the expression and location of these transcription factors in the STZ-treated neonatal rat pancreas.

MATERIAL AND METHODS

Animals

Pregnant Sprague Dawley rats from the Animal Center of Nanjing Medical University, Nanjing, China, were kept under conventional conditions and provided with a 12:12 h light-dark cycle. Litters were reduced to 12 pups at birth. Four days after birth, half of the pups in each litter was intraperitoneally injected with 70 mg/kg STZ freshly dissolved in citrate buffer (0.05 mol/L, pH 4.5). The remaining pups received vehicle only. Blood glucose was measured with a OneTouch Ultra blood glucose meter (LifeScan Inc. Milpitas, CA, USA) in blood obtained by lancing the tail vein. Body weight was recorded every two days. On the day of treatment and days 4, 8, 12, 16 and 20 after treatment, animals were killed by decapitation or by overdose of anesthesia (sodium amobarbital, amytal sodium, Sigma-Aldrich 200 mg/kg body weight). Pancreases were collected immediately and frozen in liquid nitrogen or fixed. Three to five pups from at least three separate litters were studied at each time point. All experiments were conducted in accordance with the Chinese Law for Animal Protection and were approved by Nanjing Medical University Ethics Review Committee (approval No. 200913).

Fluorescence immunohistochemistry

Tissues were fixed in 4% paraformaldehyde for 24-36 h followed by a standard protocol of dehydration and paraffin embedding. Sections (5 μ m) were cut and mounted on glass slides (Fisher Scientific, Pittsburgh, PA, USA). The paraffin sections were deparaffinized in xylene and dehydrated in graded ethanol and distilled water. The tissue sections were blocked in 1% bovine serum albumin for 1 h. For double fluorescence immunohistochemical localization of glucagon and insulin, the mouse anti-glucagon (1:100, Sigma-Aldrich, St. Louis, MO, USA) antibody was applied after blocking and revealed using goat anti-mouse IgG-FITC (1:400, Santa Cruz, Santa Cruz, CA, USA). Rabbit anti-insulin polyclonal antibody (1:100, Santa Cruz, Santa Cruz, CA, USA) was then applied and revealed by Cy3-labeled anti-rabbit IgG (1:400, Santa Cruz, Santa Cruz, CA, USA). For dual fluorescence immunohistochemical localization of Ngn3, Pax4 or Nkx6.1 and insulin, rabbit anti-neurogenin 3 (1:100, Santa Cruz, Santa Cruz, CA, USA), goat anti-Pax4 (1:100, Santa Cruz, Santa Cruz, CA, USA) or goat anti-Nkx6.1 (1:100, Santa Cruz, Santa Cruz, CA, USA) antibody were added, respectively, and revealed by rabbit anti-goat IgG-FITC (1:400, Chemicon, Temecula, CA, USA) or mouse anti-rabbit IgG-FITC (1:400, Chemicon, Temecula, CA, USA). Mouse anti-insulin (1:100, Sigma-Aldrich, St. Louis, MO, USA) was applied and revealed by Cy3 conjugated anti-mouse (1:400, Chemicon, Temecula, CA, USA) antibody. For co-localizations of Ngn3, Pax4 or Nkx6.1 and glucagon, rabbit anti-neurogenin 3 (1:100), goat anti-Pax4 (1:100) or goat anti-Nkx6.1 (1:100) antibodies were added and revealed by rabbit anti-goat IgG-FITC (1:400) or mouse anti-rabbit IgG-FITC (1:400). Mouse anti-glucagon (1:100) was applied and revealed by Cy3 conjugated anti-mouse (1:400) antibody. Sections were placed in Gel Mount Aqueous Mounting Medium (G0918, Sigma) with a cover glass, and were examined under an Olympus BX51 microscope (Olympus Optical, Tokyo, Japan) at a magnification of $\times 200$ or $\times 400$.

β -cell mass

β -cell mass was measured by point counting morphometry on the same stained sections as described above. Each section was covered systematically at a magnification of $\times 400$ using a 48-point grid to obtain the number of grid intercepts over β -cells, endocrine non- β -cells, exocrine pancreatic tissues, and non-pancreatic tissues. The relative β -cell area was calculated by dividing the number of intercepts over β -cells by the number of intercepts over total pancreatic tissue; the β -cell mass was then estimated by multiplying the relative β -cell volume by the corrected pancreatic weight. Non- β -cell mass was similarly calculated. A correction factor for pancreas weight was obtained by multiplying the pancreas weight by the ratio of intercepts over non-pancreatic tissues to intercepts over total tissues. Actual pancreas weight was then calculated by subtracting this correction factor from total pancreas weight. A monogram related to the number of points, the

Table 1 Body and pancreas weight in control and streptozotocin-treated animals after streptozotocin treatment on postnatal day 4 (mean $\pm$ SD)

	Days after STZ treatment				
	4	8	12	16	20
Body weight (g)					
Control	13.6 $\pm$ 0.3	24.4 $\pm$ 1.5	30.5 $\pm$ 1.3	34.5 $\pm$ 1.5	50.0 $\pm$ 1.5
STZ	12.4 $\pm$ 0.3	22.3 $\pm$ 1.4	26.4 $\pm$ 1.3	32.4 $\pm$ 1.7	43.9 $\pm$ 1.5
Pancreas weight (g)					
Control	24.4 $\pm$ 2.3	49.8 $\pm$ 3.2	59.8 $\pm$ 1.4	60.5 $\pm$ 3.4	187.5 $\pm$ 6.9
STZ	18.7 $\pm$ 1.4	46.8 $\pm$ 3.3	57.1 $\pm$ 1.9	57.3 $\pm$ 3.2	162.5 $\pm$ 8.4

$n = 3$ litters/18 animals per group. STZ: Streptozotocin.

volume density and the expected relative standard error of the mean ($< 10\%$) was used to determine the number of intercepts needed for a representative sampling.

Statistical analysis

The experimental data was analyzed by paired Student t test using the SPSS 17.0 software. $P < 0.05$ was considered statistically significant. Data were presented as mean $\pm$ SD.

RESULTS

Body and pancreatic weight, blood glucose and islets in STZ-treated neonatal rat pancreases

After STZ treatment, body and pancreas weight did not change significantly (Table 1). Blood glucose concentrations significantly increased within 2 d after STZ treatment (Figure 1A). However, on day 20 after treatment, there was no longer a difference in blood glucose concentrations between the two groups.

Histological analysis showed that approximately 60% of insulin immunoreactive cells within the islets were lost 4 d after STZ treatment (Figure 1B). On day 8 after treatment, an increased number of small islets was observed (Figure 1C). On day 20 after treatment, more large islets were found, which may indicate that islet function had also recovered. Similarly, calculation of β -cell mass showed a reduction in β -cell mass from 4 d after STZ treatment onwards (Figure 1D). While β -cell mass was still reduced in STZ-treated rats on day 20 after treatment, blood glucose levels were not significantly different.

Expression and location of Ngn3

We used double immunofluorescence to stain Ngn3 and insulin or glucagon at different time points after STZ treatment. We did not find Ngn3 co-located with insulin in either treated or control rats (Figure 2A). By analyzing the coexpression of Ngn3 and glucagon, we observed abundant expression of Ngn3 in the treated rat islet α -cells (Figure 2B). In the STZ group, expression of Ngn3 could be detected on day 8 and reached a peak on day 12 after treatment (Figure 2C). However, no significant changes were observed in the signal from Ngn3 in α -cells 20 d after treatment compared with the control rats. In contrast,

few α -cells expressed Ngn3 in control rats at each time point.

Expression and location of Nkx6.1

We stained Nkx6.1 and glucagon or insulin by immunofluorescence. Consistent with previous work, we found coexpression of Nkx6.1 and insulin in both the controls and the treated group (Figure 3A), while no Nkx6.1 expression was found in α -cells at any time point (Figure 3B) when we studied the coexpression of glucagon and Nkx6.1.

Expression and location of Pax4

We studied the colocalization of Pax4 and insulin or glucagon by dual immunofluorescence. Consistent with previous work, we observed coexpression of insulin and Pax4 in both the control group and the treated group (Figure 4A). We also found enhanced expression of Pax4 in STZ-treated rat pancreases compared with control rats (Figure 4A). Eight days after treatment, we observed expression of Pax4 in α -cells of the treated rats but little expression in the control rats. However, we found coexpression of glucagon and Pax4 in both treated and control rats on day 12 after treatment (Figure 4B). On day 20 after STZ treatment, we could still observe a signal of Pax4 in the α -cells. However, in the control rats, few α -cells expressed Pax4 on day 20.

DISCUSSION

It is established that neonatal β -cells are able to regenerate after subtotal β -cell damage by STZ treatment. Regeneration of neonatal β -cells after destruction mainly relies on replication of pre-existing β -cells and heterogenesis of new cells^[19]. In this article, we demonstrated a series of transcription factors expressed in pancreatic α -cells, which suggested that α -cells may be a source of β -cells during the regeneration of the STZ-treated neonatal rat pancreas.

We found that β -cells were damaged 4 d after STZ treatment. On day 8 after treatment, β -cell numbers were recovered in STZ-treated rats. By day 20 after treatment, there was still a reduction in β -cell mass but the blood glucose concentrations had reverted to normal. Although the model resulted in transient hyperglycemia, no difference in the mean body weight or pancreatic weight was seen between the two groups.

The study of pancreatic development has focused on transcription factors and transcription factor hierarchies during development. A central and heavily studied transcription factor in pancreatic development is Pdx1. Although Pdx1 is a key component of pancreatic specification, we found no significant difference in α or β -cells between STZ-treated rats and control animals. This indicates that Pdx1 is not involved in the regeneration of β -cells in STZ-treated animals.

After pancreatic formation, which is mediated by Pdx1, Ngn3 regulates the differentiation of endocrine pancreas. Lack of Ngn3 leads to an absence of islets^[20], and the ectopic expression of Ngn3 in other cells converts these

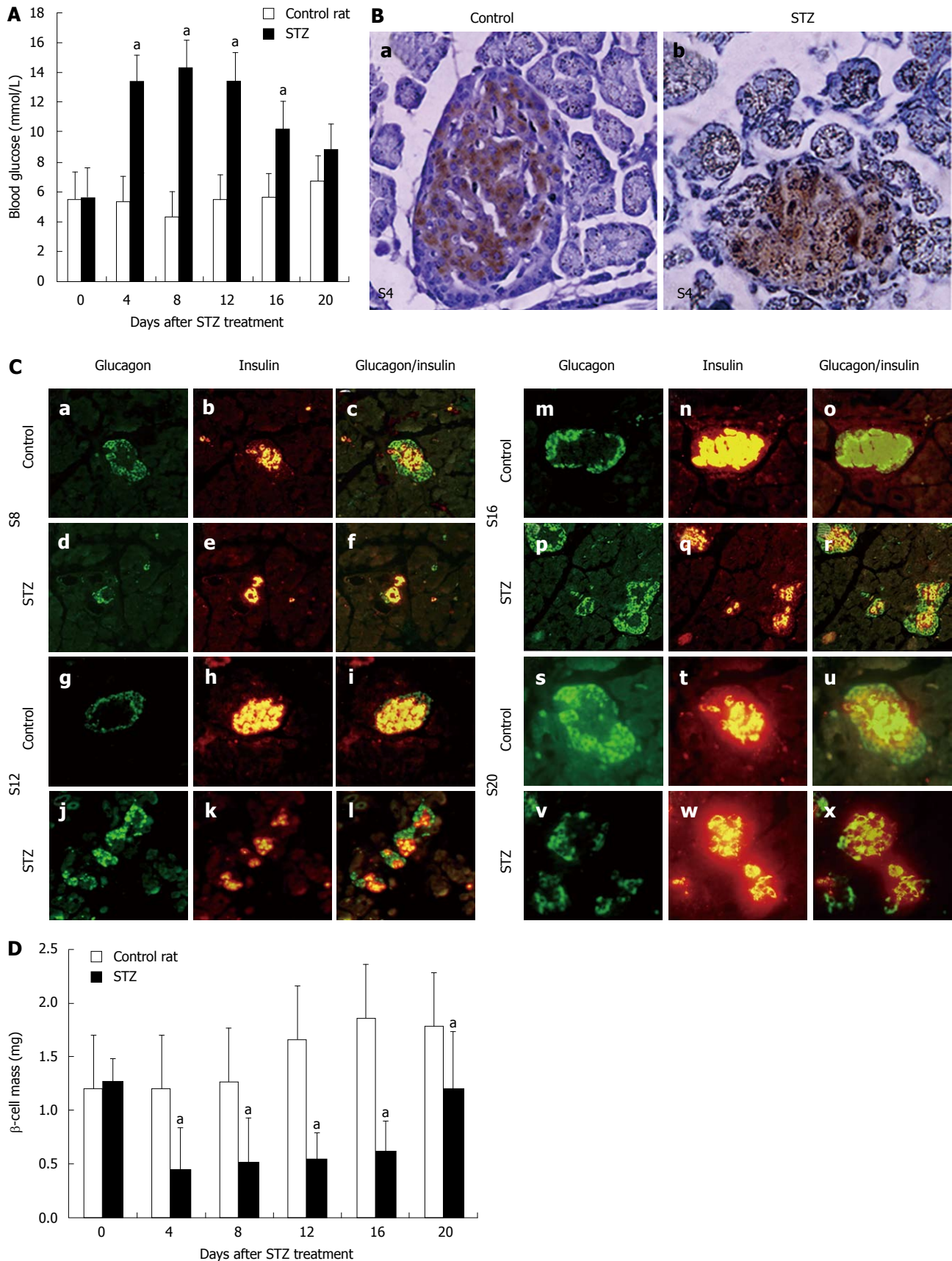


Figure 1 Body and pancreatic weight, blood glucose, islets and β -cell mass in streptozotocin-treated neonatal rat pancreas. A: Concentrations of fasting blood glucose in control rats or rats treated with streptozotocin (STZ) between day 0 and day 20 after STZ treatment. Data were obtained from 12-18 animals at each time point. ^a $P < 0.005$ vs control; B: Immunohistochemical location of insulin in sections of rat pancreas in the control (a) and 4 d after STZ treatment; (b). Original magnification, $\times 400$; C: Structure of islets in STZ-treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-glucagon antibody (green) and anti-insulin antibody (red). Original magnification, $\times 400$. Mean $\pm$ SD; D: β -cell mass in control rats or rats treated with STZ between day 0 and day 20 after STZ treatment. Data were obtained from three rats per time point. ^a $P < 0.05$ vs control rats.

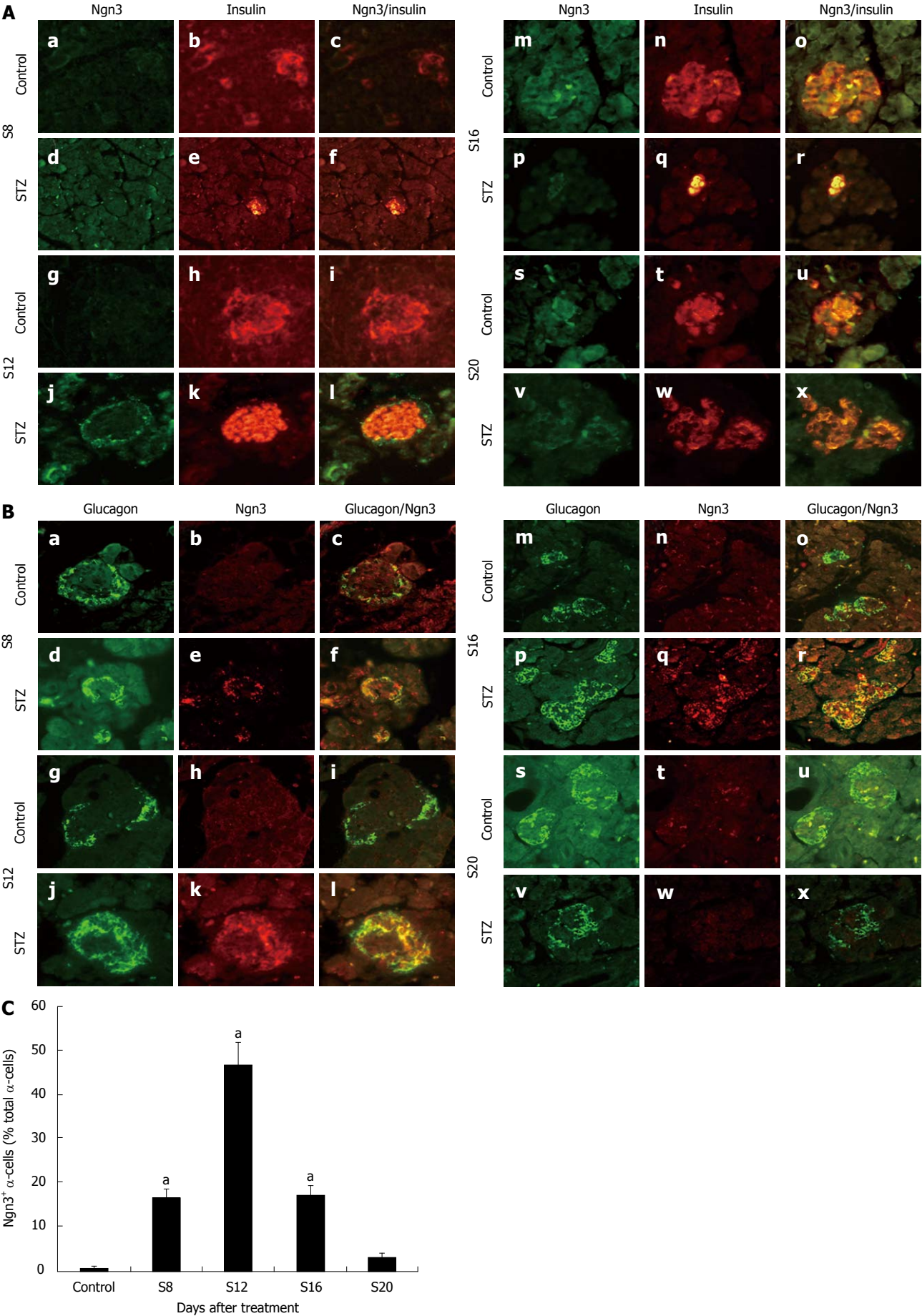


Figure 2 Expression and location of Ngn3. A: Immunofluorescent colocalization of Ngn3 and insulin in streptozotocin (STZ)-treated rats (d-f, j-l, p-r and v-x) and

control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-Ngn3 antibody (green) and anti-insulin antibody (red). Original magnification, $\times 400$; B: Immunofluorescent colocalization of Ngn3 and glucagon in STZ-treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-glucagon antibody (green) and anti-Ngn3 antibody (red). Original magnification, $\times 400$; C: Proportion of Ngn3+ / glucagon+ cells in total α -cells after treatment (Y). $^aP < 0.05$ vs control rats.

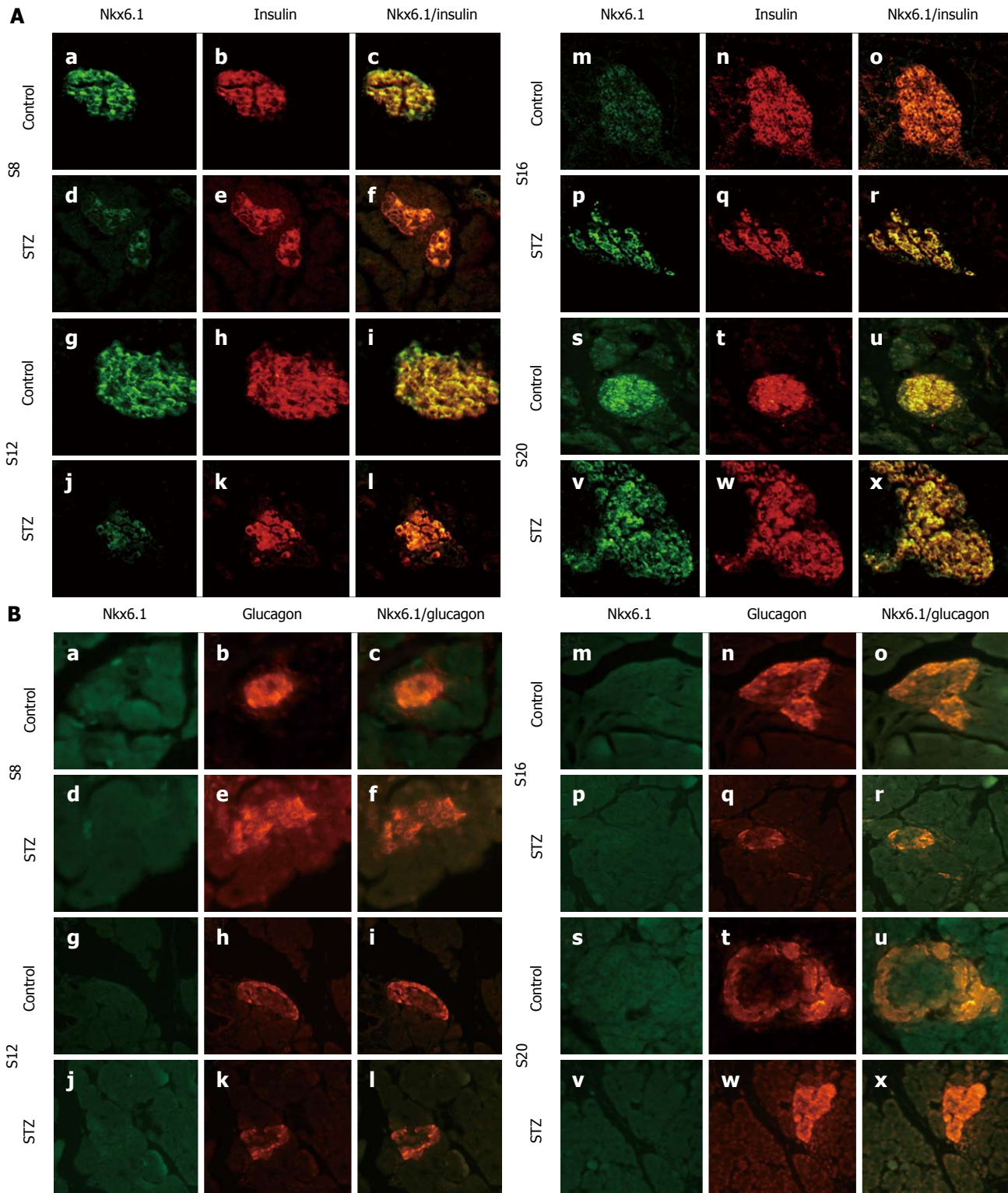


Figure 3 Expression and location of Nkx6.1. A: Immunofluorescent colocalization of Nkx6.1 and insulin in streptozotocin (STZ)- treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-Nkx6.1 antibody (green) and anti-insulin antibody (red); B: Immunofluorescent colocalization of Nkx6.1 and glucagon in STZ-treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-Nkx6.1 antibody (green) and anti-glucagon antibody (red). Original magnification, $\times 400$.

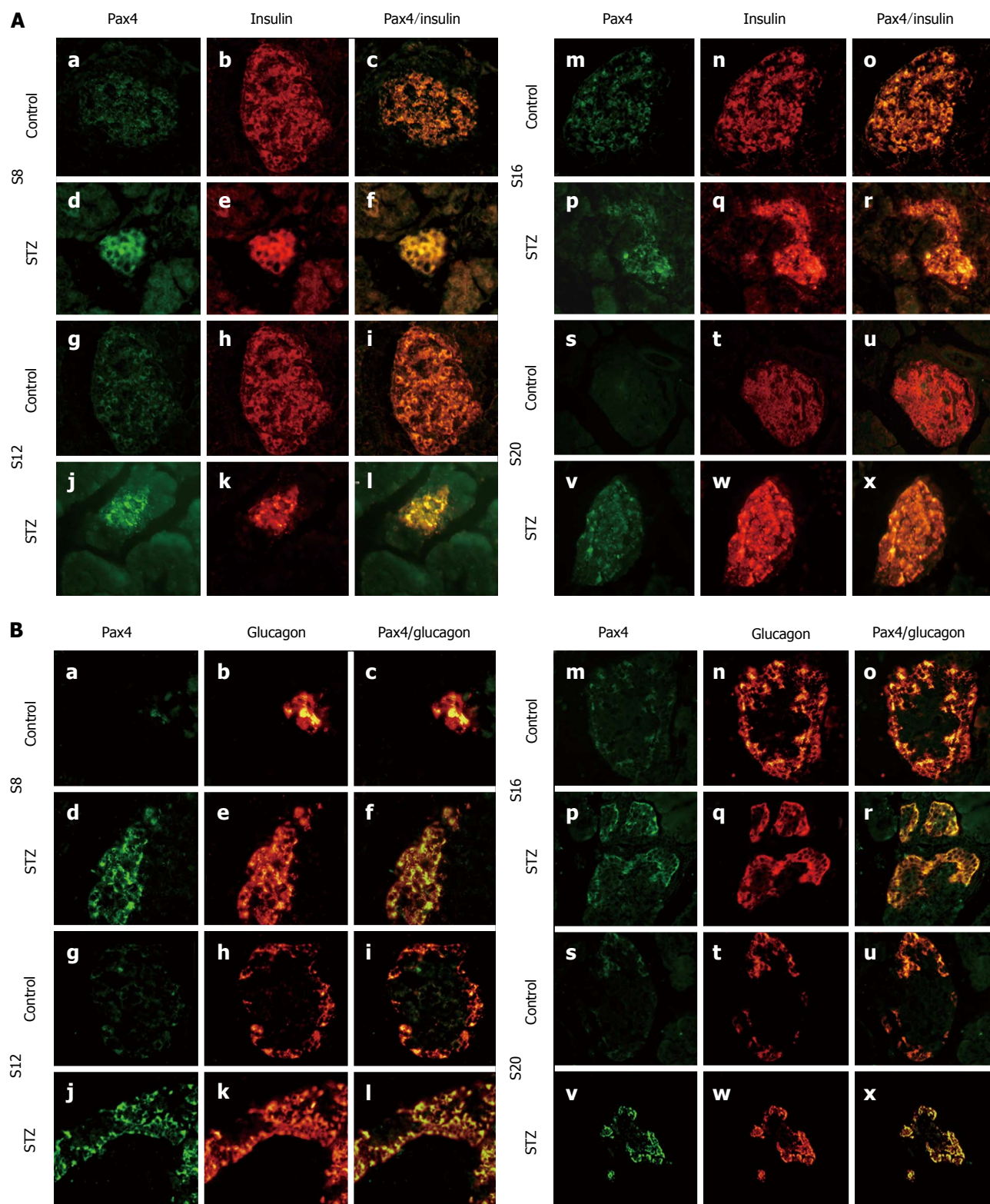


Figure 4 Expression and location of Pax4. A: Immunofluorescent colocalization of Pax4 and insulin in streptozotocin (STZ)-treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-Pax4 antibody (green) and anti-insulin antibody (red); B: Immunofluorescent colocalization of Pax4 and glucagon in STZ-treated rats (d-f, j-l, p-r and v-x) and control rats (a-c, g-i, m-o and s-u) on d 8 (a-f), 12 (g-l), 16 (m-r) and 20 (s-x) after STZ treatment. Pancreatic sections were immunostained with anti-Pax4 antibody (green) and anti-glucagon antibody (red). Original magnification, $\times 400$.

cells into endocrine cells^[21]. We observed Ngn3 expression in the α -cells of treated rats, which reached a peak on day 12 after STZ treatment. It has been reported that Ngn3 is

activated through partial duct ligation in the adult mouse pancreas^[22]. However, Ngn3 is absent in the β -cells of mice that underwent partial pancreatectomy^[23]. The dif-

ferent results among these three models indicate that the mechanism of β -cell regeneration in different pathological situations can be varied. Interestingly, we observed abundant expression of Ngn3 in STZ-treated rats but not in control rats. The expression of Ngn3 in α -cells after STZ treatment indicated that α -cells dedifferentiated into precursor cells and may be candidates for β -cell formation. It has been suggested that high Ngn3 expression at an inappropriately early time in the developing mouse pancreas may result in a pancreas entirely consisting of small clusters of glucagon-positive cells^[21,24]. Furthermore, by overexpression of Ngn3 in human^[25] or mouse^[26,27] pancreatic duct cells, the pancreatic duct cells could become endocrine cells. Apparently, the expression of Ngn3 is necessary for the transdifferentiation of α -cells to β -cells.

Next to Ngn3 induction, a complex network of transcription factors, including Pax4, progressively and differentially promotes the particular endocrine fates^[28,29]. The expression of Pax4 is first observed around E9.5 in dorsal pancreatic buds of mouse embryos and vanishes shortly after birth^[29,30]. Pax4 specifies the β -cell lineage into β and δ precursor cells^[31]. In mice lacking Pax4, mature pancreatic and δ -cells were absent^[29]. Conversely, ectopic expression of Pax4 in the mouse pancreas converted α -cells into β -cells. Moreover, the transgenic adult mice could survive after STZ-induced hyperglycemia^[32]. Activation of Pax4 in endocrine progenitor cells may be mediated by Ngn3 since it binds to the Pax4 regulatory region and is necessary for Pax4 expression^[33]. Ngn3 is required for ectopic Pax4 expressing α -cells to acquire a β -cell phenotype^[34]. Interestingly, we observed expression of Pax4 in α -cells of both control and STZ-treated rats. In the STZ-treated rats, the expression of Pax4 reached a peak on day 16 after the treatment. The expression of Pax4 in the control animals suggests that Pax4 expression is characteristic of the pancreatic remodeling phase. Both cell differentiation and maturation occur during remodeling of the pancreas, which explains the presence of transcription factors in islet cells. After STZ treatment, the expression of Pax4 increased and a Pax4 signal could still be observed in α -cells 20 d after the treatment. This suggests that STZ treatment exaggerates and extends the period of remodeling.

Another transcript factor which lies downstream of Ngn3 is Nkx6.1, and it is associated with the development and maturation of β -cells. Nkx6.1 appears to be a marker for multipotent pancreatic progenitor cells^[35]. At later developmental stages and in the adult pancreas, Nkx6.1 becomes completely restricted to insulin-expressing cells. Consistent with previous researches, we observed coexpression of Nkx6.1 and insulin in both STZ-treated and control rats. However, we did not find any Nkx6.1-positive α -cells. Immunoblotting revealed that the expression of Nkx6.1 decreased 4 d after STZ treatment, and reached normal levels on day 12 after treatment. Although Nkx6.1 is critical for the development of β -cells, it does not affect the generation of β -cells from α -cells.

It has been established that regeneration of neonatal rat β -cells after subtotal destruction by STZ occurs by two mechanisms of equal significance. The first mechanism

is the replication of surviving β -cells in the islet compartment, the second mechanism is the replication of cells from a β -cell pool outside the islet compartment. In this article, we have demonstrated that α -cells may also be a source for β -cell regeneration. Mature α -cells converted to β -cells after partial duct ligation plus alloxan treatment, and the contribution of α -cells to the emergence of new β -cells was proportional to the degree of β -cell ablation^[36]. However, α -cells could only convert to β -cells when the proportion of β -cell loss reached 99%^[37].

In conclusion, during the period of pancreatic remodeling, the islets are not completely matured and the dedifferentiation of α -cells into endocrine precursor cells contributes to the recovery of β -cell mass after impairment by STZ.

COMMENTS

Background

Streptozotocin-induced β -cell loss in neonatal rat pancreas can trigger transient hyperglycemia. β -cell mass recovers 20 d after treatment. It is unknown whether Ngn3, Pax4 and Nkx6.1 participate in the regeneration of β -cells after streptozotocin (STZ) treatment during the remodeling phase of the pancreas.

Research frontiers

It has been shown that mature α -cells converted to β -cells after partial duct ligation plus alloxan treatment, and that the contribution of α -cells to the emergence of new β -cells was proportional to the degree of β -cell ablation.

Innovations and breakthroughs

There is little information on the differentiation factors that are involved in the remodeling of the rat pancreas. This study was designed to determine the expression and location of these transcription factors in the STZ-treated neonatal rat pancreas. The authors for the first time found the expression of Ngn3 and Pax4 in α -cells during remodeling of rat pancreas after STZ treatment.

Applications

Insulin deficiency caused by a reduced pancreatic islet β -cell number underlies the progression of both type 1 and type 2 diabetes, prompting efforts to develop β -cell replacement therapies. This study demonstrated the dedifferentiation of α -cells into endocrine precursor cells may contribute to the recovery of β -cell mass after impairment by STZ and this may provide an alternative way for β -cell replacement therapies.

Terminology

After birth, many major developmental changes occur, including β -cell apoptosis, replication, and exogenesis. This stage is referred to as the remodeling of pancreas.

Peer review

The study is well conducted and the results are interesting. This paper puts up the fact that α -cells dedifferentiate to endocrine precursor cells.

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Pathological and MR-DWI study of the acute hepatic injury model after stem cell transplantation

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Abstract

AIM: To investigate apparent diffusion coefficient (ADC) values as an indication of reconditioning of acute hepatic injury (AHI) after allogeneic mononuclear bone marrow cell (MBMC) transplantation.

METHODS: Three groups were used in our study: a cell transplantation group ($n = 21$), transplantation control group ($n = 21$) and normal control group ($n = 10$). AHI model rabbits in the cell transplantation group were injected with 5 mL of MBMC suspension at multiple sites in the liver and the transplantation controls were injected with 5 mL D-Hanks solution. At the end of the 1st, 2nd and 4th wk, 7 rabbits were randomly selected from the cell transplantation group and transplantation control group for magnetic resonance diffusion-weighted imaging (MR-DWI) and measurement of

the mean ADC values of injured livers. After MR-DWI examination, the rabbits were sacrificed and the livers subjected to pathological examination. Ten healthy rabbits from the normal control group were used for MR-DWI examination and measurement of the mean ADC value of normal liver.

RESULTS: At all time points, the liver pathological scores from the cell transplantation group were significantly lower than those in the transplantation control group (27.14 ± 1.46 vs 69.29 ± 6.16 , 22.29 ± 2.29 vs 57.00 ± 1.53 , 19.00 ± 2.31 vs 51.86 ± 6.04 , $P = 0.000$). The mean ADC values of the cell transplantation group were significantly higher than the transplantation control group ($(1.07 \pm 0.07) \times 10^{-3} \text{ mm}^2/\text{s}$ vs $(0.69 \pm 0.05) \times 10^{-3} \text{ mm}^2/\text{s}$, $(1.41 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$ vs $(0.84 \pm 0.06) \times 10^{-3} \text{ mm}^2/\text{s}$, $(1.68 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$ vs $(0.86 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$, $P = 0.000$). The pathological scores of the cell transplantation group and transplantation control group gradually decreased. However, their mean ADC values gradually increased to near that of the normal control. At the end of the 1st wk, the mean ADC values of the cell transplantation group and transplantation control group were significantly lower than those of the normal control group [$(1.07 \pm 0.07) \times 10^{-3} \text{ mm}^2/\text{s}$ vs $(1.76 \pm 0.03) \times 10^{-3} \text{ mm}^2/\text{s}$, $(0.69 \pm 0.05) \times 10^{-3} \text{ mm}^2/\text{s}$ vs $(1.76 \pm 0.03) \times 10^{-3} \text{ mm}^2/\text{s}$, $P = 0.000$]. At any 2 time points, the pathological scores and the mean ADC values of the cell transplantation group were significantly different ($P = 0.000$). At the end of the 1st wk, the pathological scores and the mean ADC values of the transplantation control group were significantly different from those at the end of the 2nd and 4th wk ($P = 0.000$). However, there was no significant difference between the 2nd and 4th wk ($P = 0.073$ and 0.473 , respectively). The coefficient of correlation between the pathological score and the mean ADC value in the cell transplantation group was -0.883 ($P = 0.000$) and -0.762 ($P = 0.000$) in the transplantation control group.

CONCLUSION: Tracking the longitudinally dynamic

change in the mean ADC value of the AHI liver may reflect hepatic injury reconditioning after allogeneic MBMC transplantation.

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Key words: Stem cells; Transplantation; Hepatic injury; Magnetic resonance imaging; Diffusion weighted imaging

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INTRODUCTION

Mononuclear bone marrow cells (MBMCs) are adult stem cells that have multi-potential differentiation capabilities and low immunogenicity. Direct allogeneic MBMC transplantation can repair various organ injuries such as hepatic injury without obvious immune rejection^[1]. There are many studies evaluating the therapeutic effect of MBMC transplantation therapy for hepatic injury. However, few studies have been undertaken to determine the feasibility of magnetic resonance diffusion-weighted imaging (MR-DWI) to evaluate the therapeutic effect of MBMC transplantation therapy on models of acute hepatic injury (AHI).

MR-DWI is an atraumatic and functional imaging technique that is very sensitive to molecular diffusion from the random and microscopic translational motion of molecules known as Brownian motion^[2]. MR-DWI can image the difference in microscopic diffusion movements of water molecules in various tissues. The most noticeable merit of MR-DWI is providing an apparent diffusion coefficient (ADC) value that can distinguish the microscopic diffusion movement of water molecules in different tissues *in vivo* by assigning numerical values^[3-7]. When a tissue has a pathological change, the microscopic diffusion movement of water molecules changes and the mean ADC value should also change. It has been generally accepted that MR-DWI is valuable in qualitatively and quantitatively diagnosing cerebral ischemia in the hyper-inchoate period^[8]. During recent years, many studies of hepatic pathological changes using MR-DWI have been reported^[3-7]. These showed that MR-DWI of the liver seems promising for the characterization of many diseases (especially focal liver lesions) by calculating ADC values.

Similarly, after MBMC transplantation therapy, there should be a dynamic change in the microscopic diffusion movement of water molecules in hepatic tissue during the repair process of AHI. Thus, the aim of our study was to evaluate the contribution of the mean ADC value in reflecting the repair process of AHI after MBMC

transplantation therapy by comparison with the pathological change. The pathological mechanisms behind the dynamic change of the mean ADC value from injured hepatic tissue will be discussed in further detail.

MATERIALS AND METHODS

Material and instruments

Experiments were performed using 57 healthy, male New Zealand White rabbits weighing -2.5 kg with an average age of -2 mo. All animal work was conducted in accordance with the guidelines provided by the Institutional Animal Control and Utilization Committee. Five rabbits were randomly selected and used to isolate MBMCs. Dulbecco's modified Eagle's medium and fetal bovine serum were purchased from Gibco (New York, USA). Mononuclear cell separation medium was purchased from Tianjin Haoyang Company (Tianjin, China). D-Hanks solution, an electronic balance, 3% pentobarbital sodium, sterile surgical instruments, an optical microscope, cell separation tools and 2% trypan blue were supplied by the Second Xiangya Hospital. D-galactosamine (D-GalN) was purchased from Jiangsu Nantong Tonglu Co. Ltd. (Nantong, China). Imaging was performed using a 1.5-Tesla Signa Twinspeed MR scanner (General Electric Medical Systems, USA) with a small diameter cylindrical brain radiofrequency coil.

Study groups and the establishment of AHI models

Acute hepatic injury was induced by D-galactosamine (D-GalN). D-GalN was dissolved in sterile 0.9% NaCl at a concentration of 10 g/100 mL (w/v). Forty-two rabbits were randomly selected to establish the AHI models. According to the weight of each rabbit, D-GalN solution was injected into the upper abdomen at a dosage of 1.0 g/kg. This amount was determined by preliminary experiments. The rabbits' weight, drug dosage and detailed administration times were recorded. The 42 AHI rabbits were randomly and equally divided into 2 groups: a cell transplantation group and a transplantation control group. Liver function assays were performed 24 h after drug administration and pathological examinations of liver sections taken during cell transplantation were performed to verify the establishment of the AHI model. The remaining 10 healthy rabbits were assigned to the normal control group, and only MR-DWI examination was performed for measurement of the normal liver mean ADC value.

Isolation and transplantation of MBMCs

After being sacrificed by air injection into the ear vein, the bodies of 5 healthy male rabbits were sterilized by incubation in 75% ethanol. Their limb bones were then isolated and bone marrow was repetitively flushed using D-Hanks solution containing heparin. Soft tissue clumps were removed with 100 pore filters. Recovered cell suspensions were aliquoted into multiple centrifuge tubes. MBMCs were then obtained through density gradient centrifugation. Cell number was counted and the viabil-

Table 1 Criteria for the acute injured liver pathological score

Score	Cellular necrosis and liver hyperplasia	Inflammatory cell infiltration in the area of the header and lobule	Injury of vascular endothelium and thrombus
0	Without	Without	Without
1	Spotty liver cell degeneration, necrosis without change of hepatic sinusoid and lobule shape	Infiltration area < 1/3 lobule or low inflammatory cell infiltration in the area of the header	Hyperemia of hepatic sinusoid or thrombus
2	Scattering severe liver cell degeneration, necrosis of whole lobule or unobvious liver cell hyperplasia	Infiltration area: 1/3-2/3 of lobule or comparatively wide-bound inflammatory cell infiltration	Injury of vascular endothelium or inflammatory cell infiltration under vascular endothelium
3	Large sheet liver cell degeneration and necrosis involving multiple lobules	Infiltration area: > 2/3 of lobule or inflammatory cells surround header	Extensive injury of vascular endothelium and thrombus

Obvious liver cell hyperplasia score: -2; Not obvious liver cell hyperplasia score: +2.

ity examined using trypan blue. The percentage of live cells had to be > 95%. The MBMCs were resuspended in D-Hanks solution at a density of $4 \times 10^6/\text{mL}$. Five milliliters of cell suspension was aliquoted into 10 mL glass syringes and kept in an incubator at 37°C with 5% CO₂ for a short time before transplantation.

MBMC transplantations were performed between 24 and 48 h after establishing the AHI models. Each AHI rabbit from the cell transplantation group was properly anesthetized and immobilized on an operating table. The skin of the upper abdomen was prepared and sterilized, then the liver was exposed with a 2 cm cut beneath the xiphoid process. After slowly injecting 5 mL of the MBMC suspension at multiple sites in the liver, the needle was withdrawn and the wound sutured to stop bleeding. The wound was treated with penicillin and covered with a sterile dressing. After transplantation, each model rabbit was given intramuscular injections of penicillin in the buttocks over a 3-d period with normal feeding. In addition to 5 mL of D-Hanks solution substituted for the MBMC suspension, manipulations of the rabbits in the transplantation control group were the same as those in the cell transplantation group.

Pathological management of the liver

At the end of the 1st, 2nd and 4th wk after transplantation, 7 rabbits were randomly selected for MR-DWI examination of the liver at each time point in the cell transplantation group and transplantation control group. Then they were sacrificed for histological examination. Rabbit liver tissue blocks were fixed in 4% paraformaldehyde and were processed for paraffin embedding. Microsections were prepared and stained with hematoxylin and eosin, then examined under an optical microscope. The criteria for the liver pathological scores were established according to the characteristic of this study, histology activity index and previous studies^[9] (Table 1). Six pathological microsections from each model rabbit were randomly selected to count the pathological scores by 2 experienced pathologists using a double-blind method. The sum of the pathological scores from 10 random high power fields (400×) from each microsection was regarded as the pathological score of that microsection.

MR-DWI protocol

Rabbits in the normal control group were subjected only

to liver MR-DWI examination. At the end of the 1st, 2nd and 4th wk after transplantation, 7 rabbits from the cell transplantation group and from the transplantation control group were randomly selected at each time point for liver MR-DWI examination.

Rabbits were anesthetized and immobilized, then MR-DWI (axial) was carried out with a 1.5-Tesla Signa Twin-speed MR scanner equipped with a small diameter cylindrical brain radiofrequency coil. The scanning parameters of the MR-DWI included a spin echo echoplanar imaging series, b value 0 and 400 s/mm², repetition time 6000 ms, echo time 45 ms, all diffusion directions, frequency coding direction R/L, field of view 20 cm × 15 cm, number of excitations 8, thickness layer 3 mm, 0.5 mm space, and matrix 128 × 128.

ADC values were obtained using Function Software on a GE workstation. Three different regions of interest (ROIs) (-50 mm² each) were chosen in the liver parenchyma in every clear axial slice of each liver and their ADC values were measured. The mean value of the above was considered to be the ADC value of each liver.

Statistical analysis

Based on the mean ADC values from ROIs and the pathological scores, the differences between the various groups and time points, and the correlation between the mean ADC value and pathological score were assessed. The statistical significance was calculated by an independent sample *t*-test, analysis of variance and linear correlation using SPSS 11.0 software. *P* values < 0.05 were considered to indicate statistical significance.

RESULTS

Mean ADC values from each group and analysis

The mean ADC value of the normal control group was $(1.76 \pm 0.03) \times 10^{-3} \text{ mm}^2/\text{s}$. At all time points after transplantation, the mean liver ADC values from the cell transplantation group were significantly higher than those of the transplantation control group (*P* = 0.000) (Table 2, Figure 1).

The mean liver ADC values from the cell transplantation group and transplantation control group gradually increased to near those of the normal control group over time. At the end of the 1st wk after transplantation,

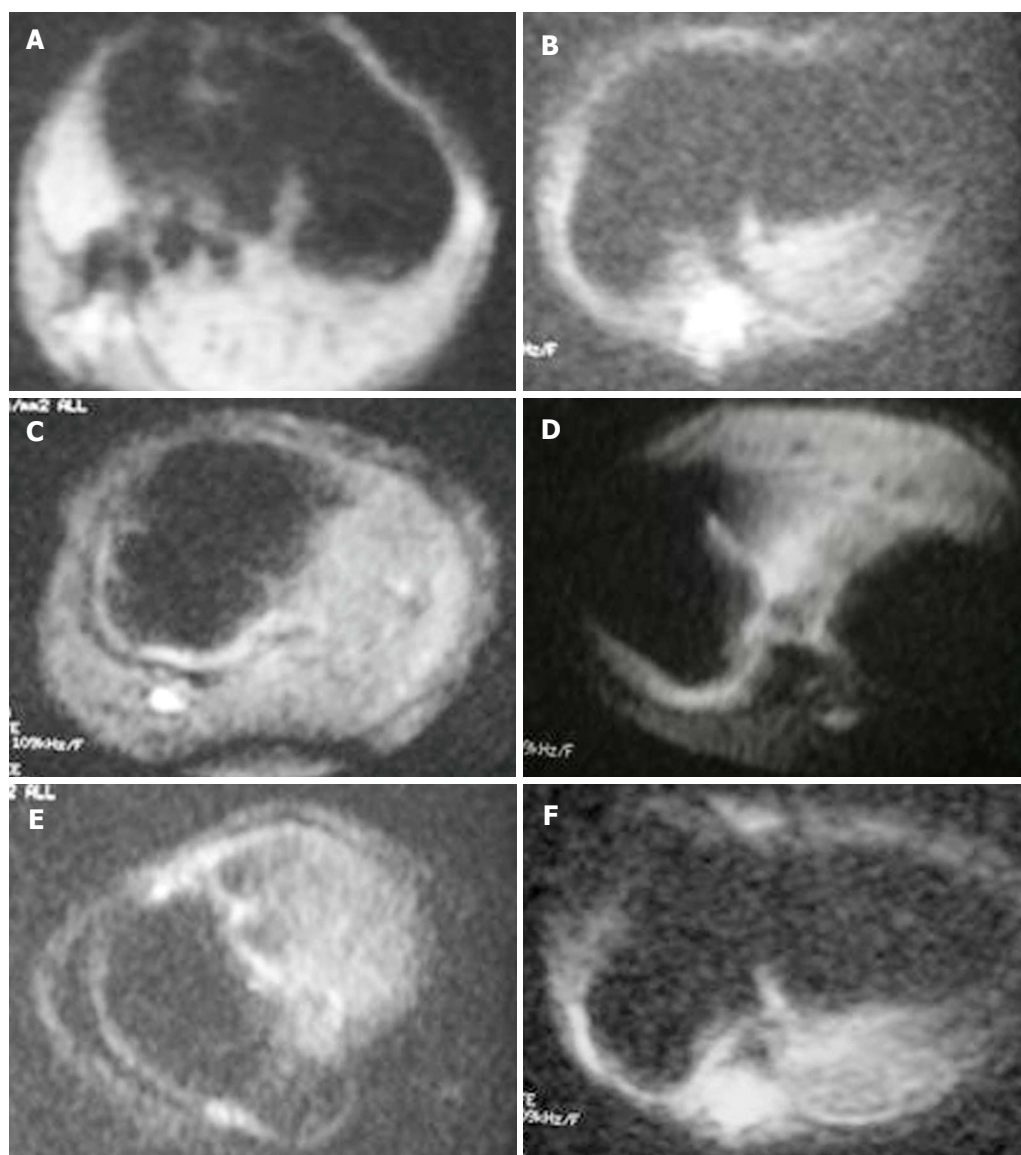


Figure 1 Diffusion-weighted imaging of hepatic injury at different time point. A: At the end of the 1st wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the transplantation control group was $(0.69 \pm 0.05) \times 10^{-3} \text{ mm}^2/\text{s}$; B: At the end of the 1st wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the cell transplantation group was $(1.07 \pm 0.07) \times 10^{-3} \text{ mm}^2/\text{s}$; C: At the end of the 2nd wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the transplantation control group was $(0.84 \pm 0.06) \times 10^{-3} \text{ mm}^2/\text{s}$; D: At the end of the 2nd wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the cell transplantation group was $(1.41 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$; E: At the end of the 4th wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the transplantation control group was $(0.86 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$; F: At the end of the 4th wk after transplantation, the mean apparent diffusion coefficient value of the acute hepatic injury liver in the cell transplantation group was $(1.68 \pm 0.04) \times 10^{-3} \text{ mm}^2/\text{s}$.

Table 2 Mean apparent diffusion coefficient values from the cell transplantation group and transplantation control group at each time point (mean $\pm$ SD) $\times 10^{-3} \text{ mm}^2/\text{s}$

Group	1st wk	2nd wk	4th wk
Cell transplantation group	1.07 ± 0.07	1.41 ± 0.04	1.68 ± 0.04
Transplantation control	0.69 ± 0.05	0.84 ± 0.06	0.86 ± 0.04
<i>t</i>	11.452	21.735	37.876
<i>P</i>	0.000	0.000	0.000

they were both significantly lower than those of the normal control group ($t = 23.612$, $P = 0.000$; $t = 52.416$, $P = 0.000$).

Between any 2 time points, the differences in the mean liver ADC values from the cell transplantation group were statistically significant ($P = 0.000$). At the end of the 1st wk after transplantation, the mean ADC values from the transplantation control group were significantly lower than those at the end of the 2nd and 4th wk ($P = 0.000$). However, there was no significant difference between the end of the 2nd and 4th wk ($P = 0.473$).

Pathological scores and analysis

The livers' pathological scores from the cell transplantation group and transplantation control group gradually decreased over time (Table 3, Figure 2). At all time

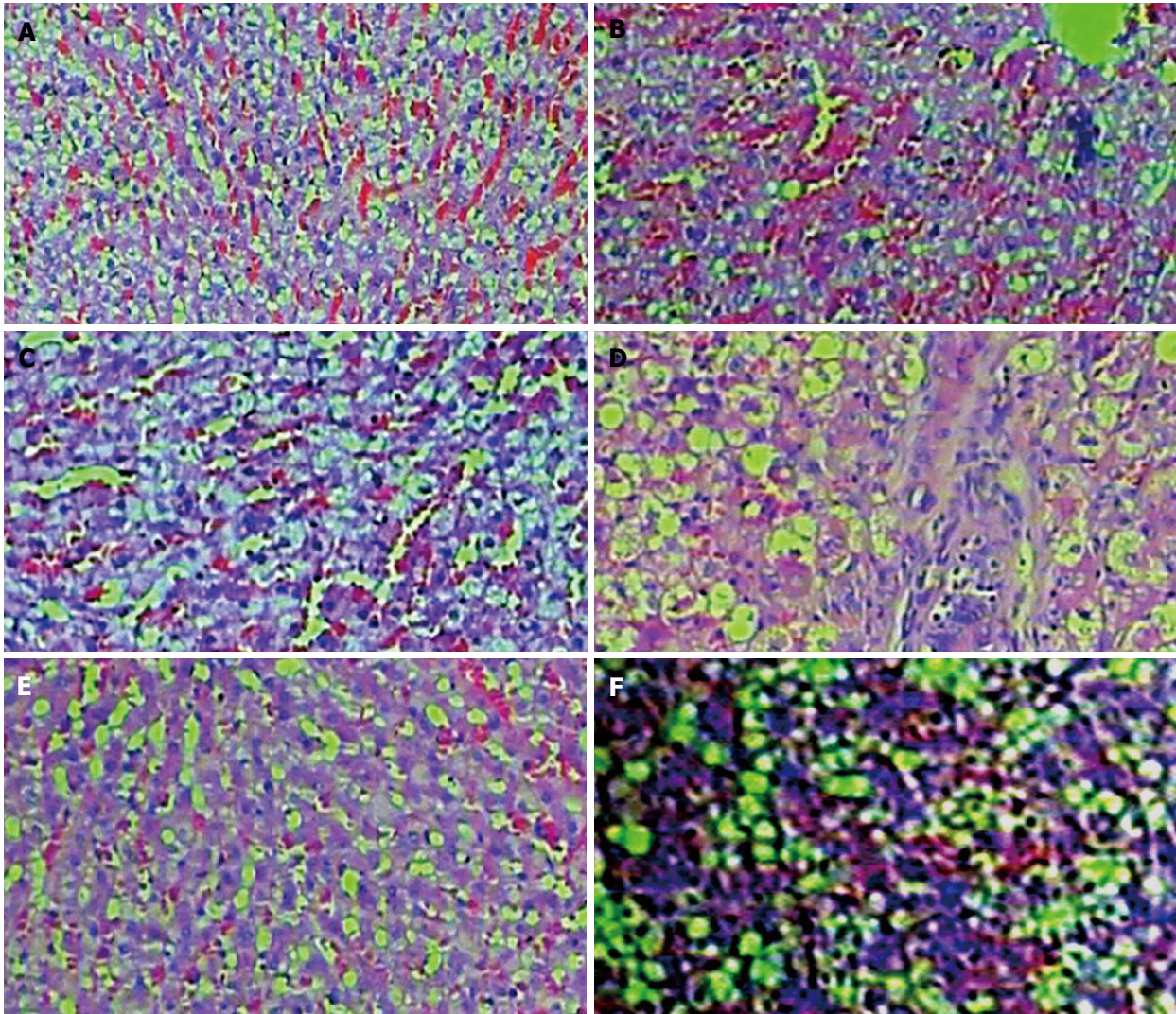


Figure 2 Pathological change of hepatic injury at different time point (Hematoxylin and eosin $\times 100$). A: At the end of the 1st wk after transplantation, the pathological sections of the cell transplantation group showed extensive hepatic cell degenerations, few binucleate cells, abnormal hepatic cords and local inflammatory cell infiltration; B: At the end of the 1st wk after transplantation, the pathological sections of the transplantation control group showed obvious and extensive edema of hepatic cells, spotty hepatolysis, abnormal hepatic cords, local inflammatory cell infiltration and injured vascular endothelium; C: At the end of the 2nd wk after transplantation, the pathological sections of the cell transplantation group showed extensive edema of hepatic cells, abnormal hepatic cords, imperceptible inflammatory cell infiltration and few scattered binucleate cells. (Hematoxylin and eosin $\times 100$); D: At the end of the 2nd wk after transplantation, the pathological sections of the transplantation control group showed obvious and extensive edema of hepatic cells, an increased number of binucleate cells and obvious inflammatory cell infiltration around the header; E: At the end of the 4th wk after transplantation, the pathological sections of the cell transplantation group showed scattering edema of the hepatic cells, hepatic cords, sinusoid near normal and hyperemia in local sinusoid; F: At the end of the 4th wk after transplantation, the pathological sections of the transplantation control group showed scattering and sheet edema of the hepatic cells, hyperemia in local sinusoids and an increased number of binucleate cells.

Table 3 Pathological scores from the cell transplantation group and transplantation control at each time point (mean $\pm$ SD)

Group	1st wk	2nd wk	4th wk
Cell transplantation group	27.14 $\pm$ 1.46	22.29 $\pm$ 2.29	19.00 $\pm$ 2.31
Transplantation control	69.29 $\pm$ 6.16	57.00 $\pm$ 1.53	51.86 $\pm$ 6.04
<i>t</i>	-17.619	-33.379	-13.444
<i>P</i>	0.000	0.000	0.000

points after transplantation, the pathological scores of the livers from the cell transplantation group were significantly lower than those from the transplantation control

group ($P = 0.000$) (Table 3, Figure 2).

Between any 2 time points, the differences in pathological scores from the cell transplantation group were statistically significant ($P = 0.000$). At the end of the 1st wk after transplantation, the pathological scores from the transplantation control group were significantly higher than those at the end of the 2nd and 4th wk after transplantation ($P = 0.000$). However, there was no significant difference between the end of 2nd and 4th wk ($P = 0.073$).

Correlation analysis

When the *b* value was 400 s/mm², there was a significant negative correlation between the pathological score and

mean ADC value in the cell transplantation group and transplantation control group ($r = -0.883$, $P = 0.000$; $r = -0.762$, $P = 0.000$).

DISCUSSION

The efficacy of allogeneic MBMC transplantation therapy for AHI has already been proven^[10,11]. Our results showed that the pathological changes such as cellular edema and inflammatory cell infiltration in the hepatic tissue of the transplantation control group were more obvious than those in the cell transplantation group at any similar time point. The pathological scores from the cell transplantation group were significantly lower than those of the transplantation control group at all time points. These results imply that allogeneic MBMC transplantation into an acute injury of the liver could improve hepatic injury reconditioning. This trend is similar to that found in other studies^[10,11].

Because of the high resolution and sensitivity, recent studies have focused on *in vivo* real-time tracking and detecting the fate of transplanted stem cells with MRI^[11,12]. However, there are few studies using MR-DWI to evaluate the therapeutic efficacy of MBMC transplantation for acute hepatic injuries.

When the b value is more than 300 s/mm^2 , physiological factors such as perfusion have little influence on the mean ADC value of hepatic tissue^[13-15]. Therefore, in our study we performed the MR-DWI examination of rabbit liver with 400 s/mm^2 for the b value, as determined by preliminary experiments.

Our study showed that at the end of the 1st wk after transplantation, the mean liver ADC values from the cell transplantation group and transplantation control group were much lower than the normal control group and both gradually increased to near the normal control over time. The correlation between the pathological scores and mean ADC values in the cell transplantation group or transplantation control group was significantly negative. This suggests the possibility of determining the reconditioning of an injured liver after allogeneic MBMC transplantation by tracking the longitudinally dynamic change of the mean ADC value from the AHI liver tissue.

By observing the pathological sections from the cell transplantation group and transplantation control group, we found the main pathological change was varying degrees of cytotoxic edema of the hepatocytes in all pathological sections. Therefore, we hypothesized that the pathological mechanism behind the change of the mean ADC value in hepatic tissue was mainly connected with cytotoxic edema of the hepatocytes in our study. Because the D-GalN injected into the peritoneal cavity was absorbed to injure the hepatic tissue causing Na-K pumps to be dysfunctional, the concentration of intracellular electrolytes increases. This causes water molecules inside cells to increase significantly, while extracellular water molecules decrease significantly. The cytotoxic edema of hepatocytes causes a decrease in

gaps between hepatocytes, so that the space where extracellular water molecules can randomly move decreases. Therefore, the mean ADC value of hepatic tissue in the AHI model started to decrease^[13-18] and was lower than that of the normal hepatic tissue.

In our study, the mean ADC values from the cell transplantation group and transplantation control group gradually increased over time and their pathological scores gradually decreased. The pathological sections showed their hepatic tissue injury gradually healed. At any similar time point, the mean ADC values from the cell transplantation group were significantly higher than those from the transplantation control group, and the pathological scores of the cell transplantation group were significantly better than those of the transplantation control group. According to previous studies^[19-22] and our pathological sections, we hypothesized that there were 2 main hepatic reconditioning mechanisms causing these results. Firstly, the transplanted MBMCs promoted hepatic tissue reconditioning. Secondly, the hepatic injury caused the autologous hepatic reconditioning mechanism to activate. Because of the hepatic reconditioning, the hepatic cells' cytotoxic edema gradually decreased, and the number of extracellular water molecules and the space where extracellular water molecules could move randomly both gradually recovered. Thus, the macroscopic mean ADC values from the cell transplantation group and transplantation control group gradually increased^[23,24]. Because of the 2 mentioned hepatic reconditioning mechanisms, the reconditioning in the cell transplantation group was faster than the transplantation control group without transplanted MBMCs. Therefore, at any time point, the mean ADC values from the cell transplantation group were significantly higher than those from the transplantation control group.

Of course, if there were extensive hepatolysis and necrosis, the number of extracellular water molecules and the space where extracellular water molecules randomly move in the AHI model liver would greatly increase. This would cause the mean ADC value of the hepatic tissue in the AHI model to exceed that of the normal hepatic tissue^[25,26]. However, we did not observe this phenomenon in our study. Through observing pathological sections from all time points, we found sporadic scattering but no extensive hepatolysis and necrosis. The dominant pathological change in the hepatic tissue was varying degrees of hepatocellular cytotoxic edema. Perhaps the reason was that the dosage of D-GalN used was not high enough to cause extensive hepatolysis in our study. Considering the influence of hepatolysis on the ADC value of hepatic tissue, we chose many ROIs in all clear images from each AHI model's liver to measure ADC values. The mean ADC value was calculated from all ROIs and ADC values from each AHI liver. Thus, we could increase the accuracy of the ADC value of each AHI model's liver to the utmost extent.

In conclusion, when the b value is equal to 400 s/mm^2 , tracking the longitudinally dynamic change of the mean ADC value of the AHI liver could determine injured he-

patic tissue reconditioning after allogeneic MBMC transplantation.

COMMENTS

Background

Many studies have proven that allogeneic mononuclear bone marrow cell (MBMC) transplantation therapy is an effective way to repair liver injury. The most notable merit of magnetic resonance diffusion-weighted imaging (MR-DWI) is the provision of an apparent diffusion coefficient (ADC) value that can distinguish the microscopic diffusion movement of water molecules in various tissues in vivo by assigning a numerical value. After MBMC transplantation therapy, there should be a dynamic change in the microscopic diffusion movement of water molecules in the hepatic tissue during the repair process of acute hepatic injury. Thus, the authors attempted to use MR-DWI to evaluate the contribution of the acute injured liver's mean ADC value in reflecting the repair process after MBMC transplantation therapy.

Research frontiers

Allogeneic MBMC transplantation therapy can accelerate the repair of liver injury. Many studies are focusing on the mechanisms behind the transplanted MBMCs repair of the liver injury. Recently, some researchers have been attempting to track and detect the fate of transplanted MBMCs with magnetic resonance imaging.

Innovations and breakthroughs

It has been proven that allogeneic MBMC transplantation can repair liver injury. There are many studies on evaluating the therapeutic effect of MBMC transplantation therapy for hepatic injury, but few studies have determined the feasibility of MR-DWI to evaluate the therapeutic effect of MBMC transplantation therapy on models of acute hepatic injury.

Applications

The results of this study suggest that the dynamic change of the mean ADC value of the acute hepatic injury model's liver can determine the injured liver's reconditioning after allogeneic MBMCs transplantation.

Terminology

MR-DWI is a functional imaging technique that can image the difference in microscopic diffusion movements of water molecules in various tissues. This technique only requires the examinee to lie still on the examining table while the examination is carried out. It is atraumatic and very safe.

Peer review

This article investigates the role of MR diffusion-weighted images for detection of acute liver injury following allogeneic bone marrow cell transplantation in a rabbit model. The conclusion reached confirmed the value and usefulness of this modality. The method is non-traumatic and easily performed. The methodology and design of the study was sound. This study is of significance in the field of bone marrow transplantation.

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***NOD2* and *ATG16L1* polymorphisms affect monocyte responses in Crohn's disease**

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monocytes from Crohn's disease (CD) patients.

METHODS: Monocytes were isolated from peripheral blood of CD patients of known genotype for common single nucleotide polymorphisms of *NOD2* and *ATG16L1*. Monocytes were challenged with MAP and bacterial persistence assessed at subsequent time-points. Cytokine responses were assayed using a Milliplex multi-analyte profiling assay for 13 cytokines.

RESULTS: Monocytes heterozygous for a *NOD2* polymorphism (R702W, P268S, or 1007fs) were more permissive for growth of MAP ($P = 0.045$) than those without. There was no effect of *NOD2* genotype on subsequent cytokine expression. The T300A polymorphism of *ATG16L1* did not affect growth of MAP in our model ($P = 0.175$), but did increase expression of cytokines interleukin (IL)-10 ($P = 0.047$) and IL-6 ($P = 0.019$).

CONCLUSION: CD-associated polymorphisms affected the elimination of MAP from *ex vivo* monocytes (*NOD2*), or expression of certain cytokines (*ATG16L1*), implying independent but contributory roles in the pathogenesis of CD.

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Key words: Inflammatory bowel disease; Mycobacterium avium subspecies paratuberculosis; Cytokine; CARD15; Autophagy

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Abstract

AIM: To assess whether polymorphisms in *NOD2* and *ATG16L1* affect cytokine responses and mycobacterium avium subspecies paratuberculosis (MAP) survival in

INTRODUCTION

Crohn's disease (CD) has been proposed as being the product of chronic inflammation caused by a dysfunctional interaction between the intestinal immune system and commensal gut microbiota^[1]. The inflammation seen in CD is characterized by pronounced Th1 and Th17/23 responses involving the cytokines interleukin (IL)-1, IL-6, tumor necrosis factor (TNF)- α , IFN- γ ^[1-3], IL-23 and IL-17^[4-6].

Although the commensal intestinal microflora appear to play an important role in the etiology of CD, certain bacterial species have also been implicated as putative causal agents of CD. These include *Pseudomonas maltophilia*^[7], *Chlamydia trachomatis*^[8], *Bacteroides fragilis*^[9], *Yersinia species*^[10], adherent invasive *Escherichia coli* (*E. coli*)^[11] and *Mycobacterium avium* subspecies paratuberculosis (MAP)^[12]. The role of MAP in the etiology of CD is unclear. However, MAP causes chronic intestinal inflammation in ruminants (Johne's disease) with similar pathophysiology to CD^[13] and it has been reported as a causative agent of regional enteritis with similarities to CD in a number of monogastrics, including two primate species^[14,15]. MAP has also been cultured from both resected tissue^[16] and peripheral blood of CD patients^[17], and has been visualized inside macrophages from CD patients^[18]. Meta-analyses of epidemiological studies confirm an association of MAP with CD^[19,20], although it remains unknown whether MAP is pathogenic in humans, or whether this association reflects a defective host immune system permissive for the survival of MAP.

Twin and family studies have demonstrated a significant genetic component to the development and progression of CD^[21-23]. Linkage analysis, candidate gene approaches and, most recently, genome-wide association studies (GWAS) have identified over 30 risk genes for CD^[24-26], many of which are involved with bacterial recognition (e.g. *NOD2*) or processing and elimination of bacteria through the autophagy pathway (e.g. *IRGM*^[27] and *ATG16L1*^[25]).

In this study, we developed an *ex vivo* monocyte model to assess the impact of the CD-associated single nucleotide polymorphisms (SNPs) in *NOD2* (rs2066842, P268S; rs2066844, R702W; and 1007fs, rs2066847) and *ATG16L1* (rs2241880, T300A) on cytokine responses to the putative pathogen MAP. MAP can survive and replicate within phagocytic cells, and consequently we also evaluated the impact of these polymorphisms on the intracellular persistence of MAP. The use of *ex vivo* monocytes allows functional evaluation of SNPs associated with CD, and may provide a more realistic insight into the impact that genotype has on CD compared to studies which involve abrogation of protein expression or whole gene deletion.

MATERIALS AND METHODS

Patient recruitment

Patients for the current study were selected from a New Zealand population-based Caucasian inflammatory bowel disease (IBD) cohort recruited to investigate genetic and environmental factors that contribute to IBD etiology^[28-32]. Inclusion criteria for the current study were a confirmed diagnosis of CD and negative MAP status as ascertained by IS900 PCR in peripheral blood^[28].

The genotype combinations and patient phenotype information are detailed in Table 1. Briefly, the potential impact of *ATG16L1* and *NOD2* polymorphisms were assessed separately. For analysis of *ATG16L1*, monocytes were collected from CD patients who had a wild-type *NOD2* genotype and were homozygous for either the major (G) allele ($n = 6$) or minor (A) allele ($n = 6$) of *ATG16L1* 1138G > A (rs2241880). Conversely, for experiments evaluating the effect of *NOD2* genotype, monocytes were collected from patients who were *ATG16L1* 1138G homozygotes and were heterozygous for one of the three *NOD2* SNPs previously associated with CD; 2104C > T (R702W, rs2066844), 2722G > C (G908R, rs2066845), or 3020insC (1007fs, rs2066847), and were heterozygous for the background variant 802C > T (P268S, rs2066842). A total of 12 patients were recruited, 6 carried the polymorphisms described, and 6 were homozygous at these *NOD2* loci (Table 1). None of the patients included in this study had the SNPs rs13361189 and rs4958847. These SNPs are in complete linkage disequilibrium with a 20 kb insertion/deletion polymorphism which has been shown to alter expression of the autophagy gene *IRGM*^[33].

Preparation of monocytes from peripheral blood

Blood (40 mL) was drawn into heparin tubes (Sigma-Aldrich), divided into 20 mL aliquots, and 15 mL of Phosphate Buffered Saline (PBS) was added to each. Ficoll-Paque™ PREMIUM (10 mL) (GE Healthcare Bio-Sciences Uppsala, Sweden) was layered under each aliquot and the samples centrifuged (1000 $\times$ g, 20 min). Mononuclear cells collected from the interface were added to 30 mL of PBS, centrifuged (350 $\times$ g, 10 min) and resuspended in 15 mL of PBS. In order to standardize the number of monocytes used in experiments, mononuclear cells were enumerated using a hemocytometer and a 200 μ L aliquot was analyzed on a Beckman Coulter FC500 MPL flow cytometer to determine the percentage of monocytes based on forward and side scatter characteristics. After centrifugation (350 $\times$ g, 10 min), cells were resuspended in RPMI medium 1640 supplemented with 10% fetal bovine serum (FBS) (Invitrogen, Carlsbad, CA, USA) to a concentration of 4×10^5 monocytes/mL. Then 500 μ L of this preparation were plated per well in a 24-well tissue culture plate (Nunc, Roskilde, Denmark). Monocytes were left to adhere for 1 h in a humidified incubator at 37°C with 5% CO₂ and non-adherent cells were removed by washing three times with 1 mL of room temperature (RT) PBS.

Table 1 *IRGM*, *ATG16L1*, and *NOD2* genotypes of Crohn's disease patients from whom monocytes were collected for *ex vivo* experiments

Patient	<i>IRGM</i>		<i>ATG16L1</i>		<i>NOD2</i>			Clinical characteristics			
	rs13361189 ¹	rs4958847 ¹	T300A 1138G > A rs2241880	R702W 2104C > T rs2066844	P268S 802C > T rs2066842	G908R 2722G > C rs2066845	1007fs 3020insC rs2066847	Gender	Time since diagnosis (yr)	Disease location	Harvey bradshaw index ²
1	TT	GG	AA	CC	CC	GG	00	M	53	Ileal	0
2	TT	GG	AA	CC	CC	GG	00	M	5	Ileo-colonic	0
3	TT	GG	AA	CC	CC	GG	00	F	5	Colonic	0
4	TT	GG	GG	CC	CC	GG	00	M	25	Ileo-colonic	2
5	TT	GG	AA	CC	CC	GG	00	F	6	Ileo-colonic	1
6	TT	GG	AA	CC	CC	GG	00	F	9	Ileal	3
7	TT	GG	AA	CC	CC	GG	00	M	1	Ileal	0
8	TT	GG	GG	CC	CC	GG	00	M	6	Colonic	2
9	TT	GG	GG	CC	CC	GG	00	F	10	Colonic	5
10	TT	GG	GG	CC	CC	GG	00	M	24	Ileo-colonic	1
11	TT	GG	GG	CC	CC	GG	00	F	11	Colonic	0
12	TT	GG	GG	CC	CC	GG	00	F	7	Ileo-colonic	4
13	TT	GG	GG	CT	CT	GG	00	F	5	Colonic	4
14	TT	GG	GG	CT	CT	GG	00	F	9	Ileo-colonic	0
15	TT	GG	GG	CT	CT	GG	00	M	17	Ileal	0
16	TT	GG	GG	CT	CT	GG	00	F	18	Colonic	4
17	TT	GG	GG	CC	CT	GG	0C	M	7	Ileal	1
18	TT	GG	GG	CT	CT	GG	00	F	16	Ileo-colonic	4

¹SNPs located upstream (5') to *IRGM*; ²Non-invasive clinical index used to assess disease activity in patients with Crohn's disease. A score of ≥ 7 indicates active disease.

Adherent monocytes were incubated overnight in 500 μ L of RPMI 1640/10% FBS.

Culture of MAP

MAP strain Dominic (ATCC 43545) was inoculated into 10 mL volumes of Difco™ Middlebrook 7H9 broth (BD Biosciences, Sparks, MD, USA) supplemented with 10% v/v BBL™ Middlebrook OADC Enrichment (BD Biosciences), 0.05% v/v Tween 80 (Sigma-Aldrich, St Louis, MO, USA) and 2 mg/mL Mycobactin J (Allied Monitor, Fayette, MO, USA) and grown at 37°C. A standard growth curve of MAP was obtained by measuring the optical density at 600 nm (OD₆₀₀) of an aliquot of bacterial suspension during the log phase, which had been passed repeatedly through a 25-gauge needle, and enumerating the bacteria by plating on the same medium supplemented with 1.5% agar (Invitrogen, Carlsbad, CA, USA).

Monocyte challenge experiments

Bacteria were grown to mid log phase (approximately 1×10^8 cells/mL, with reference to previously obtained growth curve data) and harvested by centrifugation ($13000 \times g$, 5 min). Bacteria were resuspended in 500 μ L of PBS and passed ten times through a 25-gauge needle to break up clumps of cells. One 500 μ L aliquot of MAP was heat-inactivated at 90°C for 5 min and then both aliquots were diluted to 4×10^6 cells/mL in RPMI 1640/10% FBS. The optimal temperature and incubation time for heat-inactivation had been previously confirmed by plating heat-treated MAP cells onto agar. Growth medium was removed from the monocytes and 500 μ L of the MAP suspension was added to each well. Challenge experiments were performed in triplicate for each time-point/genotype combination. After incubation for 4 h at 37°C, 5% CO₂, the supernatant

was removed and stored at -80°C as a zero time-point sample for cytokine assays. Monolayers were washed three times with 1 mL of PBS to remove extracellular bacteria. A zero time-point lysate to assess bacterial uptake and persistence was removed by incubating 500 μ L of a 0.1% sodium deoxycholate (Sigma-Aldrich, St Louis, MO, USA) solution with the monolayer for 5 min at RT. Lysates were centrifuged ($13000 \times g$, 5 min) and resuspended in 200 μ L of PBS. Serial dilutions of the lysates were made with PBS and 50 μ L were spread on to a Middlebrook agar plate. The agar plates were left to incubate for four weeks at 37°C before counting MAP colonies. Subsequent samples at time-points of 24, 48, 72 and 96 h were similarly processed.

Confirmation of genotypes of study participants

ATG16L1 genotypes were confirmed at recruitment by direct DNA sequencing of PCR products. Briefly, genomic DNA was extracted from fresh peripheral blood using GenElute™ (Sigma-Aldrich, St Louis, MO, USA) spin columns according to manufacturer's protocols. A 480 bp fragment containing the *ATG16L1* 1138G > A SNP was amplified for DNA sequencing from patient genomic DNA using the following primers: 5'-CCACAG-GTTAGTGTGCAGGA-3' (forward primer) and 5'-CA-CAGCTGACAGAGCCAAAA-3' (reverse primer). PCR was carried out in a 20 μ L volume containing 1 μ L of genomic DNA, 0.3 μ mol/L of each primer, 200 μ mol/L dNTPs, 0.75 mmol/L MgCl₂, $1 \times$ TAQ-Ti reaction buffer (Thermo Fisher Scientific, Pittsburgh, PA, USA) and 0.25 U of TAQ-Ti DNA polymerase (Thermo Fisher Scientific). After an initial denaturation step of 94°C for 2 min, 35 cycles were performed at 94°C for 30 s, 60°C for 30 s and 72°C for 30 s. Five microlitres of each PCR product was checked on 1% agarose. Another 5 μ L aliquot was

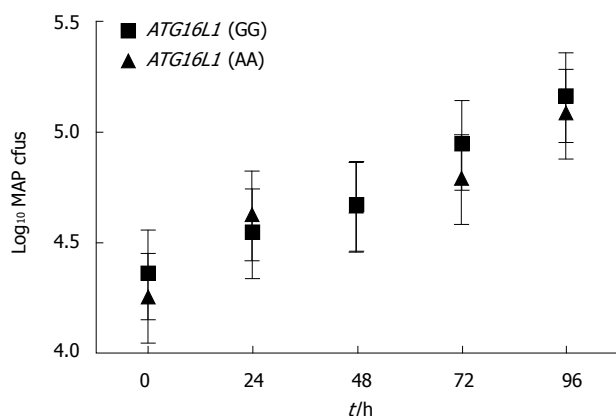


Figure 1 Effect of *ATG16L1* T300A variant on mycobacterium avium subspecies paratuberculosis numbers. Time course of mycobacterium avium subspecies paratuberculosis (MAP) growth in the context of the *ATG16L1* 1138 G > A variant. Monocytes were derived from subjects homozygous for either *ATG16L1* allele and carrying *NOD2* wild-type alleles ($n = 6$ for each group). MAP growth is expressed as colony forming units (cfu).

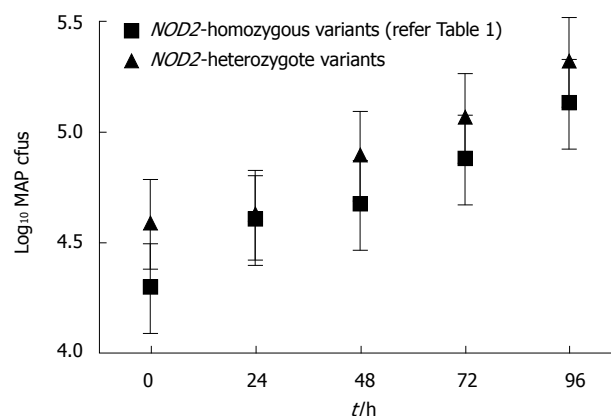


Figure 2 Effect of *NOD2* variants on mycobacterium avium subspecies paratuberculosis numbers. Time course of mycobacterium avium subspecies paratuberculosis (MAP) growth in the context of *NOD2* genetic variation. Monocytes were derived from subjects homozygous for the *ATG16L1* 1138G allele and with/without *NOD2* genetic variants ($n = 6$ for each group). MAP growth is expressed as colony forming units (cfu).

purified with Exo-SAP-IT (USB Corporation, Ohio, USA) and sequenced using BigDye chemistry (Applied Biosystems, California, USA) on an ABI 3730 Genetic Analyzer (Foster City, California, USA). The *NOD2* and *IRGM* genotypes of study participants were established as previously described using allele-specific PCR and pre-designed TaqMan SNP genotyping assays, respectively^[34,35].

Multiplex cytokine analysis

Cytokine analysis was performed using a 13-plex MILLIPLEX™ MAP human cytokine kit according to manufacturer's recommendations (Millipore) for the following: IFN γ , IL-10, IL-12p40, IL-12p70, IL-17, IL-1b, IL-2, IL-4, IL-5, IL-6, IL-8, TNF α , TNF β .

Statistical analysis

Data from the five time-points were analyzed by repeated measures ANOVA, with fixed effects for time (as categorical variable) and random effects for subject i.e. genotype. For cytokine analyses, where readings were below the threshold for detection (3.2 pg/mL) they were included as 3.2 pg/mL. Results were considered significant at $P \leq 0.05$.

Ethical considerations

Informed written consent was obtained from all participants in this study and ethical approval for this work was granted by the Upper South B Regional Ethics Committee of New Zealand.

RESULTS

Bacterial persistence ATG16L1

Numbers of MAP increased from a mean log₁₀ colony forming units (cfu) of 4.24 at 0 h to 5.08 at 96 h for the AA genotype, and from log₁₀ cfu of 4.47 to 5.29 for the GG genotype (Figure 1). There was no evidence (T-testing)

for the effect of the *ATG16L1* T300A polymorphism on MAP numbers at any individual time-point, or overall (pooled time-points ANOVA, $P = 0.175$) (Figure 1).

NOD2

MAP also grew in the monocytes with different *NOD2* genotypes, from a mean log₁₀cfu of 4.30 at 0 h to 5.12 for the cells homozygous for the major alleles of the *NOD2* variants, and from log₁₀cfu of 4.58 to 5.42 for cells heterozygous for any *NOD2* variant (Figure 2). There was no significant effect (T-testing) of *NOD2* genotype on MAP numbers at any individual time-point. However, analysis of all time-points indicated that monocytes heterozygous for a *NOD2* polymorphism were more permissive for growth of MAP (ANOVA, $P = 0.045$) (Figure 2).

Multiplex cytokine panels

Thirteen cytokines were evaluated from *ex vivo* monocyte supernatants using a MILLIPLEX™ MAP human cytokine kit. Each time-point/genotype combination was assayed in triplicate. All assays passed quality controls and r^2 values for the standard curves were ≥ 0.99 .

Of the thirteen cytokines analyzed in the multiplex format, only four, IL-10, IL-6, IL-8 and TNF α , had measurable responses above the detection threshold (> 3.2 pg/mL) on the multiplex ELISA platform used. Where samples had values of < 3.2 pg/mL, they were considered to be 3.2 pg/mL for statistical purposes.

Effect of ATG16L1 genotype

Cytokine expression results are shown in Figure 3. The AA genotype of *ATG16L1* was associated with greater expression of cytokines IL-10 and IL-6 in response to challenge with MAP ($P = 0.047$ and $P = 0.019$, respectively). No significant difference was seen between *ATG16L1* genotypes AA and GG for expression of either IL-8 or TNF α ($P = 0.758$ and $P = 0.289$, respectively) (Figure 3).

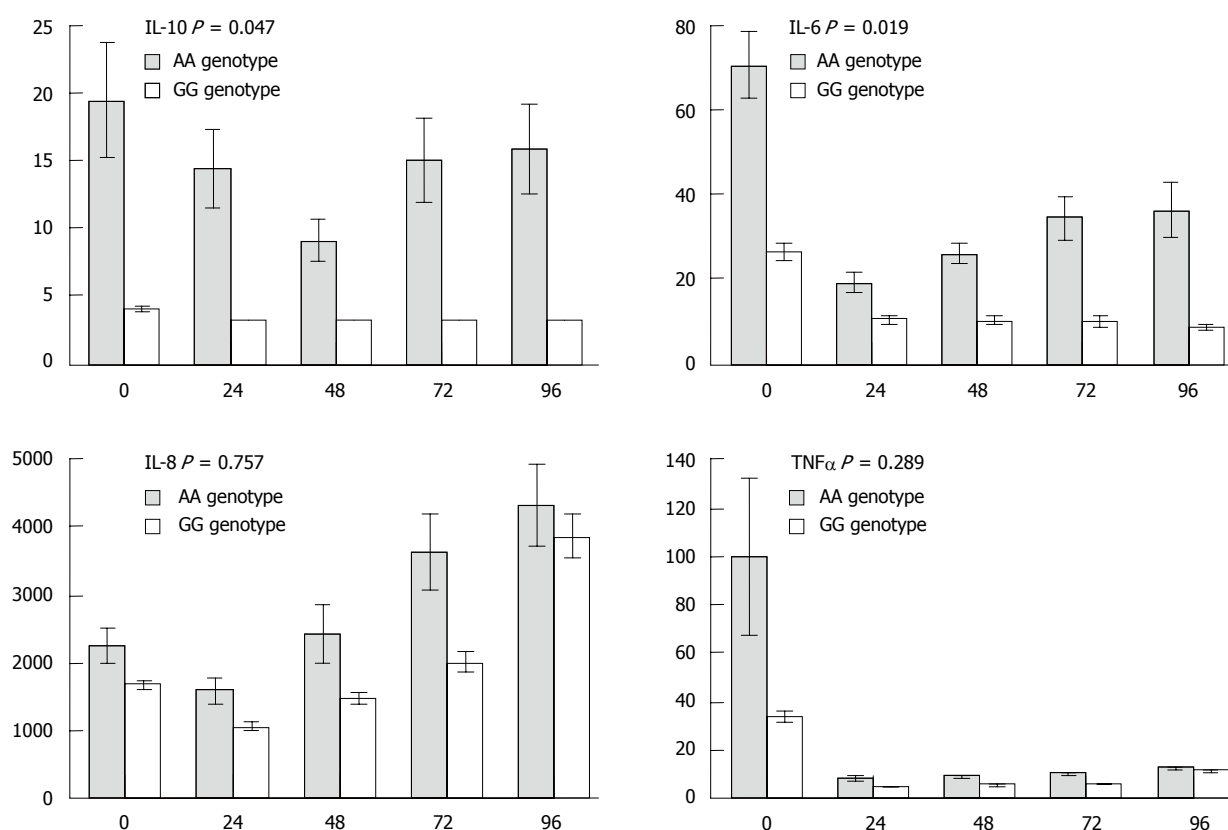


Figure 3 Effect of the *ATG16L1* T300A polymorphism on expression of cytokines following challenge with mycobacterium avium subspecies paratuberculosis. Cytokine concentrations are in pg/mL. Results are the means (and standard error of the mean) of triplicate samples from patients in Table 1. *P*-values are derived from repeated measures ANOVA testing for the effect of genotype on cytokine expression. Fixed effects for time (categorical variable) and *ATG16L1* genotype, random effect for subject. IL: Interleukin; TNF: Tumor necrosis factor.

Effect of *NOD2* genotype

Cytokine expression changes for IL-10, IL-6, IL-8 and TNF α by cells of different *NOD2* genotypes are shown in Figure 4. In general, the presence of a *NOD2* polymorphism resulted in a trend of lower expression of these four cytokines throughout the time-course, compared to monocytes without *NOD2* variants.

However, this effect was not significant, with *P*-values of 0.56, 0.32, 0.41 and 0.97 for cytokines IL-10, IL-6, IL-8 and TNF α , respectively (Figure 4).

DISCUSSION

Numerous genetic association studies have indicated a strong role for *NOD2* and *ATG16L1* in the etiology of CD. However, functional studies have yet to fully elucidate whether, and to what extent, polymorphic variation in these genes affects bacterial clearance and inflammation in CD. Models of gene/environment interaction have mostly used epithelial or monocyte cell lines in vitro with bacterial pathogens such as *Salmonella typhimurium* that are not generally associated with CD. Also, the use of gene silencing or ablation techniques in these models may assist our understanding of the function of these genes, but may not be representative of the effects of SNPs which have been associated with CD. In this study we developed an *ex vivo* cellular model using monocytes from CD patients and a

putative CD pathogen, MAP, in order to assess the effect of SNPs in *NOD2* and *ATG16L1* on bacterial survival and subsequent inflammatory response.

NOD2 is located in the cytoplasm, and plays an important role in cellular responses to bacterial infection^[36] through recognition of muramyl dipeptide (MDP), a sub-unit of bacterial peptidoglycan (PGN)^[37]. Furthermore, the R702W, G908R and 1007fs *NOD2* variants, which confer susceptibility to CD, have been shown to impair responses to the bacterial antigen lipopolysaccharide^[38].

We found the effect of *NOD2* polymorphisms appeared to be primarily on bacterial persistence/growth, with heterozygosity at R702W or 1007fs making monocytes from CD patients significantly more permissive to growth of MAP. Indeed, a recent study has observed that these variants are associated with an impairment of monocyte phagocytosis and the development of bacteremia in intensive care unit patients^[39]. Despite the increased bacterial load, no differences were seen in subsequent cytokine responses for the different host *NOD2* genotypes. Whilst there has been no prior published research with respect to MAP in this type of model of CD, the functional effects of *NOD2* SNPs have been examined for adherent invasive *E. coli* (AIEC). No differences were found in the persistence or growth of AIEC in monocytes from patients who were heterozygous or homozygous for the minor allele of *NOD2* variants R702W, G908R and 1007fs compared to

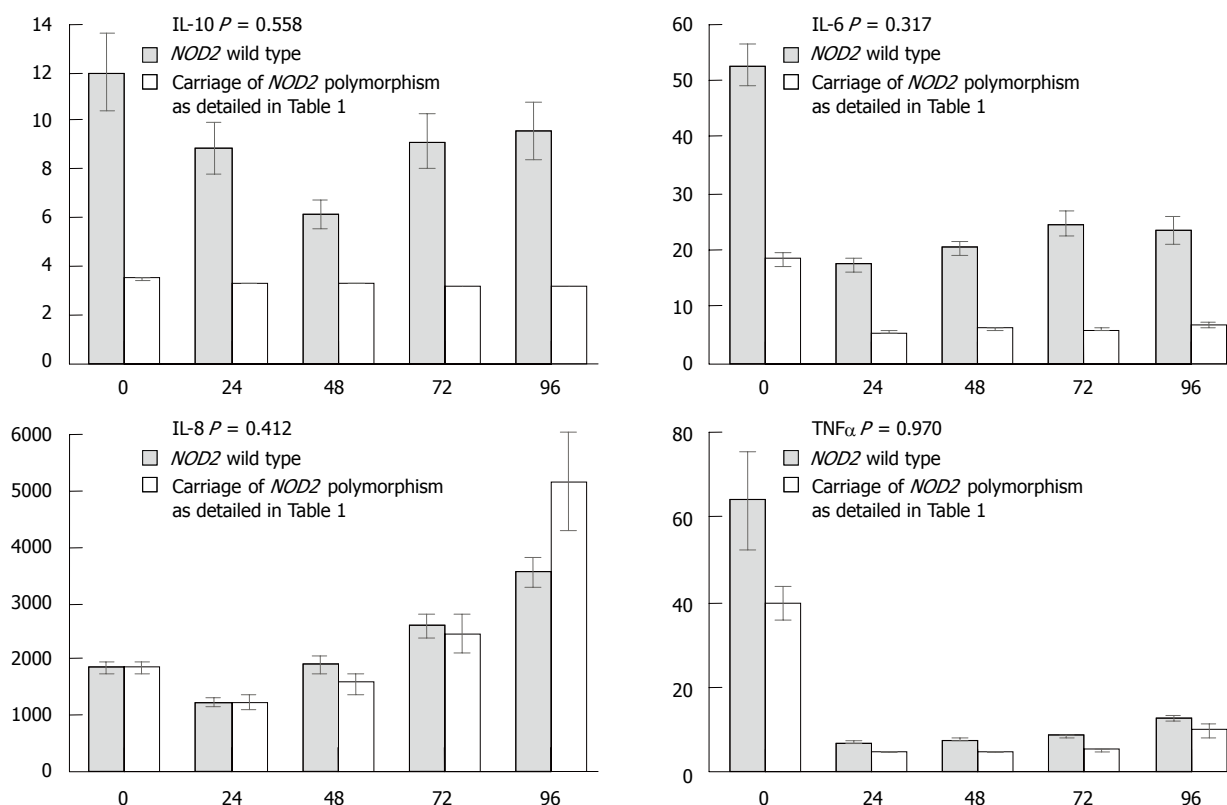


Figure 4 Effect of *NOD2* polymorphisms on expression of cytokines following challenge with mycobacterium avium subspecies paratuberculosis. Cytokine concentrations are in pg/mL. Results are the means (and standard error of the mean) of triplicate samples from patients in Table 1. *P*-values are derived from repeated measures ANOVA testing for the effect of genotype on cytokine expression. Fixed effects for time (categorical variable) and *NOD2* genotype, random effect for subject. IL: Interleukin; TNF: Tumor necrosis factor.

NOD2 major allele homozygotes^[40]. It has also been shown that in peripheral blood mononuclear cells from CD patients, homozygosity for R702W does not affect the cytokine response to Gram-negative (*Helicobacter pylori*) bacterial peptidoglycan^[41], although homozygosity for the 1007 fs mutation did. In our study we recruited no 1007fs homozygotes and only a single 1007 fs heterozygote so were unable to make any direct comparisons with this previous study. Comparative studies for a broader range of bacterial species in *ex vivo* cells from patients who are homozygous for these *NOD2* SNPs will help clarify the role of this genotype in disease pathogenesis.

Both MAP and AIEC are capable of intracellular survival and growth in monocytes and macrophages, and it appears that the presence of *NOD2* polymorphisms may influence their respective intracellular survival and growth in different ways^[42].

Autophagy has been identified as a mechanism for clearing intracellular pathogens, and two autophagy genes, *ATG16L1* and *IRGM*, have been associated with CD^[25,27]. In our study, we investigated the effect of the *ATG16L1* T300A polymorphism, and controlled for genotypic variation in *IRGM* (Table 1). *ATG16L1* T300A (rs2241880; 1138G > A) is a common non-synonymous SNP where the G major allele confers greater disease risk and results in a threonine-to-alanine substitution at amino acid position 300 of the *ATG16L1* protein (T300A). This SNP appears to account for all of the disease risk conferred by

this locus^[43], and functionally, this polymorphism has been proposed to contribute to defective macrophage killing of bacteria^[44]. This assertion is supported by the results of two *in vitro* studies. Kuballa *et al.*^[45] found that the T300A variant impaired handling and autophagy of *Salmonella* within human epithelial cells, and Lapaquette *et al.*^[46] showed that siRNA knockdown of *ATG16L1* led to loss of autophagy of intracellular AIEC bacteria by HeLa cells. Transfection of affected HeLa cells with wild-type *ATG16L1* restored autophagic function, whereas transfection with the T300A polymorphic form did not. In contrast, *ATG16L1* T300A had no effect on the survival of either *S. typhimurium* or group A *Streptococcus* in mouse embryonic fibroblasts^[47]. Although direct comparison of different model systems is complex and potentially misleading, our results with MAP in *ex vivo* monocytes generate the question as to whether the T300A polymorphism of *ATG16L1* affects autophagic clearance of certain intracellular bacteria as profoundly as indicated by knockdown or silencing models of gene function.

In our study, the T300A polymorphism was associated with significant changes in production of the cytokines IL-6 and IL-10 in response to bacterial challenge with MAP. These two cytokines are components of the Th1 (pro-inflammatory) and Th2 (modulatory) pathways of inflammation, respectively, and it is likely that CD results from an imbalance between these two pathways. It is tempting to speculate that the relative levels of the two

cytokines that were induced are indicative of an imbalance, but extrapolating from a very specific model to describe a complex disease state would be misleading and clearly further comparative work is required in this area in disease-relevant models.

Our study is the first to investigate the effect of *NOD2* and *ATG16L1* genotype on the response of *ex vivo* human monocytes to the putative CD pathogen MAP. Although our results are preliminary and need to be replicated in a larger sample, they provide novel insights into the effect of disease-associated SNPs in innate immunity genes on detection, handling, and elimination of bacteria, and ultimately CD pathogenesis. Our observations indicate that *NOD2* SNPs R702W, P268S, or 1007 fs impair the elimination of MAP yet do not impact on cytokine production. They may, therefore, increase susceptibility to prolonged intracellular bacterial infection. Conversely, the *ATG16L1* T300A polymorphism significantly alters the expression of certain Th1 and Th2 cytokines after MAP challenge, but does not seem to affect the autophagic clearance of this putative CD pathogen.

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COMMENTS

Background

Polymorphisms of the genes *NOD2* and *ATG16L1* have been associated with susceptibility to Crohn's disease (CD). These genes are important for an effective innate immune response against potential bacterial pathogens [such as *Mycobacterium avium* subspecies *paratuberculosis* (MAP)] which may trigger or exacerbate inflammation. Monocytes from CD patients of known genotype were used to determine whether polymorphisms in *NOD2* and *ATG16L1* alter cytokine responses and bacterial survival following challenge with MAP.

Research frontiers

Previous research has investigated the role of polymorphisms in *NOD2* and *ATG16L1* in various model systems. In general, these have used gene silencing strategies that may not realistically reflect the biological consequences of single nucleotide changes in these genes, or model bacterial pathogens that have little relevance to CD. None have reported the functional consequences of the naturally occurring single nucleotide polymorphisms using patient-derived cells and bacteria such as MAP that have been implicated in CD etiology.

Innovations and breakthroughs

The authors' findings indicate that monocytes heterozygous for a *NOD2* polymorphism were more permissive for the intracellular growth of MAP than those without. However, these polymorphisms did not affect subsequent cytokine expression. The T300A polymorphism of *ATG16L1* did not affect growth of MAP in our monocyte model but did result in increased expression of certain cytokines - interleukin (IL)-10 and IL-6.

Applications

By understanding how naturally occurring disease-related polymorphisms of *NOD2* and *ATG16L1* influence bacterial survival and also the production of inflammatory mediators, the authors may gain insight into the contribution of these genetic changes to the function of the host innate immune system. Development of this model system that utilizes patient cells with known single nucleotide changes in key CD-susceptibility genes will provide another research tool to assist better understanding of disease pathogenesis related to bacterial handling.

Terminology

NOD2 (CARD15) - nucleotide oligomerization domain 2 - is a cytosolic pattern recognition receptor that recognizes muramyl dipeptide, a component of bacterial peptidoglycan. Polymorphisms in *NOD2* have been associated with altered susceptibility to CD in many genetic studies. *ATG16L1* - autophagy-related 16-like 1 - is a key component of the autophagic apparatus that is involved with uptake and digestion of intracellular bacteria. The T300A polymorphism of *ATG16L1* has also been associated with altered susceptibility to CD. MAP is an intracellular bacterium that has been cited in several studies as a putative causal agent of CD.

Peer review

This is a very well-designed and well-written study, with interesting and important scientific merit. Not just simple polymorphism descriptions, but their effect on human monocyte cytokine production and intracellular pathogen survival were examined with a very functional methodology. Their *ex vivo* model is much closer to the real pathogenesis of CD than any earlier one. Using the author's concept, more descriptive polymorphism analysis of CD and other diseases may be placed into functional analysis.

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Is the schatzki ring a unique esophageal entity?

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23.4% of the 64 patients who had endoscopic and/or radiological examinations before their first presentation to our clinic, was the SR previously diagnosed. At presentation, the mean ring diameter was 13.9 ± 4.97 mm. One hundred and sixty-two (97%) patients showed a sliding hiatal hernia. Erosive reflux esophagitis was found in 47 (28.1%) patients. Twenty-six (15.6%) of 167 patients showed single or multiple esophageal webs; five (3.0%) patients exhibited eosinophilic esophagitis; and four (2.4%) had esophageal diverticula. Four (7%) of 57 patients undergoing esophageal manometry had non-specific esophageal motility disorders.

CONCLUSION: Schatzki rings are frequently associated with additional esophageal disorders, which support the assumption of a multifactorial etiology. Despite typical symptoms, SRs might be overlooked.

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Key words: Schatzki ring; Dysphagia; Food impaction; Gastroesophageal reflux disease; Esophageal web

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Abstract

AIM: To study, whether the association of Schatzki rings with other esophageal disorders support one of the theories about its etiology.

METHODS: From 1987 until 2007, all patients with newly diagnosed symptomatic Schatzki rings (SRs) were prospectively registered and followed. All of them underwent structured interviews with regards to clinical symptoms, as well as endoscopic and/or radiographic examinations. Endoscopic and radiographic studies determined the presence of an SR and additional morphological abnormalities.

RESULTS: One hundred and sixty-seven patients (125 male, 42 female) with a mean age of 57.1 ± 14.6 years were studied. All patients complained of intermittent dysphagia for solid food and 113 (79.6%) patients had a history of food impaction. Patients experienced symptoms for a mean of 4.7 ± 5.2 years before diagnosis. Only in

INTRODUCTION

Lower esophageal (Schatzki) rings are found in 6%-14% of routine barium radiographs^[1-4]. Even though most Schatzki rings (SRs) are asymptomatic, they are considered to be the most common cause of episodic dysphagia for solids and food impaction in adults^[5,6]. Since their first

description in 1944^[7], the etiology and pathogenesis of the SRs has remained obscure and little is known about their association with other structural and functional abnormalities of the esophagus. Theories about their origin include congenital, anatomical, and inflammatory factors as the most likely events that lead to a circular constriction of the esophagogastric junction^[8-12].

Therefore, the aims of this study were: (1) to investigate whether the lower esophageal (Schatzki) ring is associated with other esophageal disorders; (2) to determine whether dysphagia is due to the presence of SRs or additional esophageal disorders; and (3) to determine whether one of the pathogenic theories could be supported.

MATERIALS AND METHODS

From 1987 until 2007, all patients with newly diagnosed symptomatic SRs were prospectively registered and followed. The diagnosis of SRs was based on the results of radiographic and/or endoscopic studies. In 119 patients, radiographic and endoscopic studies showed an SR. Fourteen patients had only radiographic and 34 only endoscopic studies. All patients underwent structured interviews to assess clinical symptoms.

Evaluation of symptoms

At the initial investigation and at each follow-up visit, structured interviews were performed. Questions concentrated on clinical symptoms such as the occurrence of food impaction, and frequency of dysphagia, heartburn and regurgitation (less than once a week, weekly, daily, or several times a day).

Radiographic studies

Radiographic studies ($n = 133$) were performed by senior staff radiologists using the prone-oblique, full-column technique. To distend the lower esophagus maximally, patients were asked to take a deep breath and to perform a Valsalva maneuver during the course of swallowing. Diagnosis of SR (Figure 1A) was based on the presence of a fixed, symmetric, thin (< 4 mm) structure, which intersected the esophagus perpendicular to its long axis, at the squamocolumnar junction^[6,13]. The diameter of the lower esophageal ring was measured directly from the radiographic picture in the area of the narrowing. An esophageal web is defined as a thin (< 2 mm) eccentric membrane that can occur anywhere in the esophagus^[14]. A sliding hiatal hernia was diagnosed when a pouch was visible between the tubular esophagus and the diaphragmatic narrowing (length of the pouch ≤ 3 cm = small hernia, > 3 cm = large hernia)^[15]. Diagnosis of diverticulum was based on the presence of a pouch in the esophagus (Zenker's diverticulum: pouch in the pharyngoesophageal area; midesophageal diverticulum: pouch in the mid esophagus; epiphrenic diverticulum: pouch just proximal to diaphragm)^[14].

Endoscopic procedures

Upper gastrointestinal endoscopy ($n = 153$) was performed

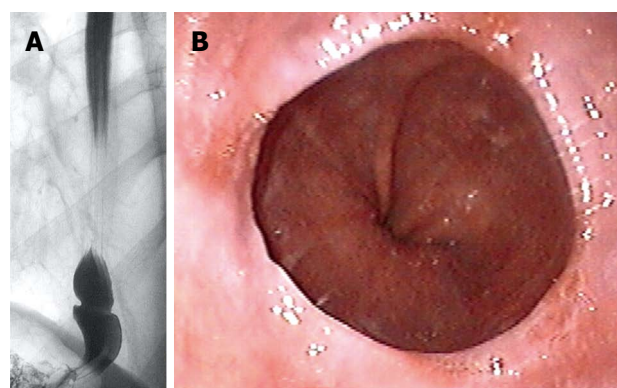


Figure 1 Radiographic (A) and endoscopic (B) image of the lower esophageal (Schatzki) ring.

by senior staff gastroenterologists using a variety of upper gastrointestinal endoscopes (Olympus, Hamburg, Germany), which varied in caliber from 8.5 to 9.5 mm. The endoscopic mucosal appearance determined the presence or absence of esophagitis as well as further morphological abnormalities of the upper gastrointestinal tract. SR (Figure 1B) was defined as a thin, symmetric, mucosal structure located at the esophagogastric junction^[3]. A sliding hiatal hernia was diagnosed when gastric mucosa extended for > 1.5 cm above the diaphragm^[16]. An esophageal web was defined as a thin (no more than 1.5 mm), eccentric membrane, located above the esophagogastric junction^[14]. The degree of esophagitis was classified into four stages according to Savary and Miller^[17]. If there were mucosal alterations in addition to reflux esophagitis, biopsies were taken from the esophagus. The presence of ≥ 20 eosinophils per high-power field in the histopathological examination was used as the criterion to diagnose eosinophilic esophagitis^[18].

Esophageal manometry

To exclude an esophageal motility disorder, 57 patients underwent esophageal manometry. Stationary esophageal manometry was performed with the use of a low-compliance capillary perfusion system (Mui Scientific, Mississauga, ON, Canada), using an eight-channel multi-lumen catheter with a 4.5-mm diameter. The four distal openings were 1 cm apart and the four proximal openings were 5 cm apart. Both sets were radially oriented. The manometric tracings were recorded by a computer polygraph system (Standard Instruments, Karlsruhe, Germany). Manometry was performed using a stationary pull-through method with the catheter introduced transnasally into the stomach. Manometry was carried out and interpreted according to the recommendations of the American Society of Gastroenterology^[19]. Non-specific motor disturbance was defined as contractile abnormalities that are insufficient to establish a diagnosis of achalasia, diffuse esophageal spasm or typical scleroderma-like esophageal dysfunction^[19,20].

Statistical analysis

Numerical variables are expressed as mean $\pm$ SD, counts

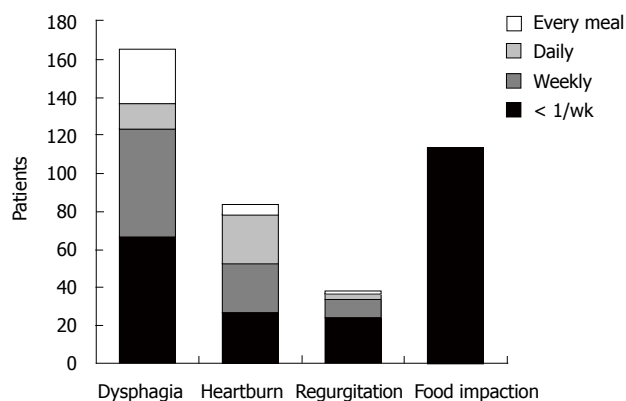


Figure 2 Clinical symptoms of 167 patients with Schatzki rings.

and ranges. Categorical variables are described using frequencies and percentages. Statistical significance of the differences between groups was assessed by Mann-Whitney *U* test for metric variables, by the Mantel-Haenszel χ^2 test for trends for ordered categorical variables and by Pearson χ^2 test for binary variables. A two-tailed *P* value < 0.05 was considered statistically significant. The analysis was performed using SPSS for Windows version 15.0 (SPSS, Chicago, IL, USA).

RESULTS

Demographic data and esophageal imaging at initial investigation

One hundred and sixty-seven patients (124 male, 43 female) with a mean age of 57.1 ± 14.6 years were studied. Patients experienced symptoms for a mean of 4.7 ± 5.2 years before diagnosis. Sixty-four (38.3%) of the 167 patients had endoscopic and/or radiological examinations before their first presentation to our clinic, but only in 15 (23.4%) of these patients was SR was previously diagnosed. In 35 (87.5%) of the 40 patients who received an endoscopic examination, the SR had not been diagnosed, and in 14 (70%) of the 20 patients who underwent radiological examinations, the diagnosis could not be determined.

One hundred and twelve patients received radiological and endoscopic examinations at their initial presentation to our hospital. Endoscopy or a barium swallow accurately diagnosed the SR in all 112 patients in whom both methods were used. In the 34 patients who were only examined by endoscopy, the correct diagnosis was made in all cases, whereas the diagnosis was only made in 14 (66.7%) of the 21 patients who underwent radiological examinations first. In the seven patients without an initial radiological diagnosis, the SR was identified on subsequent endoscopy.

Clinical findings at initial investigation

Clinical symptoms at initial presentation are shown in Figure 2. All patients complained of intermittent dysphagia for solid food: 66 patients (39.5%) less than once per week, 58 (34.7%) weekly, 14 (8.4%) daily, and 29 (16.4%) with every meal. One hundred and thirteen

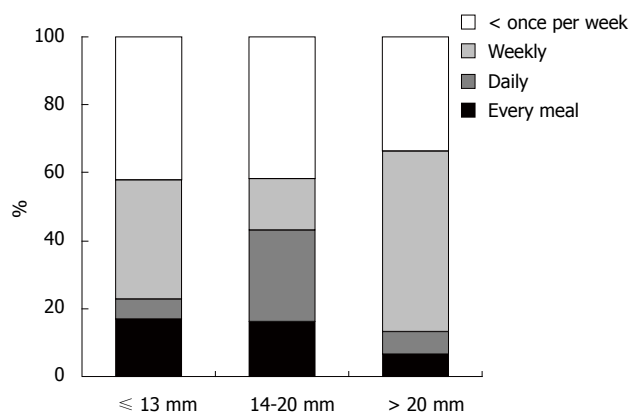


Figure 3 Frequency of dysphagia in relation to the ring size.

Table 1 Demographic data, ring size and clinical symptoms of all patients with Schatzki rings, Schatzki rings and additional erosive esophagitis, and with Schatzki rings and additional esophageal webs (mean $\pm$ SD)

Variables	SR (n = 167)	SR with erosive esophagitis (n = 47 ¹)	SR with esophageal webs (n = 26 ¹)
Age (yr)	57.1 $\pm$ 14.6	58.4 $\pm$ 13.7	54.4 $\pm$ 18.9
Sex (n)			
Male	124	33	18
Female	43	14	8
Ring size (mm)	13.9 $\pm$ 4.97	14.1 $\pm$ 5.3	12.2 $\pm$ 3.8
Dysphagia, n (%)			
Every meal	29 (17.4)	7 (14.9)	8 (30.8)
Daily	14 (8.4)	3 (6.4)	3 (11.5)
Weekly	58 (34.7)	17 (36.2)	6 (23.1)
< 1 x/wk	66 (39.5)	20 (42.6)	9 (34.6)
Food impaction, n (%)	113 (79.6)	34 (72.3)	18 (69.2)
Heartburn, n (%)	86 (57.1)	29 (61.7)	12 (46.1)
Regurgitation, n (%)	40 (23.9)	11 (23.4)	6 (23.1)

¹In two patients, erosive esophagitis as well as esophageal webs could be diagnosed. SR: Schatzki ring.

(79.6%) of the 167 patients had a history of food impaction. Forty (23.9%) patients described regurgitation and 87 (52.1%) complained of occasional heartburn.

The diameter of the lower esophageal ring was evaluated in 126 patients undergoing radiographic studies, and in 27 patients, endoscopic estimation was used with open biopsy forceps (7 mm) being the reference standard. In 14 patients, no measurement was performed. At initial presentation, the mean ring diameter was 13.9 ± 4.97 mm (range: 5-25 mm). Eighty-three (54.2%) of 153 patients had a ring size ≤ 13 mm, and 15 (9.8%) had a ring size > 20 mm. There was no correlation between ring size and frequency of dysphagia ($P = 0.29$, Figure 3). Also, sex ($P = 1.0$) and age ≤ 40 or > 40 years ($P = 0.93$) had no influence on the frequency of dysphagia. Demographic data, ring size and clinical findings of all patients with Schatzki rings are shown in Table 1.

Additional findings and their influence on symptoms

A sliding hiatal hernia was found in 162 (97%) of 167

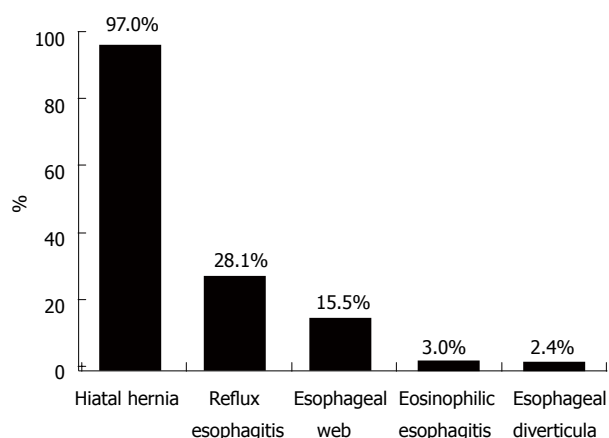


Figure 4 Additional structural abnormalities of the esophagus.

patients ($n = 28$ radiographic examinations, $n = 29$ endoscopic examinations, $n = 105$ radiographic and endoscopic examinations). One hundred and nineteen patients exhibited a small hernia and 43 had a large one. data, ring size and clinical findings of patients with Schatzki rings and additional erosive esophagitis, and /or esophageal webs are demonstrated in Table 1.

Further structural and functional abnormalities of the esophagus were diagnosed in 87 (52%) of 167 patients (Figure 4). The most frequent additional endoscopic finding was erosive reflux esophagitis, which was found in 47 (28.1%) patients; 40 (85.1%) of whom had stage I esophagitis, whereas seven (14.9%) presented with stage II and III, and none with stage IV. All but one patient with reflux esophagitis showed a hiatal hernia. Twenty-six (15.6%) of 167 patients showed single ($n = 15$) or multiple ≥ 2 ($n = 11$) esophageal webs, and four (2.4%) patients had esophageal diverticula. Two of the four patients with esophageal diverticula showed a Zenker's diverticulum, and in two patients, midesophageal diverticula were diagnosed. Four patients exhibited erosive reflux esophagitis in addition to esophageal webs. Five (16.6%) of the 30 patients in whom biopsies of the esophagus were taken exhibited histopathological signs of eosinophilic esophagitis. All but one patient complained of food impaction, whereas the frequency of dysphagia varied in this subgroup of patients (two patients, every meal; one patient, daily; and two patients, less than once per week).

Four (7%) of 57 patients undergoing esophageal manometry showed pathological results (two with non-specific motor disturbance, one with low contraction amplitudes, and one with diffuse esophageal spasm). Patients with an additional motility disorder of the esophagus showed a higher frequency of dysphagia than patients without ($P = 0.03$), although there was no difference in ring diameter (patients with motility disorders, 13.53 ± 3.6 mm; patients without, 13.7 ± 4.1 mm; $P = 0.92$).

The mean ring diameter in patients with additional esophageal webs (12.3 ± 3.8 mm) was smaller than in patients without webs (14.2 ± 5.1 mm) ($P = 0.057$). However, there were no differences in the frequency of dysphagia in patients with further structural abnormalities of

the esophagus (sliding hernia, $P = 0.1$; erosive esophagitis, $P = 0.48$; and esophageal webs, $P = 0.15$) in comparison to the patients with an SR alone.

DISCUSSION

The lower esophageal SR is a common clinical finding and the most common cause of intermittent dysphagia, especially after consumption of solid food^[6,21]. However, little is known about its etiology, its pathogenesis, or its association with other esophageal disorders. In addition, the clinical importance of associated disorders has not been described.

In our study, we were able to show that symptomatic SRs cannot always be diagnosed with a single imaging technique, and that the SR is not a unique entity. It is frequently associated with other esophageal disorders, such as hiatal hernias, reflux esophagitis and esophageal webs. In addition, ring size and most other structural abnormalities do not predict symptoms. In contrast, dysphagia was more common in patients with an additional motility disorder, and food impaction was the most common presentation in patients with eosinophilic esophagitis. Whether the frequent association with hiatal hernias and inflammatory esophagitis plays a pathogenic role remains unclear, but a multifactorial etiology is suspected.

In the present study, we confirmed previous observations that patients with symptomatic SRs complain about episodic dysphagia for solid food (mean duration 4.7 years prior to diagnosis), and more than two-thirds develop food impaction. Despite the typical clinical presentation, there was a significant diagnostic delay. Prior to presentation to our hospital, diagnosis of an SR was made in less than half of symptomatic patients; a surprisingly low number of patients. One of the difficulties in detecting lower esophageal rings might be related to the fact that the radiographic and endoscopic visualization depends on proper distension of the esophagogastric region beyond the caliber of the ring, which is often not accomplished^[22]. This is especially true for wider rings with a luminal diameter > 13 mm^[23]. In such instances, the radiographic examination has been shown to be superior to endoscopy in detecting lower esophageal rings^[24]. In contrast, the present study could show a better diagnostic yield of endoscopy as compared with a barium swallow. This is most likely related to our special attention to membranous structures. Our findings suggest that a second imaging study should be performed in patients with typical clinical presentation if the first study fails to make the diagnosis of SR.

The current investigation showed that SRs are not a unique entity, but associated with additional esophageal disorders in 57% of symptomatic patients. Besides the nearly unanimous association with a hiatal hernia^[2,24], we found a common association with reflux esophagitis and esophageal webs. In addition, esophageal diverticula were occasionally diagnosed. However the presence of additional structural abnormalities of the esophagus did not change the clinical presentation. Dysphagia was not more common in these patients. Even in patients with addition-

al esophageal webs, whose ring diameters were generally smaller, dysphagia was not more common. These findings suggest that the ring diameter alone may not be responsible for the observed symptoms.

In contrast, dysphagia was more frequently observed in patients with non-specific motility disorders, regardless of ring size, which suggests that the motility disorder may be responsible for the symptoms. Therefore, manometry should be considered in patients with wide ring diameters and symptoms of dysphagia. In addition, we found that intermittent bolus obstructions were a very frequent finding in those patients with an additional diagnosis of eosinophilic esophagitis, and clinicians should keep this clinical entity in mind. Therefore, the presence of an SR should not deter the endoscopist from taking esophageal biopsies in a patient in whom eosinophilic esophagitis remains a possibility. In fact, ring-like structures are common in eosinophilic esophagitis, and we became aware of this entity only a decade ago. Although an association of eosinophilic esophagitis and SRs has been previously suggested, it is not known if this is caused by shared clinical and endoscopic findings, or rather a shared pathogenesis^[25,26]. Common clinical features might also explain the frequent coexistence of esophageal webs and eosinophilic esophagitis in our study. However, it is not clear if the additional esophageal disorders occur by chance, or if there is a common pathogenesis. The etiology of SRs remains obscure, and several theories about their etiology and pathogenesis exist. One of these is the developmental theory that holds that the presence of a congenital mucosal ridge at the esophagogastric junction is a rather frequent anatomical phenomenon that could fold in a valve-like fashion to create the ring^[3,8]. Arguing against this, is the fact that the majority of symptomatic individuals were over the age of 40 years in the present and previous studies^[27]. In the so called plication theory, Stiennon has postulated that longitudinal shortening in the presence of a hiatal hernia may lead to folding of redundant esophageal mucosa^[11]. Consistent with this theory is the fact that most of the patients in the present study had a sliding hiatal hernia. However, it still remains unclear why some patients with a hernia develop an SR and others do not. Therefore, the plication theory is unlikely to be the only cause for the development of SRs. Currently, the inflammation theory with gastroesophageal reflux as the main cause of inflammation, is the most popular theory^[28], and consequently, some authors have recommended an antireflux regimen to prevent symptomatic recurrence^[29,30]. Others have pointed out that, if less than two-thirds of patients are found to have pathological gastroesophageal reflux^[31,32], it might not be the main pathogenic factor. Similar to the latter findings, even if reflux esophagitis were one of the most frequent associated esophageal disorders in the present study, less than one-third of all investigated patients showed endoscopic signs of erosive esophagitis, and only half complained of occasional heartburn, which suggests that gastroesophageal reflux is not the only cause for the development and narrowing of the SR. Therefore, we assume that the etiology of SR is multifactorial.

In conclusion, SRs might be overlooked in endoscopic and/or radiological examinations. Therefore, in patients with a typical clinical presentation, a second diagnostic imaging should be considered. Other esophageal disorders are frequently observed and should be kept in mind; most of which do not alter clinical presentation. Non-specific motility disorders and eosinophilic esophagitis should be considered, especially when frequent dysphagia or food impaction is present. With regard to the etiology of SRs, the present findings suggest a multifactorial genesis, which supports the inflammation theory as well as the plication theory.

COMMENTS

Background

The Schatzki ring (SR) is the most common cause of episodic dysphagia to solid food. Nevertheless its etiology and pathogenesis remains unknown and little is known about its association with other structural and functional abnormalities of the esophagus. Theories regarding its origin include inflammatory, developmental, and congenital factors as the most likely events leading to a circular constriction of the esophagogastric junction. In addition, the clinical importance of associated disorders has not been described.

Research frontiers

Currently, the 'inflammation theory' with gastroesophageal reflux disease (GERD) as the main cause of inflammation, is the most popular theory. However, prospective studies have documented an association with GERD in less than two thirds of patients, suggesting that additional pathogenic factors might be responsible for the development of the SR.

Innovations and breakthroughs

It is known that SRs are associated with hiatal hernias and reflux esophagitis, whereas this is the first study that could show the frequent association of SRs with additional esophageal disorders, most of which do not alter clinical presentation. Nonspecific motility disorders and eosinophilic esophagitis should be considered, especially when frequent dysphagia or food impactions are present, respectively. In regards to the etiology of SRs the present findings suggest a multifactorial pathogenesis. Furthermore, despite the typical clinical presentation SRs might be overlooked in endoscopic and/or radiological examinations.

Applications

SRs are frequently associated with other esophageal disorders. These should be sought, especially when frequent dysphagia or food impaction is the presenting symptom. SRs might be overlooked on radiographic or endoscopic examinations, therefore, a second diagnostic modality should be used when suspicion remains high.

Terminology

"Stiennon's plication theory", postulated that longitudinal shortening in the presence of an hiatal hernia may lead to folding of a redundant esophageal mucosa, creating the SR.

Peer review

The manuscript reads very well and flows nicely. The conclusions are supported by the data and the limitations are well addressed. In addition, the study is novel and the topic chosen is original.

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Factors influencing lower esophageal sphincter relaxation after deglutition

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CONCLUSION: LES relaxation seemed to be caused by the peristaltic wave pushing the bolus from behind against the LES gate.

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Key words: Deglutition; Lower esophageal sphincter; Peristalsis; Relaxation; Upper esophageal sphincter

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Abstract

AIM: To study the relationship between upper esophageal sphincter (UES) relaxation, peristaltic pressure and lower esophageal sphincter (LES) relaxation following deglutition in non-dysphagic subjects.

METHODS: Ten non-dysphagic adult subjects had a high-resolution manometry probe passed transnasally and positioned to cover the UES, the esophageal body and the LES. Ten water swallows in each subject were analyzed for time lag between UES relaxation and LES relaxation, LES pressure at time of UES relaxation, duration of LES relaxation, the distance between the transition level (TL) and the LES, time in seconds that the peristaltic wave was before (negative value) or after the TL when the LES became relaxed, and the maximal peristaltic pressure in the body of the esophagus.

RESULTS: Relaxation of the LES occurred on average 3.5 s after the bolus had passed the UES and in most cases when the peristaltic wave front had reached the TL. The LES remained relaxed until the peristaltic wave faded away above the LES.

INTRODUCTION

Swallowing dysfunction with esophageal food retention is a common problem in an adult population with hiatus hernia. Most articles reporting lower esophageal sphincter (LES) studies depict LES relaxation caused by neurogenic mechanisms^[1] in gastroesophageal reflux (GER). The ability of the LES to allow esophagogastric transit after deglutition has received little attention. Efforts have been made to prove that LES relaxation is triggered by a neurogenic reflex following deglutition^[2], that the LES and the upper esophageal sphincter (UES) relaxations are simultaneous events and that the cervical portion of the vagus nerve mediates inhibitory and excitatory changes in LES pressure^[3]. In a recent study, a biodynamic approach was proposed for LES opening when GER takes place in hiatal hernia and the gastric wall tension pulls open the LES^[4]. As long ago as 1978^[5], LES was suggested to be a biodynamic gate which is forced to open when a bolus is propelled by esophageal peristalsis. We decided to further

challenge the idea of LES as an esophagogastric pressure zone dependent on complex neuro-humoral factors.

The recent development of high-resolution solid-state manometry (HRM) systems with closely spaced circumferential pressure sensors has made it possible to display simultaneous recordings along the entire esophagus in color-coded pressure plots (Figure 1) and has dramatically improved the diagnostic assessment of esophageal function and disease. With conventional esophageal manometry, simultaneous events in the UES and LES have been difficult to display especially since deglutition often will displace the pressure sensors due to shortening of the esophagus. The HRM technique enables, therefore, a unique possibility to study UES and LES pressure during the entire deglutition period and independent of any sphincter dislocation. In order to find out if there is an interplay between pulling forces and LES opening, the aim was therefore to study the relationship between UES relaxation, peristaltic pressure and LES relaxation following deglutition using the HRM technique.

MATERIALS AND METHODS

The HRM system (ManoScan 360 A-100, ManoView analysis software ver. 2.0.1 from Sierra Scientific Instruments Inc., Los Angeles, CA) uses a solid state catheter (Ø 4.2 mm) with closely spaced circumferential pressure sensors with 1 cm intervals over 36 cm. The HRM catheter was passed transnasally and positioned to be recording simultaneously from the hypopharynx, through the body of the esophagus, to the stomach. The catheter was calibrated outside the patient before and immediately after the investigation using the thermal compensation option in the software.

We performed a prospective HRM study in 10 adult patients (median age 45 years, range 38–63 years; 7 women, 3 men) who were admitted to an esophageal laboratory for suspected dyspepsia. It can be claimed that our patients with dyspepsia are not representative for studies of normal LES and UES function. Dyspepsia is a diagnosis without organic lesion and with diffuse symptoms predominantly in the gastric region. The patients did not have any symptoms of dysphagia and reflux, they were free of medication, and the presence of hiatus hernia was excluded at gastroscopy and HRM. It is therefore regarded that confounding factors have been excluded in the study material.

The investigation comprised ten swallows of a 10 mL water bolus in a supine position. The characteristics analyzed were: (1) the time lag between UES relaxation and LES relaxation; (2) the LES pressure at time of UES relaxation; (3) the duration of LES relaxation; (4) the length of the esophagus between UES and LES; (5) the distance between the transition level (TL) and the LES; (6) time in seconds that the peristaltic front wave was before (negative value) the TL or after the TL when the LES pressure dropped to nadir; and (7) the maximal peristaltic pressure in the esophagus. The eight best readable swallow recordings in each subject (a total of 78 swallows) were calculated upon, and the mean values of each individual item are given.

TL is defined as an esophageal zone with striated-to-smooth muscle fiber transition^[6] showing as a short loss of peristaltic pressure (Figure 1).

RESULTS

Individual values and the mean of all values are presented in Table 1. The LES relaxed on average 3.5 s after the UES had opened. The mean LES pressure was 26 mmHg at time of UES opening. The mean duration of LES remaining relaxed was 6.7 s. The mean length of the esophagus between UES and LES was 26 cm. The mean distance between the TL and the LES was 18 cm, corresponding to on average 72% of the total length. The mean time that the peristaltic wave was before (negative value) the TL or after the TL when the LES opened was -0.5 s. The mean maximum pressure of the peristaltic wave was 138 mmHg. The time lag between UES and LES relaxation was never over 6.4 s. The individual LES pressure, as well as the maximum peristaltic pressure, varied remarkably from swallow to swallow (Table 1).

DISCUSSION

This study shows quite clearly that the LES becomes relaxed several seconds (on average 3.5 s) after the water bolus has passed the UES. This corresponds with findings by Nguyen *et al.*^[7] when impedance and manometry techniques were used. They found a mean latency between bolus entry into the esophagus and LES relaxation of 3.6 s. This is also in agreement with the esophageal transit time (3.8 s) as assessed with the biomagnetic technique^[8]. The LES pressure did not change in our study at time of UES opening. Therefore, it seems unlikely that LES relaxation is triggered by the start of deglutition.

It seems as if opening of the LES coincides with the peristaltic wave front reaching close to the TL, which is an esophageal level with striated-to-smooth muscle fiber transition. Reasonably, this depends on the premise that the distal end of the water bolus has reached the LES, that the water bolus fills up the esophageal lumen between TL and LES, and that the peristaltic wave pushes the water bolus from behind against the LES gate. Only the combination of manometry and impedance measurement or the combination of HRM and radiography can find out whether LES relaxation and opening take place at the moment when the bolus arrives at the LES. In an impedance study of LES opening and bolus transit, it was found that LES relaxation seemed to be modulated by the bolus transit and occurred predominantly upon arrival of the bolus in the distal esophagus^[7]. This discovery clashes with the findings by Pandolfino *et al.*^[9] who used a combined impedance/manometry technique. They showed that LES relaxation did not necessary coincide with bolus passage or LES opening. The hydrostatic pressure in the esophageal body necessary to open the LES in an upright position, as shown in a combined manometric and radiographic study from 1978^[5], was approximately the same as the LES pressure before opening. If no deglutition activ-

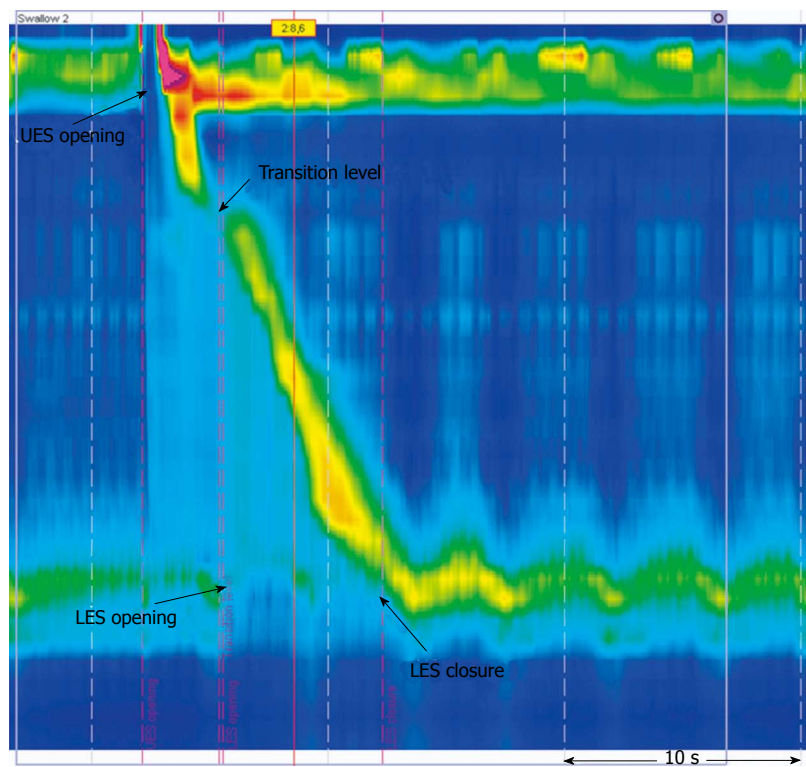


Figure 1 An high-resolution solid-state manometry recorded swallowing event. Transition level = TL, LES relaxation = LES opening to LES closure. Red $\geq$ 60 mmHg. Blue $\leq$ 0 mmHg. LES fluctuations represent respiration, upwards expiration, downwards inspiration. UES: Upper esophageal sphincter; LES: Lower esophageal sphincter.

Table 1 Different esophageal events in ten subjects											
Event	F1	F2	M3	F4	F5	F6	M7	M8	F9	F10	All 10 subjects; mean: ranges
(A) s	2.6	5.2	5.0	3.6	3.8	3.2	3.6	1.7	3.0	3.5	3.5: 1.7-5.2
(B) mmHg	21	19	20	32	13	24	23	52	29	29	26: 13-52
(C) s	5.1	4.2	4.2	6.7	5.5	7.7	10.3	8.5	7.7	7.5	6.7: 4.2-10.3
(D) cm	25	26	28	25	29	23	26	26	22	26	26: 22-29
(E) cm	16	17	20	18	20	17	19	20	16	18	18: 16-20
(F) s	-1.4	0.7	0.9	0.3	0.5	-0.2	-1.4	-2.0	-1.6	-0.3	-0.5: -2.0-0.9
(G) mmHg	109	121	123	71	102	232	187	169	152	116	138: 71-232

Different esophageal events, mean values of ten recordings in ten subjects, and mean values of all ten subjects. A: Time lag between relaxing of UES and LES; B: LES pressure when UES opened; C: Duration of LES remaining relaxed; D: Esophagus length; E: Distance between TL and LES; F: Time in seconds that the peristaltic wave was before (minus value) or after the TL when the LES relaxed; G: maximum pressure of the peristaltic wave. F: Female; M: Male. UES: Upper esophageal sphincter; LES: Lower esophageal sphincter; TL: Transition level defined as the zone when the striated muscle layer transitions into the smooth muscle layer.

ity took place and a contrast medium was instilled into the esophagus, the LES opened when the hydrostatic pressure exceeded the resting LES pressure and closed again when the hydrostatic pressure in an upright position fell short of the LES pressure. Deglution caused the LES to relax and open when the peristaltic wave reached the upper level of the infused contrast medium. These different findings indicate that the LES is a barrier which is forced to open by the peristaltic pressure. In the clinic, this would explain why, for instance, patients with achalasia cardia or with lack of esophageal peristalsis do not have any LES relaxation after deglution.

If we look upon the LES as a gate that will be pulled open, it is of interest to compare the pressure of the LES

and the maximum pressure of the peristaltic wave in the distal esophagus. In this study, the peristaltic pressure was five times stronger than the LES pressure. HRM and conventional manometry are claimed to be the same in their measurement of LES resting pressure^[10]. It has been shown that the longitudinal esophageal muscle is contracted during the peristaltic activity^[11] which will decrease esophageal wall compliance. Certainly, the peristaltic force displays an interaction between the longitudinal and circular esophageal muscles^[12], and a compliance decrease of the esophageal wall will facilitate bolus transit. The reason for the deglution-induced pressure overload in the esophageal body is therefore of importance, in order to overcome the stiffness of the esophageal wall. In the study by Babaei *et al*^[12], it was

even proposed that the longitudinal esophageal smooth muscle has an important role in the relaxation of LES. In our study, the LES remained relaxed as long as the peristaltic wave was present in the esophagus. This indicates that there is a close interplay between LES function and peristaltic activity. It is reasonable to believe that the LES will be pulled open when the pulling direction is either from the esophagus or from the stomach^[12].

In conclusion, LES opening seems to be caused by the peristaltic wave pushing the bolus from behind against the LES gate. Therapeutic attention in patients with dysphagia of non-stricture origin should therefore be focused on esophageal motility function rather than on drugs affecting LES pressure.

COMMENTS

Background

Swallowing problems with food retention in the gullet are present in at least 8% of an adult population. For accurate treatment, it is of importance to know whether transit from the esophagus to the stomach can be treated with drugs aimed at opening the lower esophageal sphincter (LES) or whether transit is due to dynamic properties of gullet muscles. So far, it has been claimed that LES is triggered to open by a neurogenic reflex from the upper esophageal sphincter (UES).

Research frontiers

The newly developed high-resolution manometry (HRM) system is a technical innovation and breakthrough for the understanding of dynamic esophageal events, meaning the interplay between esophageal motility and esophageal sphincter relaxations.

Innovations and breakthroughs

The esophageal HRM probe was used in ten non-dysphagic patients with dyspepsia in order to study the time relationship between UES and LES relaxation and to study where the peristaltic wave front was located when the LES relaxed after deglutition of a 10 mL water bolus in the supine position. These simultaneous activities have previously not been possible to study with conventional esophageal manometry.

Applications

The LES was shown to relax 3.5 s later than the UES after deglutition which is the average time it takes a water bolus front to reach the LES. The LES remained relaxed on average 6.8 s; that is until the propulsive force had faded away. The peristaltic front wave reached a level close to the transition level (TL), either 2 s before or 1 s after the TL.

Terminology

Esophagus-gullet. Dyspepsia-a diagnosis without any specified organic lesion and with diffuse symptoms from the gastric region. Dysphagia-swallowing difficulties. HRM-a pressure catheter with a 36 cm long segment of sensors spaced 1 cm apart giving simultaneous pressure information of sphincter and muscular activity from a total of 432 locations from UES to LES. The pressure can be displayed as a color plot offering visual information of the esophagus and its sphincters very similar to an anatomic picture. LES-lower esophageal sphincter. Manometry-pressure measurement. Smooth muscle-a muscle under autonomic, non-volitional control. Striated muscle-a muscle under volitional control. TL, transition level-the

level in the esophagus between the upper striated muscle level and the lower smooth muscle level which is located about 7 cm distal of the UES.

Peer review

More emphasis on why HRM is a great technique and the knowledge it provides compared to conventional esophageal manometry has now been given in the Methods section. The reason why we believe that dyspepsia patients can be regarded as normal people with regard to esophageal transit studies is addressed in the Materials section. The previous conclusion, regarding older theories of a neurogenic reflex causing LES relaxation, has been omitted and basic data for this are given in the discussion.

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Effects of sargentgloryvine stem extracts on HepG-2 cells *in vitro* and *in vivo*

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RESULTS: SSE treatment could not only inhibit HepG-2 cell proliferation in a dose- and time-dependent manner but also induce apoptosis and cell cycle arrest at the S phase. The number of colonies formed by SSE-treated tumor cells was fewer than that of the controls ($P < 0.05$). SSE induced caspase-dependent apoptosis accompanied by a significant decrease in Bcl-xl and Mcl-1 and elevation of Bak expression ($P < 0.05$). Tumor necrosis factor α in the xenograft tumor tissue and the liver functions of SSE-treated mice showed no significant changes at week 8 compared with the control group ($P > 0.05$). Systemic administration of SSE could inhibit the HepG-2 xenograft tumor growth with no obvious toxic side effects on normal tissues.

CONCLUSION: SSE can induce apoptosis of HepG-2 cells *in vitro* and *in vivo* through decreasing expression of Bcl-xl and Mcl-1 and increasing expression of Bax.

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Key words: Sargentgloryvine stem extract; Apoptosis; Human hepatocellular carcinoma; HepG-2; *Bcl-2* family

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Wang MH, Long M, Zhu BY, Yang SH, Ren JH, Zhang HZ. Effects of sargentgloryvine stem extracts on HepG-2 cells *in vitro* and *in vivo*. *World J Gastroenterol* 2011; 17(23): 2848-2854 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v17/i23/2848.htm> DOI: <http://dx.doi.org/10.3748/wjg.v17.i23.2848>

Abstract

AIM: To observe the effects of sargentgloryvine stem extracts (SSE) on the hepatoma cell line HepG-2 *in vitro* and *in vivo* and determine its mechanisms of action.

METHODS: Cultured HepG-2 cells treated with SSE were analysed by 3-(4,5-Dimethyl-thiazol-2-yl)-2,5-Diphenyltetrazolium bromide and clone formation assay. The cell cycle and apoptosis analysis were conducted by flow cytometric, TdT-Mediated dUTP Nick End Labeling and acridine orange/ethidium bromide staining methods, and protein expression was examined by both reverse transcriptase-polymerase chain reaction and Western blotting. The pathological changes of the tumor cells were observed by haematoxylin and eosin staining. Tumor growth inhibition and side effects were determined in a xenograft mouse model.

INTRODUCTION

Although significant progress has been made over the past decades in cancer prevention and treatment, the development of effective treatment regimens remains one of the greatest challenges in the area of cancer che-

motherapy. Recently, plant-derived natural products are becoming important as anti-cancer derivatives, including vincristine, vinblastine, paclitaxel and camptothecin, which are invaluable contributions of nature to modern medicine^[1-4]. However, the quest to find novel therapeutic compounds for cancer treatment is a never-ending venture, and diverse plant species are being studied to identify prospective anti-cancer agents^[5,6]. Sargentgloryvine stem of *Sargentodoxa cuneata* (Oliv.) has been widely used as an ingredient in Chinese medicine according to the Chinese herbal medicine principles for thousands of years in the treatment of several kinds of diseases, such as chronic pelvic cavity inflammation, rheumatism and appendicitis. Sargentgloryvine stem extract (SSE) as a chemotherapeutic adjuvant can enhance the efficacy and ameliorate the side effects of cancer chemo- or radio-therapy. Because SSE has been used in Chinese herbal medicine as a bioactive constituent in a complex herbal mixture, an important question is whether its biological activity can be largely or exclusively ascribed to one or more individual compounds present in this herb. To address this question, we prepared SSE and studied its effects. Our previous research showed that SSE possesses potent anticancer activities^[7]. However, the molecular mechanisms underlying the anticancer effects of SSE are poorly understood and need to be elucidated. To identify potential anticancer mechanisms of SSE in human hepatocellular carcinoma (HCC), the molecular effects of SSE on HepG-2 cells were examined. Down-regulation of the two anti-apoptotic Bcl-2 family proteins Bcl-xl and Mcl-1 may be responsible for antiproliferative and cell apoptotic effects of SSE on HepG-2 cells. Meanwhile, HepG-2 xenograft nude mice treated systemically with SSE were also monitored in tumor growth inhibition and toxicity *in vivo*. The purpose of this study was to observe the effects of SSE on the hepatoma cell line HepG-2 *in vitro* and *in vivo*, and preliminarily analyse its mechanisms of action.

MATERIALS AND METHODS

Materials

SSE was extracted from 10 g dried powder of *Sargentgloryvine* stem in a rotary shaker with 200 mL of 50 mL/L ethanol at 60°C for 24 h. The extract was then filtered, concentrated using a rotary evaporator to remove the solvent, and finally lyophilised in a freeze-dryer to obtain crude freeze-dried powder. The same batch of SSE was used in all studies in order to keep the results reliable. The powder was dissolved in DMEM culture medium at a stock solution of 5 g/L for further use. The hepatoma cell line HepG-2 was preserved in our laboratory. Specific pathogen-free male athymic BALB/c nude mice of 6-7 wk of age with a body mass of 20-30 g were purchased from the Animal Experimental Centre of the Fourth Military Medical University. HepG-2 cells were cultured in DMEM supplemented with 100 mL/L foetal calf serum, 100 kU/L penicillin, 0.1 g/L streptomycin and 250 µg/L amphotericin B, incubated at 37°C in a humidified atmosphere of

50 mL/L carbon dioxide. The primers for PT-PCR detection of transcript are described in Table 1.

Methods

Cell viability and clone formation assay: HepG-2 and ECV304 cells (control cells) were cultured in 96-well plates at a density of 3×10^8 cells/L with 100 µL per well in DMEM. Cells were treated with 1.5, 15, 45, 60 and 90 mg/L SSE for 6, 12, 24, 36 and 48 h or medium only as a control (DMEM-treated) group. After incubation, cell proliferation was detected by 3-(4,5-dimethyl-thiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay, and cytotoxicity was studied with a commercial assay kit (Beyotime Biotechnology, China) following the manufacturer's instructions. Absorbance was measured at 570 nm using the Bio-Rad 550 microplate reader. The protracted cell growth curves and the inhibition of cell growth were calculated based on the absorbance (*A*) value as follows: inhibitory rate = $(1 - A_{\text{treated}} / A_{\text{control group}}) \times 100\%$. For the colony formation assay, a total of 3×10^2 HepG-2 and control cells, and ECV304 tumor cells were plated in 75 mm culture dishes and treated with SSE at a concentration of 30 mg/L. After incubation for an additional 10-14 d, the cells were fixed with methanol and stained with 1 g/L crystal violet (Sigma, USA), and colonies of > 50 cells were manually counted. All experiments were performed in independent triplicates.

Cell apoptosis and cycle analysis: For apoptosis, HepG-2 cells and ECV304 cells were treated with SSE at concentrations of 15, 30 or 60 mg/L, or no drug as a control for 24 h. The cells were harvested and washed twice with cold PBS and resuspended in binding buffer. FITC-labelled annexin V and propidium iodide (PI) were added and incubated for 10 min at room temperature, and the cell suspensions were immediately analysed by flow cytometry. For cell cycle detection, the cells treated with 45 mg/L SSE for 24 h were fixed with 700 mL/L cold ethanol and resuspended in phosphate-buffered saline containing 20 mg/L PI and then analysed for PI fluorescence intensity by flow cytometry to measure the cellular DNA content. The HepG-2 cells were suspended in 75 mm plates and treated with SSE at a concentration of 45 mg/L for 24 h or an equal volume of culture medium as the control. The total volume of each well was one mL. The cells were collected, and a TdT-Mediated dUTP Nick End Labeling assay (Keygen Biotech Co., Ltd., Nanjing, China) was performed as suggested by the manufacturer to detect the incorporation of labelled nucleotides into DNA. At least 300 cells were counted under a light microscope, and apoptotic cells were identified. All experiments were performed in triplicate. The negative control cells were set up with no TdT enzyme added, and positive control cells were pretreated with DNase during the staining process.

Apoptosis quantification and Δψ_m detection: HepG-2 cells were cultured in 6-well plates and treated with SSE at a concentration of 45 mg/L for 24 h. Acridine orange/ethidium bromide staining was performed following the

Table 1 The primers for detection of transcript

Gene	Sense sequence 5'-3'	Antisense sequence 5'-3'
<i>β-actin</i>	GACTTAGTTGCGTTACACCTTTC	TGCTGTACACCTTCACCGTTC
<i>Bax</i>	ATGGACGGGTCCGGGGAG	TCAGCCCATCTTCTCCAGAT
<i>Bak</i>	ATGGCTTCGGGGCAAGGC	TCATGATTGAAGAATCTTCGTACC
<i>Bal-2</i>	ATGGCGCACGCTGGGAGAACG	GTACTCAGTCATCCACAGGGC
<i>Bcl-xl</i>	ATGTCTCAGAGCAACCGGGAGCT	TCATTTCGACTGAAGAGTGAGC
<i>Mcl-1</i>	TGCCGCTGCTGGAGTTGGT	TTACAGTAAGGCTATCTTATTAGAT
<i>Bcl-w</i>	CTCTGGTGGCAGACTTTGTAG	CCGTCCCCGTATAGAGCTGTGA
<i>Bcl-b</i>	ATGGCCGACTCGCAGGACCCA	TTATAAACGTTTCCATATAAAA
<i>Blf-1</i>	ATGAGTGATCCAGAAACCAG	TTAATCCTCTTCTGAACCTTCA

manufacturer's instructions (Keygen Biotech Co., Ltd., Nanjing, China). Acridine orange is a vital dye and can stain both live and dead cells. Ethidium bromide can only stain the cells that have lost membrane integrity. Live cells appear uniformly green, while early apoptotic cells stain green but contain bright green dots in the nuclei as a consequence of chromatin condensation and nuclear fragmentation. Late apoptotic cells incorporate more ethidium bromides and therefore stain orange and show condensed and often fragmented nuclei. At least 300 cells were counted under a fluorescence microscope to quantify apoptosis. All experiments were performed independently in triplicate. Additionally, HepG-2 cells were harvested following treatment with SSE at 45 mg/L for 12 and 24 h. After washing twice with PBS, 1×10^6 cells were incubated with 10 mg/L of Rh123 (Sigma, USA), a cationic lipophilic fluorochrome that is taken up by mitochondria in proportion to the $\Delta\psi_m$, for 30 min at 37°C. Fluorescence intensities were determined by flow cytometry (Becton Dickinson Inc., USA).

Gene expression study: Total RNA from 1×10^6 SSE-treated (45 mg/L for 24 h) HepG-2 cells and control cells were extracted by Trizol™ reagent (Invitrogen, USA), and 1 µg total RNA was used to synthesise cDNA with the superscript first-strand synthesis kit (Takara BioTechnology, Dalian, China) following the manufacturer's instructions. One microliter cDNA was used to amplify the specific genes by reverse transcriptase-polymerase chain reaction (RT-PCR). To normalize cDNA loading, the *β-actin* gene was also amplified from each sample. RT-PCR was performed with the primers listed above. HepG-2 cells treated with SSE (45 mg/L for 24 h) and control cells were harvested by suspension in lysis buffer. The cell extracts were clarified by centrifugation, and the protein concentrations were determined using the Bio-Rad protein assay kit. Each protein extract (25 µg) was electrophoresed on a 100 g/L SDS-polyacrylamide gel, transferred to a membrane and blocked in 50 g/L skimmed milk in tris buffered saline-Tween 20 for 1 h at room temperature. Membranes were probed with anti-Bax, -Bak, -Bcl-xl, -Mcl-1, -caspase-8, -caspase-9, -cytochrome C and -β-actin antibodies overnight at 4°C. Primary antibodies were removed, and the blots were extensively washed with TBS-T three times. Blots were then incubated for 1 h at 37°C with the secondary antibodies in 10 g/L skimmed milk dissolved in TBS-T. After removal of the secondary antibody, blots were extensively washed

and developed using the enhanced chemiluminescence kit in the dark (Santa Cruz Biotechnology). The primary antibodies used in this experiment were monoclonal mouse anti-human Bax, Bcl-xl, Mcl-1, cytochrome C, caspase-8 and -9 (latter two from Abcam, UK) and β-actin and polyclonal goat anti-human Bak (Santa Cruz). Goat anti-mouse and rabbit anti-goat IgG coupled to horseradish peroxidase (Santa Cruz Biotechnology) were used as secondary antibodies for detection of protein expression.

Solid tumor growth assay: Athymic BALB/c nude mice were housed in laminar flow cabinets under specific pathogen-free conditions. All animal studies were performed in compliance with the Institutional Guidelines of the Fourth Military Medical University. Aliquots of 1.0×10^6 HepG-2 cells were suspended 1:1 in PBS and subcutaneously inoculated into the right flank of each mouse. When 300 mm³ tumors were observed, the mice were randomly assigned to two groups ($n = 5$). The mice of the treatment group received 18 mg/kg SSE suspended in 50 µL DMEM, and the mice of the control group were treated with an equal volume of DMEM *via* vena caudalis injection every 2 d for 14 d. The tumor volume was measured each time before SSE administration with callipers using a standard formula as follows: width² × length × 0.5. An average tumor volume per mouse was used to calculate the group mean tumor volume ± SD ($n = 5$). Mice were sacrificed 24 h after the last administration of SSE to harvest the tissues of tumors and the heart, liver, spleen, kidneys and lungs. All tissues were then fixed in 40 g/L paraformaldehyde overnight and sectioned, and haematoxylin and eosin staining was performed to identify the toxicity of SSE *in vivo*. The supernatants of nude mice xenografts were preserved at -70°C. After protein concentration determination, tumor necrosis factor α (TNFα) levels were detected by ELISA in tumor tissues from nude mice according to the manufacturer's instructions. Liver function (aspartate aminotransferase and alanine aminotransferase) and kidney function (creatinine) were also detected.

Statistical analysis

All statistical analyses were performed using SPSS13.0. Data were expressed as mean ± SD. Comparisons among all groups were performed with the one-way ANOVA analysis of variance test. Differences were considered significant at $P < 0.05$.

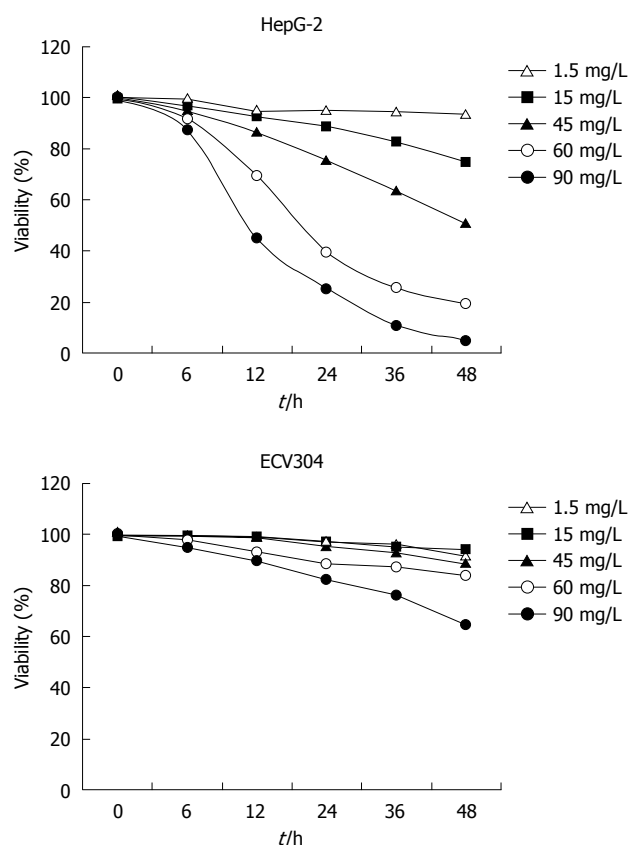


Figure 1 Effects of sargentgloryvine stem extract on HepG-2 viability *in vitro* (MTT assay). HepG-2 and ECV304 cells were treated with sargentgloryvine stem extract (SSE) at five concentrations in five different time points. MTT assay showed that cell proliferation inhibition rates were enhanced with increased SSE concentration and treatment time in HepG-2 cells but not in ECV304 cells. Experiments were repeated in triplicate.

RESULTS

Proliferation and colony formation

SSE-treatment at concentrations of 1.5 and 15 mg/L showed no significant growth inhibition of HepG-2 cells, but higher SSE concentrations of 30, 60 and 90 mg/L significantly inhibited the proliferation of the HepG-2 cells (Figure 1). At an SSE concentration of 30 mg/L, the inhibition rate (mean $\pm$ SD) increased with treatment time; the rates were 5.0 ± 1.4 , 13.7 ± 2.7 , 23.3 ± 6.0 , 34.2 ± 5.3 h and 53.7 ± 3 at 6, 12, 24, 36 and 48 h, respectively ($P < 0.05$). All concentrations showed no obvious growth inhibition on ECV304 cells. Additionally, the number of colonies of SSE treated HepG-2 cells was lower than that of the control cells (261 ± 16 vs 492 ± 21 , Student's *t* test, $P < 0.05$), but no difference was observed on the plates of ECV304 cells. Finally, SSE treatment at 45 mg/L for 24 h significantly increased the proportion of S phase HepG-2 cells from 17.8 ± 1.9 to 63.3 ± 3.3 ($P < 0.05$), but decreased the proportion of G₀/G₁ phase and G₂/M phase cells.

SSE-induced apoptosis

SSE treatment of HepG-2 cells increased the apoptosis rates in a dose-dependent manner (0.2%, 4.7%, 9.5%, 28.7%, as analysed by flow cytometry) (Figure 2). Western

blotting analysis showed that SSE treatment (45 mg/L) for 24 h significantly increased caspase-9 but not caspase-8 cleavage (Figure 3), indicating that SSE induces apoptosis through the intrinsic pathway. Additionally, SSE-treated HepG-2 cells lost $\Delta\psi_m$, as indicated by a decrease in Rh-123 fluorescence (Figure 4), which was significantly weaker than that of the control cells. Consistent with the results of fluorescence microscopy above, Western blotting analysis demonstrated that the expression of cytochrome C in plasmosin was also altered in SSE-treated HepG-2 cells (Figure 3).

Gene expression

In SSE-treated (45 mg/L) HepG-2 cells, the expression of Bak but not Bax was significantly increased, while the expression levels of Bcl-xl and Mcl-1 were significantly down-regulated compared with the control cells (Figure 5A). Western blotting analysis further confirmed the up-regulation of Bax and down-regulation of Bcl-xl and Mcl-1 (Figure 5B).

Xenograft growth in mice

Compared with DMEM-treated mice, i.v. administration of 18 mg/kg SSE every 2 d for 14 d led to an inhibition of HepG-2 cell growth (Figure 6). No lesions were found in the heart, liver, spleen, lungs or kidneys in SSE-treated xenograft mice, and their functions were also normal. Compared with the control group, the TNF α levels in SSE-treated tumor tissue showed no significant difference at week 8 (9.9 ± 6.8 mg/L vs 9.1 ± 5.7 mg/L, $P > 0.05$). In addition, the food intake, mental status and activities were similar in the two groups during the treatment.

DISCUSSION

Recently, the discovery of active compounds from natural products has gained considerable attention as a new source of anticancer drugs^[6-10]. The quest to find novel therapeutic compounds for cancer treatment is a never-ending venture. Sargentgloryvine stem, a traditional Chinese medicine, has been used for thousands of years in the treatment of several inflammatory diseases. Recently, we have successfully developed a novel extract from sargentgloryvine stem SSE that has a potent anticancer activity on HCC cells^[1]. However, the molecular mechanisms underlying the anticancer effects of SSE have not been elucidated.

Our research shows that SSE can induce apoptosis of the hepatoma cell line HepG-2 *in vitro* and *in vivo*, and its mechanism of action may be through decreasing expression of Bcl-xl and Mcl-1 and increasing expression of Bax. Compared with the control group, TNF α in the tumor tissue and liver function in SSE-treated mice had no significant changes at 8 wk ($P > 0.05$). In addition, this study provides evidence that SSE may be a potent therapeutic agent in the treatment of HCC without obvious toxic side effects.

In this study, the inhibitory effect of SSE on HepG-2 cells was tested, and ECV304 cells as the control were also studied. It was demonstrated that SSE profoundly

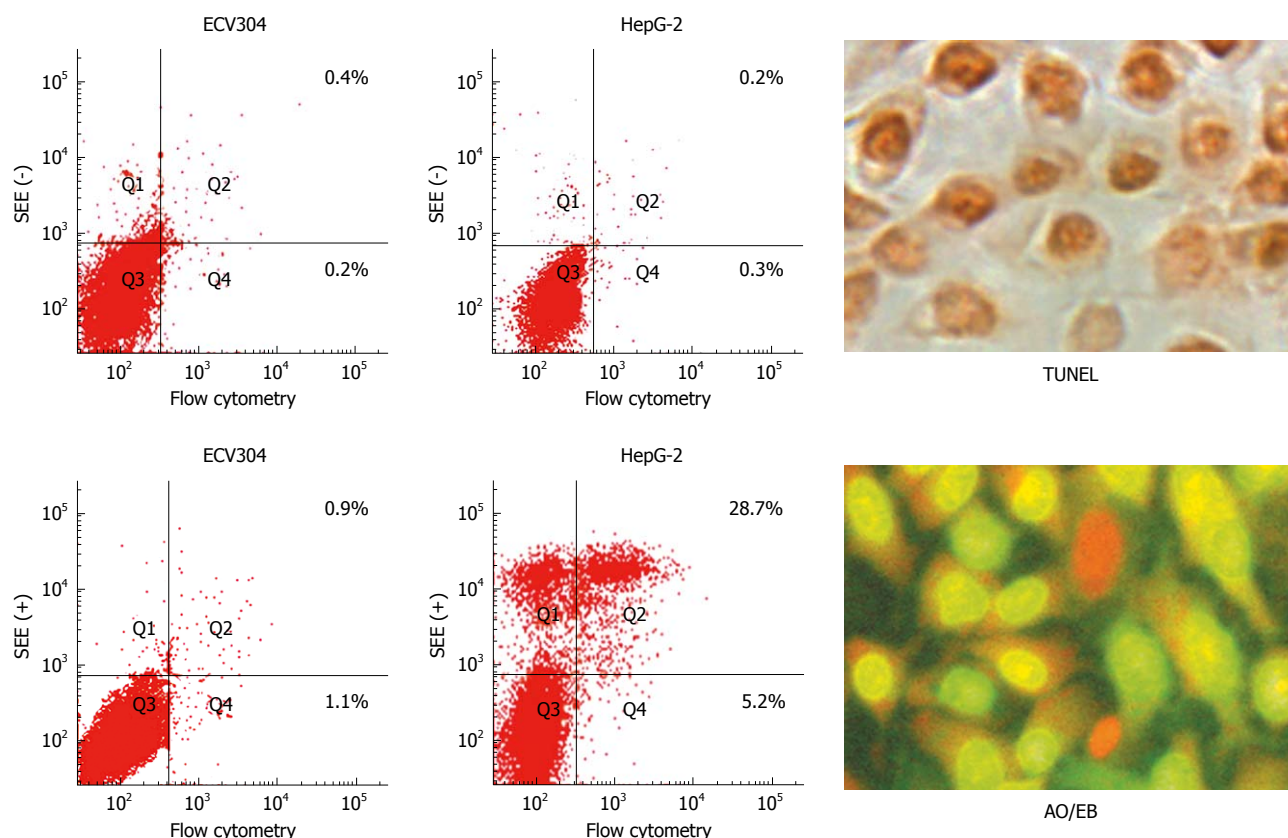


Figure 2 Apoptosis of sargentgloryvine stem extract-treated HepG-2 cells ($\times 400$). HepG-2 and ECV304 cells were treated with sargentgloryvine stem extract (SSE) at a concentration of 45 mg/mL for 24 h. Flow cytometry showed that apoptosis rate was increased obviously compared with the non-treated control cells, $P < 0.05$; while ECV304 cells did not show obvious diversity, $P > 0.05$. Positive signals in nucleus were observed obviously in SSE-treated HepG-2 cells by TdT-Mediated dUTP Nick End Labeling (TUNEL) and acridine orange/ethidium bromide (AO/EB) assays.

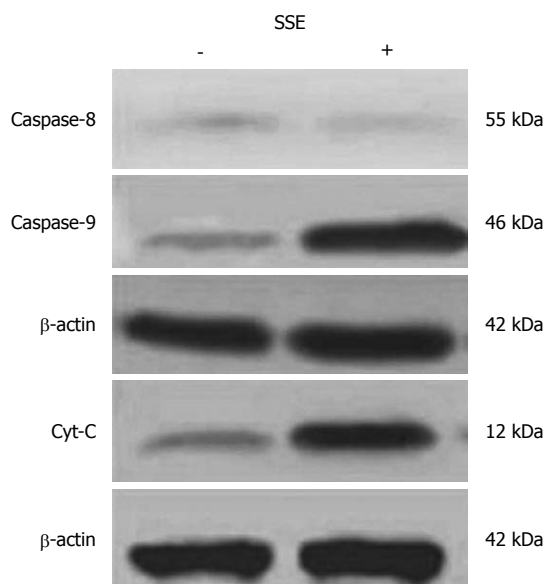


Figure 3 Caspase-8, caspase-9 and cytochrome C in sargentgloryvine stem extract-treated HepG-2 cells. Significantly up-regulated cleavage was found in caspase 9 but not in caspase 8 in HepG-2 cells treated with 45 mg/L sargentgloryvine stem extract (SSE) for 24 h. Cytochrome C in plasmin was notably increased. $P < 0.05$.

inhibited the growth of HepG-2 cells in a concentration- and time-dependent manner but not in ECV304 cells.

MTT and colony formation assays indicate that SSE possesses specific anti-HCC cell activity rather than general cytotoxicity. Additionally, the study suggested that SSE may be safe for normal cells, thus, SSE may have advantages for clinical application.

To reveal the mechanisms of the inhibitory effect of SSE on HepG-2 cells, changes in the cell cycle were analysed. It was demonstrated that the cell cycle of HepG-2 cells was blocked at S phase after 45 mg/L SSE treatment for 24 h, which indicated that the growth inhibition by SSE might be, in part, due to cell cycle arrest. Because cell cycle arrest is always accompanied with cell apoptosis, we analysed apoptosis in the SSE-treated cells. The data showed that SSE treatment induced cell apoptosis, and the apoptosis rates increased with increasing SSE concentrations^[11]. More significantly, the induction of apoptosis by SSE in HepG-2 cells was observed at an initial concentration of 30 mg/L within 24 h, further suggesting the safety of SSE for systemic use in the treatment of HCC. It is known that apoptosis is regulated by two main pathways: the extrinsic pathway, which is initiated by the binding of ligands to specific death receptors on the cell surface, and the intrinsic pathway, which is initiated in mitochondria^[12,13]. To understand the major *in vivo* pathway through which SSE induces HepG-2 cell growth suppression and apoptosis, the expression of caspase-8 and caspase-9, which play important roles in apoptosis triggered by various proapoptotic signals,

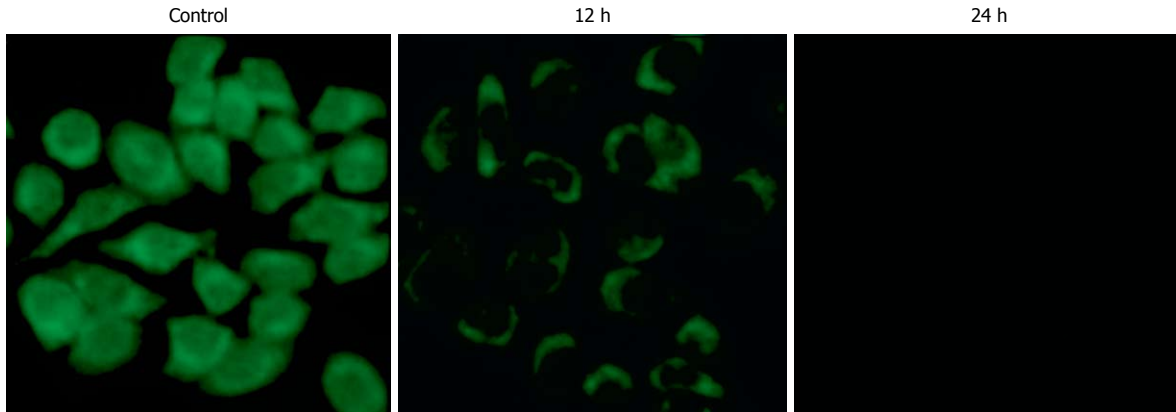


Figure 4 Rh-123 fluorescence in sargentgloryvine stem extract-treated HepG-2 cells ($\times 400$). Flow cytometry showed that fluorescent intensities in sargentgloryvine stem extract (SSE)-treated (45 mg/L) cells for 12 h maintained their $\Delta\psi_m$ and only displayed minor changes in Rh-123 fluorescence. In contrast, SSE-treated (45 mg/L) cells for 24 h, fluorescent intensities were significantly weaker than control cells.

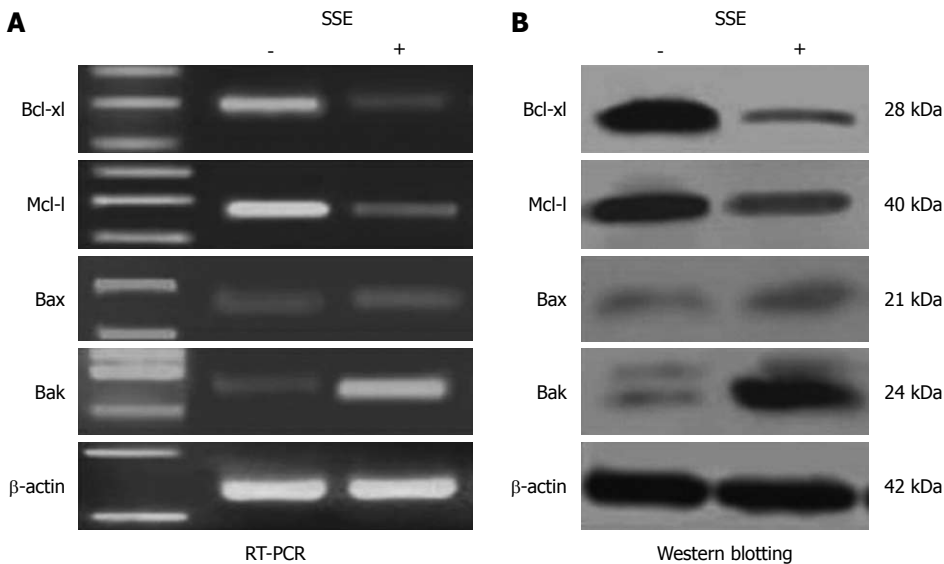


Figure 5 Gene expression in sargentgloryvine stem extract-treated HepG-2 cells. A: Semi-quantitative reverse transcription polymerase chain reaction (RT-PCR) showed that the expression of Bak but not Bax was significantly increased in HepG-2 cells treated with 45 mg/L sargentgloryvine stem extract (SSE) for 24 h, and the expression of Bcl-xl and Mcl-1 was significantly down-regulated; B: Western-blotting confirmed the SSE induced gene expression changes with up-regulated Bak and down-regulated Bcl-xl and Mcl-1 in HepG-2 cells.

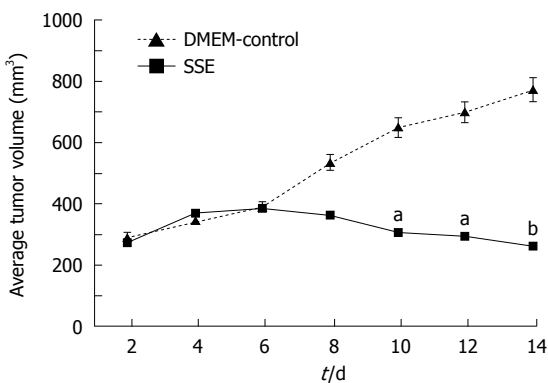


Figure 6 Tumor growth inhibition by systemic sargentgloryvine stem extract-treatment *in vivo*. HepG-2 xenograft tumor (approximately 300 mm³) growth in Athymic BALB/c nude mice injected with 50 μ L of 18 mg/kg sargentgloryvine stem extract (SSE) or DMEM-control every 2 d for 14 d. The tumor size was measured and the tumor volume was calculated as: width² $\times$ length $\times$ 0.5. ^a $P < 0.05$, ^b $P < 0.01$ vs DMEM control.

were studied^[14]. The results showed that 45 mg/L SSE treatment for 24 h significantly increased caspase-9 but not caspase-8 expression, indicating that SSE-induced apoptosis may be through the intrinsic pathway.

The intrinsic pathway for apoptosis involves several steps including mitochondrial membrane permeabilization and release of cytochrome C, followed by caspase-9 activation^[15,16]. Our results showed that treatment with SSE at 45 mg/L for 24 h led to loss of $\Delta\psi_m$ as indicated by a decrease in Rh-123 fluorescence. SSE also induced cytochrome C release from the mitochondria to cytosol in HepG-2 cells. Taken together, these results further confirmed that SSE may directly trigger the intrinsic pathway to induce the mitochondrial pathway for apoptosis in HCC cells.

Previous studies have shown that in apoptotic cells, anti-apoptotic *bcl-2* members are often inactivated whereas pro-apoptotic members, such as *bax* and *bak*, are activated

and oligomerized in the mitochondria outer membrane. This triggers mitochondrial membrane permeabilization and release of soluble apoptogenic factors such as cytochrome C into the cytosol, which results in caspase activation^[17,18]. Further studies revealed that 45 mg/L SSE treatment significantly decreased Bcl-xl and Mcl-1 expression and increased Bak expression and led to mitochondria endomembrane action. Finally, it was confirmed that SSE-induced HepG-2 cell apoptosis is mediated through the *bcl-2* pathway. These results demonstrated that SSE-induced apoptosis is mediated primarily by down-regulated expression of Bcl-xl and Mcl-1, which led to the release of Bak and ultimately activated the intrinsic apoptosis pathway.

In addition to inducing tumor cell apoptosis, systemic injection of SSE into HepG-2 xenografted mice inhibited tumor growth and significantly minimised tumor size but caused no obvious pathological changes in the heart, lungs, liver, spleen or kidneys. The levels of TNF α in the tumor tissue and liver function tests suggest that SEE treatment is relatively safe for the mice.

In conclusion, our research shows that the extract of the Chinese herb sargentgloryvine stem has *in vitro* anticancer effects including inhibition of proliferation and induction of apoptosis in the hepatoma cell line HepG-2 by mechanisms involving expression of Bcl-2 family proteins activating the intrinsic mitochondria apoptosis pathway. Moreover, an *in vivo* solid tumor growth assay further confirmed that systemic administration of the extract could inhibit tumor growth with little cytotoxicity to normal tissues. These *in vitro* and *in vivo* studies provide evidence urging the development of SSE as a novel regimen for human HCC.

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COMMENTS

Background

Plant-derived natural products have become available such as anticancer derivatives of vincristine, vinblastine, paclitaxel and camptothecin.

Research frontiers

Sargentgloryvine stem extract (SSE) as a chemotherapeutic adjuvant can enhance the efficacy and ameliorate the side effects of cancer chemo- or radiotherapy. However, the effect of SSE on the human hepatocellular carcinoma (HCC) cells remains unknown.

Innovations and breakthroughs

This study showed that SSE treatment was not only able to inhibit the proliferation of human HCC cell HepG-2 cells in a dose and time dependent manner, but also induce apoptosis and cell cycle arrest at S phase.

Applications

SEE is able to inhibit proliferation of human HCC cells and is relatively safe for the mice, and therefore it has a great potential to be a therapeutic agent in the treatment of HCC.

Terminology

SSE: Sargentgloryvine stem is the dried vine stem of *Sargentodoxa cuneata* (Oliv.) and has been widely used as an ingredient in formulated Chinese medicine for thousands of years in the treatment of diseases such as chronic pelvic cavity inflammation, rheumatism and appendicitis.

Peer review

The paper by Wang *et al* addresses an important issue, i.e. novel options for systemic therapy of HCC. In general, the paper is well written, the methods used are sound and the described approach is of potential interest.

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Sonographic features of duodenal lipomas in eight clinicopathologically diagnosed patients

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Abstract

AIM: To investigate the sonographic features and diagnostic value of endoscopic ultrasonography (EUS) for duodenal lipomas (DLs).

METHODS: A total of eight consecutive patients with DL diagnosed pathologically were included in the study. One EUS expert reviewed the ultrasonic images for all lesions, including the original layer of the duodenal wall, the echo intensity and the echo homogeneity. The size of the lesions and the perifocal structures were also investigated. The diagnosis by EUS was compared with the histological results.

RESULTS: Using routine endoscopy, only one case was correctly diagnosed as DL. Four cases were classified as submucosal tumors, and three cases were mistaken for stromal tumors. All tumors appeared as round or oval intensive hyperechoic lesions with distinct anterior

borders that originated from the submucosal layer on EUS. Tumors ranged from 8 to 36 mm in size, with an average size of 16 mm. Homogeneous echogenicity was seen in all cases except one that had a tubular structure inside the tumor. Echo attenuation was observed only in the area behind the tumors in five cases, and it was observed both inside and behind the tumors in three cases in which the posterior border was obscure or invisible. Seven (87.5%) cases were correctly diagnosed as DL, and one (12.5%) was mistaken as Brunner's gland adenoma by EUS. Pathologically, all tumors originated from the submucosal layer and consisted of mature fat cells without heteromorphism. Among the fat cells, there was a small amount of thick-wall vessels infiltrating the lymphocytes, and abundant fibrous connective tissues.

CONCLUSION: On EUS, DL is featured as an intensive homogeneous hyperechoic submucosal lesion with marked echo attenuation and without involvement of the mucosa.

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Key words: Duodenum; Lipoma; Endoscopic ultrasonography; Hyperecho; Echo attenuation

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INTRODUCTION

Gastrointestinal lipomas are uncommon benign tumors that occur anywhere along the gut. The most common location for these lesions is the colon, followed by the il-

eum and the jejunum^[1]. Lipomas found in the duodenum are rare and the literature regarding duodenal lipomas (DLs) is only limited to case reports^[2-8], and no systematic study of diagnostic means for DLs has been reported. Since preoperative diagnosis of DLs is difficult, and large DLs can mimic malignant tumors on endoscopy, patients could be subjected to extensive surgical procedures that are sometimes destructive. Endoscopic ultrasonography (EUS) is an optimal method for detecting gastrointestinal submucosal tumors (SMTs) such as stromal tumors and leiomyomas; however, the features and diagnostic value of EUS for examining DLs have not been well established because of the rareness of this disease. In this study, we studied the sonographic features and diagnostic value of EUS for identifying DLs.

MATERIALS AND METHODS

Patients

A total of eight consecutive patients with DL were included. The diagnosis of DL for all patients was pathologically established after surgical excision in five patients and endoscopic resection in three patients during the period from June 2000 to December 2010 in the First Affiliated Hospital, School of Medicine, Zhejiang University, China. The patient group was composed of five males and three females, and aged from 42 to 78 years, with a mean of 60 years. Except for one patient who was asymptomatic, DLs presented as bleeding in four patients, dyspepsia in two patients, and epigastric pain in one patient (Table 1). Laboratory examinations, including liver function tests, serum lipids, and tumor markers (carcinoembryonic antigen, carbohydrate antigen 19-9, carbohydrate antigen 125, and alpha-fetoprotein), showed no obvious abnormalities except for anemia in five patients.

Instrument

The EUS system included Olympus EU-M2000 sonogram processing equipment, an Olympus GIF-2T-240 double-cavity electronic gastroscope, Olympus MAJ drive systems with a high-frequency echo probe, UM-DP12-25R miniature ultrasonic probes with a frequency spectrum of 12-15 MHz, and a Daker WP-800 water pump (Olympus Medical System Corp., Tokyo Japan).

Methods

One EUS expert reviewed the ultrasonic image of all lesions, including the original layer of the duodenal wall, the echo intensity, and the echoic homogeneity. The size of the lesions and the perifocal structures were also investigated. The EUS diagnosis was compared with the histological results.

RESULTS

Endoscopic studies

The tumors were located at the bulb in one case and in the

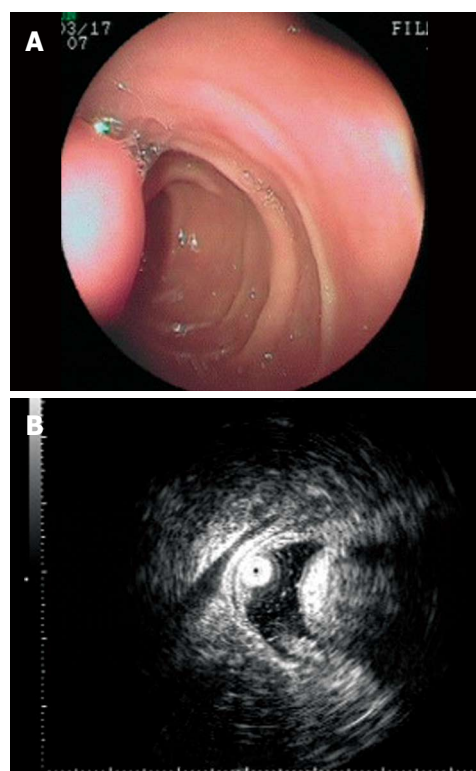


Figure 1 Endoscopic and endoscopic ultrasonography findings in Case 7. A: A submucosal tumors of the descendant duodenum with an intact surface; B: Endoscopic ultrasonography showed a hyperechoic lesion with a distinct anterior border originating from the submucosal layer. There was marked echo attenuation both inside and behind the lesion, and the posterior border was obscure.

descending part of the duodenum in seven cases. The lesions, with a hemispherical or oval shape, were sessile in six cases and had a stalk in two. The surface of the lesions was intact in three cases (Figure 1A) and had an ulcer (Figure 2A) or an erosion in five cases. Prior to EUS, only one case was correctly diagnosed as DL by routine endoscopy because of the yellowish and soft appearance (Figure 3A). Four cases were classified as SMTs, and three cases were mistaken for stromal tumors.

Endoscopic ultrasonography

The endoscopic ultrasonography (EUS) findings in all cases are shown in Table 1. All tumors appeared as intensive hyperechoic lesions with a distinct anterior border that originated from the third EUS layer without involvement of the overlying first and second layers (Figures 1B, 2B, 3B and 4). Tumors ranged from 8 to 36 mm in size, with an average size of 16 mm. The margins of the tumors were clear in five cases (Figures 3B and 4), and the posterior borders of three lesions were obscure or invisible because of marked echo attenuation (Figures 1B and 2B). Homogeneous echogenicity was seen in all cases except for one that had a tubular structure inside the tumor (Figure 2B). Echo attenuation was observed only in the area behind the tumors in five cases (Figures 3B and 4) and both inside and behind the tumors in three cases (Figures 1B and 2B). With EUS, seven patients were correctly diagnosed as having DLs, but one

Table 1 Clinical settings and endoscopic ultrasonography observations

Case	Sex	Age	Symptoms	Location	Treatment	EUS features					
						Layer	Size (mm)	Echogenicity	Homogeneity	Border	Echo attenuation
1	M	50	None	Bulb	Endoscopic resection	3rd	12	Hyperecho	Homogenous	Distinct	Behind
2	F	64	Melena	2nd portion	Surgery	3rd	10	Hyperecho	Homogenous	Distinct	Behind
3	M	63	Dyspepsia	2nd portion	Surgery	3rd	25	Hyperecho	Homogenous	Indistinct	Behind and inside
4	F	54	Melena	2nd portion	Surgery	3rd	12	Hyperecho	Homogenous	Distinct	Behind
5	M	67	Dyspepsia	2nd portion	Endoscopic resection	3rd	8	Hyperecho	Homogenous	Distinct	Behind
6	M	78	Melena	2nd portion	Endoscopic resection	3rd	11	Hyperecho	Homogenous	Distinct	Behind
7	F	62	Epigastric pain	2nd portion	Surgery	3rd	15	Hyperecho	Homogenous	Indistinct	Behind and inside
8	M	42	Melena	2nd portion	Surgery	3rd	36	Hyperecho	Heterogeneous	Indistinct	Behind and inside

EUS: Endoscopic ultrasonography; M: Male; F: Female.

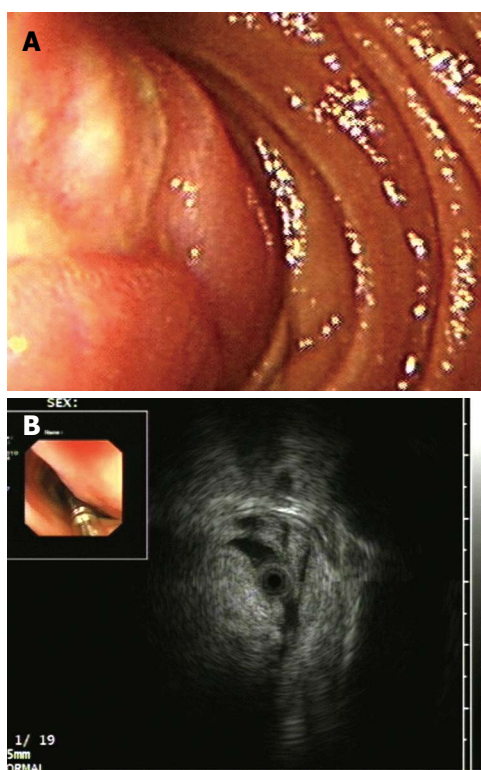


Figure 2 Endoscopic and endoscopic ultrasonography findings in Case 8. A: A lobulated submucosal tumor in the descendant duodenum with an ulcer on its surface; B: Endoscopic ultrasonography showed an intensive hyperechoic lesion with a distinct anterior border originating from the submucosal layer without involvement of the overlying mucosal layer. The posterior border of the tumor was invisible because of the marked echo-attenuation.

patient with DL was mistaken as having Brunner's gland adenoma (BGA) due to the appearance of a tubular structure.

Pathology

The pathological diagnosis after routine endoscopic biopsy was chronic inflammation of the mucosa, whereas the post-operative diagnosis after surgical excision or endoscopic resection was DL. The tumors presented by gross appearance as a node or finger in six cases and as a sub-lobe or cauliflower in two cases. All tumors originated from the submucosal layer, sometimes involving the muscularis propria, with a fully or partially coated fiber peplus. Microscopically, the

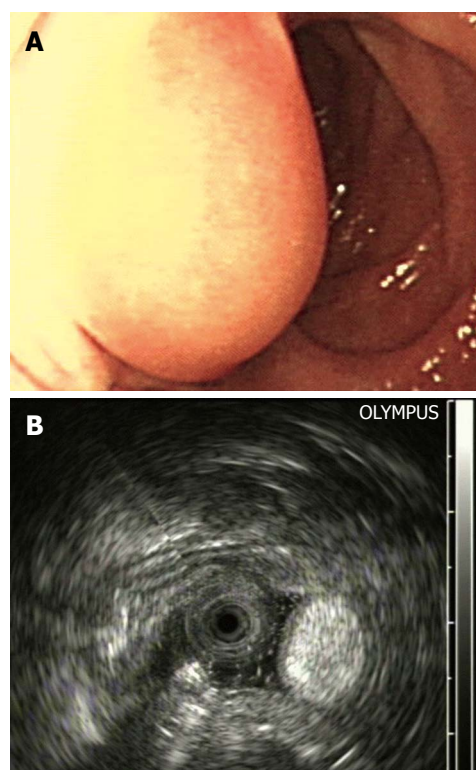


Figure 3 Endoscopic and endoscopic ultrasonography findings in Case 2. A: A submucosal tumor located in the descendant duodenum with a yellowish and soft appearance; B: Endoscopic ultrasonography showed an oval intensive hyperechoic lesion with homogeneous parenchymal echogenicity and a clear margin originating from the third layer without involvement of the overlying mucosal layers. Echo attenuation was seen at the area behind the focus.

tumors were composed of mature fat cells without heteromorphism. Among the fat cells, there were small amounts of thick-wall vessels, infiltrating lymphocytes, and abundant fibrous connective tissues (Figures 5-7).

DISCUSSION

Lipomas of the duodenum are rare, with fewer than 230 cases reported in the literature, and most of the described cases are from autopsy records rather than clinical experience^[9]. DLs were mostly detected after bleeding or obstruction occurred. Among the patients in

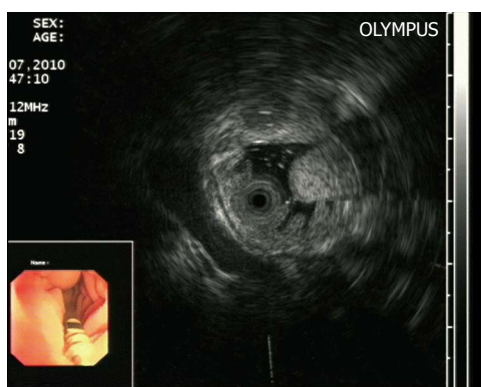


Figure 4 Endoscopic and endoscopic ultrasonography findings in Case 4. A submucosal tumor located in the descendant duodenum. Endoscopic ultrasonography showed a submucosal hyperechoic lesion with marked echo-attenuation behind the focus.

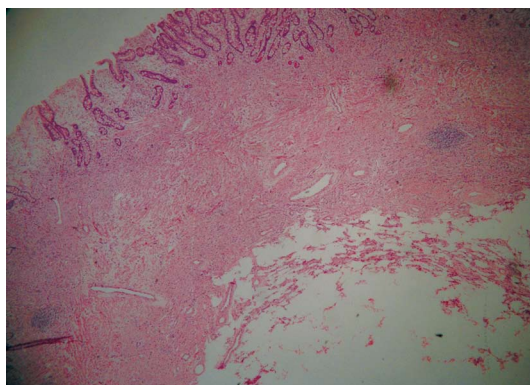


Figure 5 Pathological findings in Case 3. Microscopically, the tumor was located in the submucosa without involvement of the mucosa (HE, × 40).

this study, four (50%) experienced bleeding, two (25%) experienced dyspepsia, one (12.5%) had epigastric pain, and one (12.5%) was asymptomatic. The symptoms of DL are nonspecific, however, and they are not useful for differential diagnosis.

Endoscopy is the preferred means for detecting upper gastrointestinal diseases. However, it can only suggest the presence of submucosal protruding lesions, but cannot provide additional details even though lesions have been detected^[10,11]. In this study, four patients were diagnosed as having SMTs by endoscopy, and three patients were mistaken as having stromal tumors. Only one patient was correctly diagnosed with lipoma by routine endoscopy due to the yellowish and soft appearance of the lesion (Figure 2B).

EUS has been reported to be an effective modality for assessing gastrointestinal tumors and evaluating the original layer of the submucosal tumor, the homogeneity of the internal parenchymal echo, and the echogenicity of the lesions^[10]. The typical EUS observations of DLs are intensive homogeneous hyperechoic lesions originating from the submucosa, with echo attenuation behind and/or inside the rear area. Thus, the signs of DLs are similar to the ultrasonic features of a fatty liver.

Intensive hyperecho is the most noticeable EUS fea-

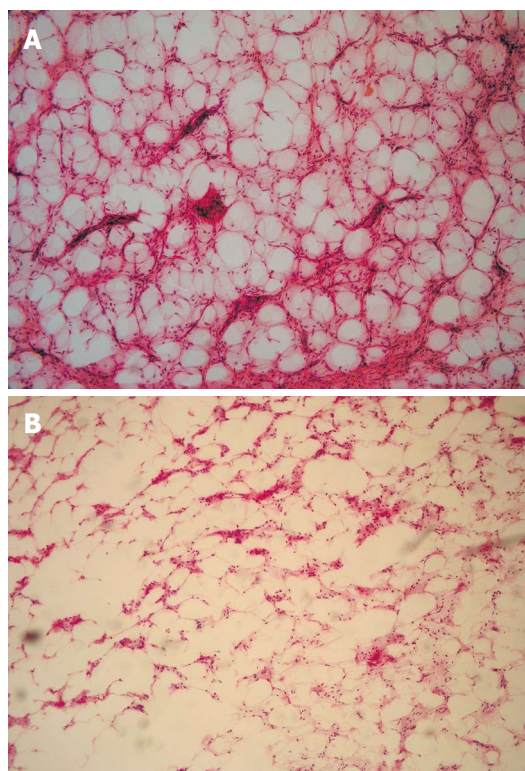


Figure 6 Pathological findings in Cases 2 and 4. A, B: The tumors consisted of mature fat cells. Abundant fibrous connective tissues were found among the fat cells (HE, × 100).

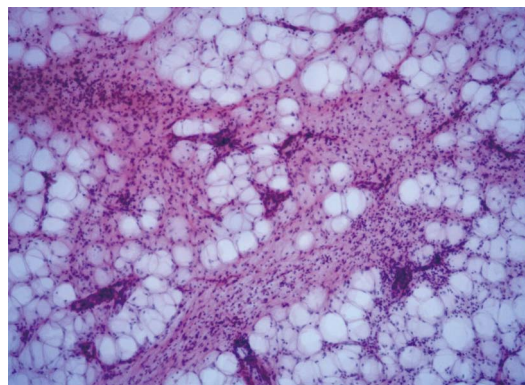


Figure 7 Pathological findings in Case 7. Massive fiber ropes were inside the tumor parenchyma (HE, × 100).

ture of DLs. A newly-devised echogenicity classification system for SMTs by Okanobu^[10] demonstrated the highest echo level of lipomas (levels 5-6). The marked echo-attenuation is another EUS feature of DLs. In our series, there was a more apparent echo decline in the area behind the focus than anywhere else in all cases regardless of the size of the lesions, suggesting a greater attenuation coefficient for DLs than for normal intestinal wall tissues. Furthermore, visible echo decline was seen inside the lesion when the size of the focus was larger than 15 mm. The anterior border was as distinct as the overlying first and second layers of the DLs; however, the appearance of the posterior border depended on the related echo de-

cline. The latter portion and the posterior border of DLs larger than 25 mm are often invisible with the 12-MHz probe. The internal parenchymal echo of DLs is generally homogenous^[11]. Occasionally, blood vessels may present as tubular structures inside the focus.

According to two ultrasonic characteristics, we could distinguish DLs from the majority of other SMTs such as leiomyomas, stromal tumors, or cysts. It is noteworthy that Brunner's gland adenomas (BGAs) also show hyperechoic lesions originating from the submucosa, and therefore, DLs may be mistaken for BGAs^[11,12]. In our study, one patient was misdiagnosed with duodenal BGA. BGAs appear primarily in the bulb portion or at the junction of the bulb and the descending duodenum, whereas DLs are located primarily in the descending portion of the duodenum. In addition, the echogenicity of BGAs is not as intensive or homogeneous as that of lipomas. Although the second EUS layer often becomes blurry or invisible in BGAs because of involvement of the lamina propria, it is always readable in DLs.

The reason why all gastrointestinal lipomas appeared as hyperechoic is not clear. Interestingly, normal subcutaneous fat tissues appeared as a hypoechoic zone with a small amount of hyperechoic fiber ropes. An earlier report showed that 29% of superficial soft tissue lipomas were hypoechoic, 22% were isoechoic, 29% were hyperechoic, and 20% were of a mixed pattern^[13]. Thus, the echo types of lipomas mostly depend on the quantity of the boundary in relation to the mixture of fat and other connective tissues. We found abundant fibrous connective tissues among the fat cells of DLs. The heterogeneous mixture generated innumerable acoustic boundaries that appeared hyperechoic because of the marked acoustic impedance difference between the fat and fibrous tissues.

In summary, EUS has significant value for the differential diagnosis of DLs. The appearance of a round or oval lesion originating from the submucosal layer with intensive homogenous hyperecho and marked echo-attenuation, without involvement of the mucosal layers, suggests a diagnosis of DL. Abundant fibrous connective tissues among the fat cells may be the acoustic basis of this appearance.

COMMENTS

Background

Lipomas located in the duodenum are rare. Because the preoperative diagnosis for duodenal lipomas is difficult to establish and some large lipomas can mimic malignant tumors on endoscopy, patients could be subjected to extensive surgical procedures that sometimes were destructive. Endoscopic ultrasonography (EUS) is the optimal method for the diagnosis of gastrointestinal stromal tumors, but its diagnostic value for duodenal lipomas has not been well established because of its rareness.

Research frontiers

Up to date, less than 230 cases of lipomas have been reported in the literature,

but most of them are from autopsy records rather than clinical experience. Clinically, duodenal lipomas are mostly revealed by bleeding or obstruction. Endoscopy can only detect the submucosal lesion but fail to judge its nature. EUS is an effective modality in the assessment of gastrointestinal submucosal tumors and evaluation of the original layer, homogeneity of internal parenchymal echo and echogenicity of the lesions.

Innovations and breakthroughs

EUS is of significant value in the diagnosis and differential diagnosis of duodenal lipomas. The sonographic features were round or oval lesions originated from submucosal layer with intensive homogenous hyperecho and marked echo-attenuation, without involvement of the mucosal layers.

Applications

According to this study, duodenal lipomas can be defined by EUS, thus need-less surgery can be avoided. By EUS, they can differentiate duodenal lipomas from other submucosal tumors. The sonographic features of duodenal lipomas can be used for the diagnosis of lipomas in esophagus, stomach and colon.

Peer review

This is an original report on the correlations of the sonographic findings and clinicopathological features of duodenal lipomas. The material is characterized by small case series but the conclusive suggestions are appropriate and interesting. Duodenal lipoma is a rare clinicopathological entity. Therefore, it is interesting to get an eight consecutive duodenal lipoma cases. The EUS is probably the best option to diagnose this pathology.

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Association between *ITGA2* C807T polymorphism and gastric cancer risk

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Author contributions: Chen J is involved in the study design, conducted polymerase chain reaction-restriction fragment length polymorphism, analyzed the data and wrote the manuscript; Li JQ and Liu NN participated in the study design and extracted genetic DNA from blood samples; Yang L, Zeng Y, Zhao XM, Xu LL and Luo X collected blood samples; Wang B and Wang XR designed and coordinated the study and revised the manuscript.

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the wild genotype CC, subjects with the variant genotypes (CT + TT) had a significantly higher risk of gastric cancer (adjusted odds ratio = 1.57, 95% CI = 1.13-2.17, $P = 0.007$). In stratified analyses, the elevated gastric cancer risk was especially evident in older individuals aged > 58 years, nonsmokers and rural subjects. Further analyses revealed that the variant genotypes were associated with poor tumor differentiation and adjacent organ invasion in the sub-analysis of gastric cancer patients.

CONCLUSION: The *ITGA2* gene C807T polymorphism may be associated with an increased risk of gastric cancer, differentiation and invasion of gastric cancer.

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Key words: Gastric cancer; Integrin; *ITGA2*; Polymorphism; Genotype

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Abstract

AIM: To evaluate the impact of the *ITGA2* gene polymorphism on gastric cancer risk.

METHODS: A hospital-based case-control study was conducted, including 307 gastric cancer patients and 307 age- and gender-matched control subjects. The genotypes were identified by polymerase chain reaction-restriction fragment length polymorphism assay.

RESULTS: The frequencies of the wild and variant genotypes in cases were significantly different from those of controls ($P = 0.019$). Compared with individuals with

INTRODUCTION

Gastric cancer remains a major public health issue as the fourth most common cancer type and the second leading cause of cancer death worldwide^[1,2]. Nearly half of the gastric cancer cases occur in China^[3]. Although the

cause of gastric cancer is largely unknown, it has been shown that diet, tobacco smoking, alcohol, gastroesophageal reflux and *Helicobacter pylori* (*H. pylori*) infection are associated with the risk of this cancer^[4-7]. As genetic polymorphisms are responsible for the inter-individual variation and diversity, they have been recently considered as the main genetic elements involved in the development of common and complex diseases, including various cancers. Like many malignancies, it is believed that gastric cancer is the result of interactions between environmental factors and genetic factors^[8]. Our previous epidemiological studies also provided the evidence that genetic polymorphisms were associated with the risk of gastric cancer^[9-12].

Integrins are members of a family of cell-surface heterodimeric proteins that mediate cell-matrix and cell-cell interactions. The 18 α -subunits and 8 β -subunits form together at least 25 different integrins, each pair being specific for a unique set of ligands. It has been demonstrated that integrins may play a crucial role in carcinogenesis, tumor behavior and metastasis^[13,14]. Several integrins such as $\alpha 2\beta 1$, $\alpha IIb\beta 3$ and $\alpha v\beta 3$ are considered as key factors for cancer development and progression. Integrin $\alpha 2\beta 1$, also known as platelet glycoprotein I a-II a, is expressed by epithelial cells, and its level of expression in tumor cells is associated with motility, invasiveness and cellular differentiation^[15-17]. Several studies have shown that integrin $\alpha 2\beta 1$ expression is closely associated with invasion and metastasis of gastric cancer^[18-21].

The integrin, $\alpha 2$ gene (*ITGA2*) is located on chromosome 5q23-31. A silent change in the coding region at nucleotide 807 (TTT/TTC at codon Phe253) has been identified. The C807T single nucleotide polymorphism (NCBI SNP ID: rs1126643) of the *ITGA2* gene was associated with the integrin $\alpha 2\beta 1$ density. The genotype 807 TT was associated with a higher receptor density and the genotype 807 CC with a lower density, whereas heterozygous individuals expressed intermediate receptor levels^[22,23].

Recent studies indicated that the *ITGA2* gene C807T polymorphism was associated with various diseases, including stroke, retinal vein occlusion, acute coronary syndrome, colorectal cancer, and breast cancer^[24-29]. To the best of our knowledge, there has been no study that assessed the association between the polymorphism and gastric cancer risk.

Given that the roles of *ITGA2* in the progression of gastric cancer as well as the effect of the polymorphism in *ITGA2* gene on the receptor function, it is plausible that the polymorphism may be associated with the risk of gastric cancer. To test the hypothesis, we performed a hospital-based case-control study in a Chinese population.

MATERIALS AND METHODS

Subjects

This hospital-based case-control study consisted of 307 consecutive inpatients with histologically confirmed gas-

tric cancers without synchronous and/or metachronous secondary malignancy and a population-based and sex- and age-matched 307 cancer-free inpatients as controls. All subjects were recruited between March 2005 and November 2009 from the patients who were admitted to the First Affiliated Hospital of Nanjing Medical University. The most common causes for hospitalization in the control subjects were hernias, appendicitis, hydrocele, cholecystitis and cataract. All subjects were of unrelated Han nationality from Jiangsu Province or its surrounding regions. Information on age, gender, smoking status, residence (urban or rural), body weight and personal medical history was collected by questionnaire. Individuals who formerly or currently smoked ≥ 10 cigarettes per day for at least 2 years were defined as smokers. Depth of tumor invasion and local lymph node status were classified according to the TNM classification criteria of International Union Against Cancer^[30]. Differentiation was graded according to World Health Organization classification. The study was approved by the Ethics Committee of Nanjing Medical University First Affiliated Hospital and informed consent was obtained from all the participating subjects.

Genotyping

The protocol for genomic DNA extraction was described in our previous study^[9]. The polymerase chain reaction (PCR)-restriction fragment length polymorphism assay was used to identify the *ITGA2* C807T genotypes. The PCR was performed in a total volume of 20 μ L reaction mixtures containing 2 μ L 10 $\times$ PCR buffer (MBI Fermentas), 1.75 mmol/L MgCl₂, 0.25 μ mol/L each primer (forward 5'-GTGTTTAACCTGAACACATAT-3', reverse 5'-ACCTTGCATATTGAATTGCTT-3'), 0.15 mmol/L dNTP, 1 unit *Taq* polymerase (MBI fermentas) and 150 ng genomic DNA. The amplification protocol is as follows: primary denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 1 min, then a final elongation at 72°C for 5 min. The 115 bp PCR products including the polymorphic site were digested at 65°C for 12 h, using restriction enzyme *Taq* I (MBI Fermentas) and then separated on a 3% ethidium bromide-stained agarose gel. The wild-type homozygotes (CC) produced two bands at 92 and 23 bp, while the variant homozygotes (TT) produced one band at 115 bp, and the heterozygous (CT) produced three bands at 115, 92 and 23 bp (Figure 1). To control the quality of genotyping, all assays were conducted by two researchers separately in a blind fashion. In addition, a 10% masked samples were randomly selected and retested, and the reproducibility was 100%.

Statistical analysis

Statistical analyses were conducted using SPSS 16.0 software (SPSS Inc., Chicago, IL, USA). All statistical tests were two-tailed and $P < 0.05$ was considered statistically significant. Quantitative variables departing from the normal distribution including age and weight were summarized as median and analyzed by Mann-Whitney rank

Table 1 Demographic information *n* (%)

Characteristics	Cases (<i>n</i> = 307)	Controls (<i>n</i> = 307)	<i>P</i> value
Gender (male)	231 (75.2)	231 (75.2)	1.000
Age ¹ (yr), (range)	59 (50-68)	58 (49-66)	0.145
Weight ¹ (kg), (range)	62 (55-70)	65 (57-72.75)	0.001
Hypertension	65 (21.17)	59 (19.22)	0.546
Diabetes	17 (5.54)	24 (7.82)	0.262
Smoking	82 (26.71)	53 (17.26)	0.005
Residence			
Rural	139 (45.28)	139 (45.28)	1.000
Urban	168 (54.72)	168 (54.72)	

¹Median (25th-75th percentiles).

sum test. Pearson's χ^2 test was used to compare the difference in the distribution of categorical variables and genotype frequencies between cases and controls. The Hardy-Weinberg equilibrium of the *ITGA2* genotypes was estimated for cases and controls by a goodness-of-fit χ^2 test. Odds ratio (OR) and 95% CI were calculated to evaluate the association between the polymorphism and the risk of gastric cancer. Carriers of the wild genotype CC were used as the reference. The crude OR was obtained using the Woolf approximation method and the adjusted OR was calculated by unconditional logistic regression method, with adjustment for age, sex, smoking status, residence, hypertension and diabetes.

RESULTS

Demographic information

A total of 614 subjects (307 cases and 307 controls) were analyzed. Baseline demographic characteristics of the study groups are shown in Table 1. The age distribution and proportion of males were quite similar due to the fact that we selected the age- and gender-matched subjects. The two groups were similar with respect to residence, history of hypertension and diabetes. Nevertheless, compared with controls, gastric cancer patients had a lower body-weight ($P = 0.001$) and more smokers were found among gastric cancer cases than among the controls (26.71% *vs* 17.26%, $P = 0.005$).

Distribution of *ITGA2* genotype in cases and controls and risk estimates

Table 2 shows the frequency distributions of the genotypes and their association with gastric cancer risk by unadjusted OR, adjusted OR and 95% CI. The genotype distributions in cases and controls were consistent with those from the Hardy-Weinberg equilibrium model ($P = 0.988$, $P = 0.675$, respectively). The frequencies of the *ITGA2* genotype were significantly different between gastric cancer cases and controls ($P = 0.019$). Compared with the control group, T allele frequency was significantly higher in the case group ($P = 0.024$). With the wild genotype CC as reference, we found that the CT genotype was associated with an increased risk of gastric cancer (adjusted OR = 1.54, 95% CI = 1.10-2.18, $P = 0.013$).

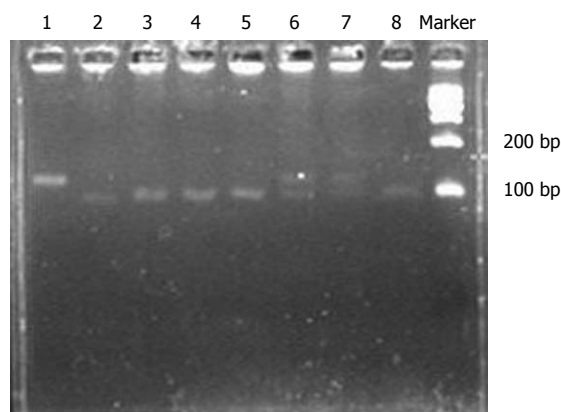


Figure 1 *ITGA2* C807T polymorphism in gastric cancer patients and controls. Amplified polymerase chain reaction products were digested with restriction enzyme *Taq* I and analyzed on a 3% agarose gel. Lane 1: The TT homozygous; Lanes 2-5, 8: The CC homozygous; Lanes 6, 7: The CT heterozygous.

Individuals with the variant genotypes (CT + TT) had a 1.57-fold increased risk of developing gastric cancer (adjusted OR = 1.57, 95% CI = 1.13-2.17, $P = 0.007$).

Stratified analysis of polymorphism and gastric cancer risk

As shown in Table 3, stratified analyses were performed by the median age of controls (58 years), sex, smoking status, and residence. The elevated risk of gastric cancer associated with the variant genotypes was noteworthy in subjects aged > 58 years (adjusted OR = 1.88, 95% CI = 1.17-3.03, $P = 0.010$), but not in subjects aged ≤ 58 years. In non-smoking subjects, the variant genotypes were associated with a 51% increased risk of gastric cancer (adjusted OR = 1.51, 95% CI = 1.05-2.18, $P = 0.028$), whereas the correlation was not statistically significant in smoking subjects. When stratified by residence, the elevated risk was evident in rural subjects (adjusted OR = 2.35, 95% CI = 1.42-3.90, $P = 0.001$), but not in urban subjects. No statistically significant difference was observed in the association of the polymorphism and susceptibility to gastric cancer between males and females.

Variant genotypes and clinicopathological characteristics of gastric cancer

We also observed the correlations between the *ITGA2* variant genotypes and clinicopathologic features of gastric cancer patients in this study (Table 4). A significantly increased risk was found in individuals with the variant genotypes in both poorly differentiated tumors (adjusted OR = 2.21, 95% CI = 1.12-4.38, $P = 0.022$) and adjacent invaded organs (adjusted OR = 2.12, 95% CI = 1.10-4.07, $P = 0.024$) of gastric cancer. However, no significant association was observed between the polymorphism and lymph node metastasis or tumor location.

DISCUSSION

In the present study, we investigated the role of *ITGA2* gene C807T polymorphism in gastric cancer susceptibility.

Table 2 Distributions of *ITGA2* genotype in cases and controls and risk estimates *n* (%)

<i>ITGA2</i> genotype	Cases ¹	Controls ¹	Crude OR (95% CI)	<i>P</i> value	Adjusted OR ² (95% CI)	<i>P</i> value
Overall	307	307				
CC	141 (45.93)	170 (55.37)	1.00		1.00	
CT	135 (43.97)	113 (36.81)	1.44 (1.03-2.01)	0.033	1.54 (1.10-2.18)	0.013
TT	31 (10.10)	24 (7.82)	1.56 (0.87-2.78)	0.133	1.62 (0.90-2.91)	0.112
CT + TT	166 (54.07)	137 (44.63)	1.46 (1.06-2.01)	0.019	1.57 (1.13-2.17)	0.007
C allele	417 (67.92)	453 (73.78)				
T allele	197 (32.08)	161 (26.22)				

¹Distributions of the *ITGA2* genotype in cases and controls were in Hardy-Weinberg equilibrium ($P = 0.988$, $P = 0.675$, respectively); ²Adjusted for age, sex, smoking status, residence, hypertension and diabetes. OR: Odds ratio.

Table 3 Stratified analyses for variant *ITGA2* genotypes in cases and controls *n* (%)

Variable	(CT + TT)/CC		Crude OR (95% CI)	<i>P</i> value	Adjusted OR ¹ (95% CI)	<i>P</i> value
	Cases	Controls				
Age (yr), (median)						
≤ 58	81 (26.4)/68 (22.1)	80 (26)/85 (27.7)	1.27 (0.81-1.97)	0.298	1.31 (0.83-2.06)	0.247
> 58	85 (27.7)/73 (23.8)	57 (18.6)/85 (27.7)	1.74 (1.10-2.75)	0.018	1.88 (1.17-3.03)	0.010
Sex						
Females	45 (14.7)/31 (10.1)	38 (12.4)/38 (12.4)	1.45 (0.76-2.76)	0.255	1.52 (0.73-2.93)	0.206
Males	110 (35.8)/121 (39.4)	99 (32.2)/132 (43)	1.21 (0.85-1.73)	0.304	1.29 (0.82-2.01)	0.287
Smoking status						
Smokers	40 (13)/42 (13.7)	19 (6.2)/34 (11.1)	1.70 (0.84-3.46)	0.141	1.87 (0.89-3.94)	0.100
Non-smokers	126 (41)/99 (32.3)	118 (38.4)/136 (44.3)	1.47 (1.02-2.10)	0.037	1.51 (1.05-2.18)	0.028
Residence						
Urban	89 (29)/79 (25.7)	84 (27.4)/84 (27.4)	1.13 (0.73-1.73)	0.585	1.17 (0.76-1.81)	0.479
Rural	77 (25.1)/62 (20.2)	53 (17.2)/86 (28)	2.02 (1.25-3.25)	0.004	2.35 (1.42-3.90)	0.001

¹Adjusted for age, sex, smoking status, residence, hypertension, and diabetes. OR: Odds ratio.

Table 4 Associations between variant *ITGA2* genotypes and clinicopathological characteristics of gastric cancer¹

Variable	CT + TT	CC	Crude OR (95% CI)	<i>P</i> value	Adjusted OR ² (95% CI)	<i>P</i> value
Tumor differentiation						
Well	42	42	1		1	
Moderate	65	69	0.94 (0.55-1.63)	0.830	0.94 (0.54-1.63)	0.828
Poor	55	27	2.04 (1.09-3.82)	0.027	2.21 (1.12-4.38)	0.022
Depth of tumor infiltration						
T1	24	30	1		1	
T2	21	17	1.54 (0.67-3.56)	0.308	1.76 (0.73-4.25)	0.208
T3	34	40	1.06 (0.53-2.15)	0.866	1.10 (0.52-2.32)	0.797
T4	83	51	2.03 (1.07-3.86)	0.030	2.12 (1.10-4.07)	0.024
Lymph node metastasis						
Negative	59	51	1		1	
Positive	103	87	1.02 (0.64-1.64)	0.923	0.98 (0.61-1.58)	0.942
Localization						
Cardia	38	41	1		1	
Non-cardia	128	100	1.38 (0.83-2.31)	0.217	1.38 (0.81-2.35)	0.231

¹Data of seven plaintively treated cases were not obtained for the inoperable tumors; ²Adjusted for age, sex, smoking status, residence, hypertension, and diabetes. OR: Odds ratio.

ity in a Chinese population. We found that the polymorphism may be associated with an increased risk of gastric cancer, differentiation and invasion of gastric cancer.

It has been reported that integrin $\alpha 2\beta 1$ is one of the key factors accelerating tumor progression and metastasis in various types of cancers^[15-21,31]. Koike *et al*^[20] found that the $\alpha 2$ integrin was expressed in the intestinal-type and

diffuse-type gastric carcinoma cells, and invasion through basement membrane and type I collagen gel was inhibited by anti- $\alpha 2$ integrin monoclonal antibody, indicating that the $\alpha 2$ integrin plays an important role in invasion of gastric carcinoma cells. Another study conducted by Lee *et al*^[32] elucidated the potential mechanisms underlying the spreading and invasiveness of gastric carcinoma

cells, the integrin transduces signaling directly *via* engagements with extracellular matrix proteins, thereby leading to the regulation of downstream intracellular signaling molecules. It also functions in collaborative (indirect) signaling, in which integrins cosignal with other membrane receptor-mediated signal pathways, e.g. growth factor receptors, G-protein coupled receptors or the transforming growth factor β 1 signaling pathway.

The *ITGA2* gene C807T polymorphism is associated with integrin density, but the precise molecular mechanism remains unclear. It is a silent polymorphism in codon 253 (Phe253Phe) and does not cause an altered structure of the integrin molecule, but in linkage disequilibrium with a yet unknown functional polymorphism affecting *ITGA2* expression. Another explanation could be a direct effect on the stability of the *ITGA2* mRNA, which resulted in a change of the amount of integrin protein being expressed.

Limited studies have reported the association between the polymorphism in *ITGA2* gene and cancer risks, although the results remain inconsistent^[27-29]. Gerger *et al*^[27] found that the *ITGA2* gene C807T polymorphism was associated with reduced colorectal cancer risk (OR = 0.77, 95% CI = 0.64-0.94, *P* = 0.011). In their another case-control study, they found that carriers of the most common *ITGA2* haplotype (807C_1648G) had a decreased risk for breast cancer (OR = 0.72, 95% CI = 0.53-0.98)^[28]. Nevertheless, Ayala *et al*^[29] reported that no association was observed between the *ITGA2* gene C807T polymorphism and breast cancer risk.

Based on these studies, we conducted this hospital-based case-control study to investigate the association between the *ITGA2* gene C807T polymorphism and the risk of gastric cancer in a Chinese population. The frequency of the variant T allele in our control group was 26.22%, which was similar to that in another study in a Chinese Taiwanese population (27.1%)^[33] and HapMap database (26.7% for Han Chinese). Our results showed that the variant genotypes had a 57% increased risk of developing gastric cancer.

In the subgroup analyses, we found that the polymorphism was associated with the increased risk of gastric cancer in the subgroup of the subjects aged > 58 years, but not in the subjects aged $\leq$ 58 years. Milne *et al*^[34] indicated that carcinogenesis is considered as accumulation of genetic events, and gastric cancer has a steep slope for age-specific increase in incidence. The increased risk observed in older subjects implies that the *ITGA2* genotype effects tend to be age specific. The polymorphism may contribute to elevated integrin α 2 β 1 levels beyond the age of 58, thus representing a significant risk factor in this age group. However, this is just a hypothesis to interpret the results of our study, and further research is warranted to clarify the mechanism underlying the interaction between the polymorphism and age.

Similarly, in statistical analyses stratified by smoking status, a significant association was observed in non-smokers, but not in smokers. Tobacco smoking has been

undoubtedly accepted as a independent risk factor for gastric cancer^[3,5,6]. The association between the polymorphism and gastric cancer risk could be masked by the overwhelming accumulated exposure to tobacco carcinogens in smokers so that the association is more evident in nonsmokers.

We also noted that increased risk of gastric cancer associated with the polymorphism was pronounced in rural subjects, but not in urban subjects. It has been suggested that the genetic differences have their strongest effects under conditions of low environmental pollution^[9,35]. Our results plausibly agree with the hypothesis that the genetic effects might be more prominent in the better environments of rural areas^[9]. However, this result may be found accidentally, further studies are needed to verify it.

In addition, in the stratified analyses by clinicopathological characteristics of gastric cancer, we observed a significant correlation of the variant genotypes with poorly differentiated tumors. Similarly, Langsenlehner *et al*^[28] suggested that a histological grade of 3 or 4 was found more often in breast cancer subjects with TT genotype. The result is consistent with our findings. In contrast, Yasoshima *et al*^[21] found no correlation between the expression of integrin α 2 β 1 and histopathological features such as the histological grade, stromal type, and infiltrating growth pattern. We also observed the significant association of the variant genotypes with adjacent organ invasions. Several studies have suggested that integrin α 2 β 1 was closely associated with invasion and metastasis in gastric cancer or tumor cells^[18-21,31]. These studies might explain the result we observed. However, no correlation between the polymorphism and lymph node metastasis or location of gastric cancer was found in the stratified analyses. Because the number of cases in the subgroups was relatively small and clinicopathological variables were obtained at the time of diagnosis, our findings should be interpreted with caution before being confirmed in further studies. Thus, large-sized studies which prospectively follow up the clinical outcome, especially the survival rate, may be required to elucidate the association between the polymorphism and gastric cancer progression as well as prognosis.

Some limitations may exist in the present study. First, our study is a hospital-based case-control study, so we can not rule out the selection and recall bias. Nevertheless, the T allele frequency in control subjects is quite similar to that reported in HapMap database for Han Chinese in Beijing (0.262 in our study *vs* 0.267 in HapMap database) and the genotype distributions of cases and controls were in Hardy-Weinberg equilibrium. The second limitation is our relatively small sample size, with 307 cases and 307 controls. So gene-environment interactions may have been underpowered in stratified analyses. However, our preliminary data certainly provides some interesting information and valuable guidance for the future studies in this area. Finally, no enough information on *H. pylori* status was available in cases and controls, because of the ethical reasons.

In conclusion, the present study provides evidence that the *ITGA2* gene C807T polymorphism is associated with an increased risk of gastric cancer in a Chinese population. The association is especially evident in older individuals, non-smokers and rural subjects, and the variant genotypes may also play a role in the differentiation and invasion of gastric cancer, indicating that the polymorphism may be a useful diagnostic marker for genetic susceptibility to gastric cancer. Further studies with larger samples and functional studies are needed to elucidate the role of genetic variations in *ITGA2* and the pathogenesis of gastric cancer.

COMMENTS

Background

Integrin $\alpha 2 \beta 1$ has been considered as a key factor for cancer development and progression, especially in gastric cancer. Polymorphisms in *ITGA2* gene is responsible for the expression of integrin $\alpha 2 \beta 1$. Recent studies indicated that the *ITGA2* gene C807T polymorphism was associated with cancer risk.

Research frontiers

Using polymerase chain reaction-restriction fragment length polymorphism method, this study explored the relationship between *ITGA2* C807T polymorphism and gastric cancer risk.

Innovations and breakthroughs

The results suggest that the polymorphism is associated with the elevated risk of gastric cancer in a Chinese population, especially in older individuals aged > 58 years, nonsmokers, and rural subjects. Further analyses revealed that the polymorphism may play a role in differentiation and invasion of gastric cancer.

Applications

The results of this study could help further understand the genetic determinants of gastric cancer. The polymorphism may be a useful diagnostic marker for genetic susceptibility to gastric cancer.

Terminology

Integrins are members of a family of cell-surface heterodimeric proteins that mediate cell-matrix and cell-cell interactions. Single nucleotide polymorphisms represent a natural genetic variability at a high density in the human genome, which are responsible for the inter-individual variation and diversity. They have been recently considered as the main genetic elements involved in the development of common and complex diseases, including various cancers.

Peer review

The current study was designed, processed and concluded well, deserving publication.

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Log-normal censored regression model detecting prognostic factors in gastric cancer: A study of 3018 cases

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Abstract

AIM: To investigate the efficiency of Cox proportional hazard model in detecting prognostic factors for gastric cancer.

METHODS: We used the log-normal regression model to evaluate prognostic factors in gastric cancer and compared it with the Cox model. Three thousand and eighteen gastric cancer patients who received a gastrectomy between 1980 and 2004 were retrospectively evaluated. Clinic-pathological factors were included in a log-normal model as well as Cox model. The akaike information criterion (AIC) was employed to compare the efficiency of both models. Univariate analysis indicated that age at diagnosis, past history, cancer location, distant metastasis status, surgical curative degree, combined other organ resection, Borrmann type, Lauren's classification, pT stage, total dissected nodes and pN stage were prognostic factors in both log-normal and Cox models.

RESULTS: In the final multivariate model, age at diagnosis, past history, surgical curative degree, Borrmann type, Lauren's classification, pT stage, and pN stage were significant prognostic factors in both log-normal and Cox models. However, cancer location, distant metastasis status, and histology types were found to be significant prognostic factors in log-normal results alone. According to AIC, the log-normal model performed better than the Cox proportional hazard model (AIC value: 2534.72 vs 1693.56).

CONCLUSION: It is suggested that the log-normal regression model can be a useful statistical model to evaluate prognostic factors instead of the Cox proportional hazard model.

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Key words: Gastric cancer; Log normal regression model; Cox proportional hazard model; Prognostic factors

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INTRODUCTION

The survival of patients with gastric cancer has recently been improved because of early detection, rational lymphadenectomy and several therapeutic modalities^[1,2]. However, gastric cancer still remains the second leading cause

of cancer mortality in the world. It is acknowledged that surgery and systemic chemotherapy can clearly improve the survival of patients with gastric cancer^[3,4]. However, a sensible treatment option must be fundamentally based on the current evaluation of prognostic factors, so a rational method to evaluate the prognostic factors is very important in establishing therapeutic strategies and evaluate prognosis.

Survival analysis is a branch of statistics which deals with death in biological organisms and failure in mechanical systems. The Cox model is the standard tool for assessing the effect of prognostic factors; however, there may be substantive differences in the estimated prognosis obtained by the Cox model rather than a log-normal model^[5]. The Cox model is semiparametric, in that the baseline hazard takes on no particular form^[6]. In contrast to Cox, a link to parametric survival models comes through alternative functions for the baseline hazard. In this case, one can let the baseline hazard be a parametric form such as log-normal. It is acknowledged that most of studies used the Cox proportional hazard model to find the relation between survival time and covariates of patients with gastric cancer^[7-9]. On the other hand, some studies reported that log-normal regression could estimate the parameter more efficiently than the Cox model^[5]. However, the efficiency of log-normal regression was still controversial.

The aim of this retrospective study was to elucidate the factors affecting the survival of patients with GC using log-normal regression, and to compare these results with the Cox model.

MATERIALS AND METHODS

Patients

In this study, three thousand and eighteen cases with gastric cancer were selected on whom an operation was performed at the China Medical University between 1980 and 2004. The selection criteria for inclusion were as follows: (1) an operation was performed; (2) lymph nodes were dissected and then pathologically examined; and (3) the patient medical records were available. All patients were periodically followed up through post letters, and/or telephone interviews with patients and their relatives. Clinical, surgical and pathological findings, and all follow-up information were collected and recorded in a database, and 5-year survival rate was calculated. The study protocol was approved by the Ethics Committee of China Medical University.

Reference standard

Lymph nodes were meticulously dissected from the en bloc specimens, and the classification of the dissected lymph nodes was determined by surgeons who reviewed the excised specimens after surgery based on the Japanese Classification of Gastric Carcinoma^[10]. Accordingly, lymphadenectomy was classified as D1, dissection of all the Group 1 lymph nodes; D2, dissection of all Group 1 and Group 2 lymph nodes; and D3, dissection of all the Group 1, Group 2 and Group 3 lymph nodes. pN

category was defined as pN0 (no metastatic lymph node), pN1 (1-6 metastatic lymph nodes), pN2 (7-15 metastatic lymph nodes) and pN3 (> 15 metastatic lymph nodes), according to the 5th Edition of UICC^[11]. The location of tumors was defined as upper, middle and lower third gastric cancer, according to JCGC^[10] and the histological grade was defined as poorly differentiated, moderately differentiated and well differentiated, according to the latest World Health Organization (WHO) classification^[12]. The Borrmann type was defined as Borrmann I, Borrmann II, Borrmann III and Borrmann IV, according to JCGC^[10]. The histological type was determined according to Lauren's classification.

Statistical analysis

All data were analyzed using STAT statistics software (Version 10.0, Stata Corp LP). Clinic-pathologic factors were entered to a log-normal censored regression, as well as a Cox proportional hazard model in univariate and multivariate analysis in order to find the prognostic factors. The term of relative risk (RR) was used to interpret the risk of death in parametric results and the term of Akaike Information Criterion (AIC) was employed to compare the efficiency of models. Disease-specific survival was analyzed using the Kaplan-Meier method. The log-rank test was used to analyze survival differences. Lower AIC indicates better likelihood. A *P* value of less than 0.05 was considered statistically significant.

RESULTS

Clinic-pathological characteristics of patients with gastric cancer

The male-to-female ratio among the 3018 patients enrolled was 2.74:1 and the mean age was 57.54 years (range: 19 to 90 years) at operation. 269, 1362 and 608 cases received D1, D2 and more than D2 lymph node dissection respectively. In addition, six hundred and fifty seven cases received palliative surgery. From 3018 cases, a total of 46081 lymph nodes were removed and examined, and the mean number of examined lymph nodes was 15.27. One thousand six hundred and forty three cases were observed lymph node metastasis. Thus, the incidence of lymph node metastasis was 54.44%. The last follow-up was Jan 1, 2009, with a total follow-up rate of 70.68%. More clinic-pathologic factors are shown in Table 1.

Multivariate analysis of prognostic factors in gastric cancer

Univariate analysis indicated that age at diagnosis, past history, cancer location, distant metastasis status, surgical curative degree, combined other organ resection, Borrmann type, Lauren's classification, pT stage, total dissected nodes and pN stage were prognostic factors in both log-normal and Cox models. In the final multivariate model, age at diagnosis, past history, surgical curative degree, Borrmann type, Lauren's classification pT stage, and pN stage were significant prognostic factors in both

Table 1 Clinicopathological characteristics of 3018 gastric cancers included in the study *n* (%)

Variable	Subgroups	Frequency
Gender ratio	Male	2211 (73.26)
	Female	807 (26.74)
Age at diagnosis (mean ± SD; yr)		57.54 ± 11.24
Past history		
	Without	2234 (74.02)
	With	784 (25.98)
Family history	Without	2467 (81.74)
	With	551 (18.26)
Cancer number	Single	2883 (96.65)
	Multiple	100 (3.35)
Cancer location	Lower stomach	1873 (62.64)
	Middle stomach	492 (16.46)
	Upper stomach	355 (11.87)
	Total stomach	270 (9.03)
Distant metastasis status	Without	2540 (85.04)
	With	447 (14.96)
Maximum tumor diameter (mean ± SD, cm)		5.85 ± 3.30
Surgical curative degree	Absolutely radical	1396 (49.73)
	Relatively radical	809 (28.82)
	Palliative	602 (21.45)
Lymph node dissection	More than D2	608 (20.99)
	D2	1362 (47.03)
	D1	269 (9.29)
	Palliative surgery	657 (22.69)
Combined other organ resection	Without	2016 (76.80)
	With	609 (23.20)
Histological type	Well differentiated	755 (27.43)
	Middle differentiated	382 (13.88)
	Poor differentiated	1615 (58.69)
Borrmann classification	I	70 (2.98)
	II	426 (18.15)
	III	1571 (66.94)
	IV	280 (11.93)
Lauren classification	Intestinal type	1170 (43.89)
	Diffuse type	1496 (56.11)
pT stage	pT1	328 (11.89)
	pT2	1486 (53.88)
	pT3	737 (26.72)
	pT4	207 (7.51)
Total dissected lymph node (mean ± SD)		15.27 ± 13.11
Pathological lymph node status	pN0	1375 (45.56)
	pN1	1039 (34.43)
	pN2	432 (14.31)
	pN3	172 (5.70)

log-normal and Cox models. However, cancer location, distant metastasis status and histology types were found as significant prognostic factors in log-normal results alone (Table 2). According to AIC, the log-normal model performed better than the Cox proportional hazard model (AIC value: 2534.72 *vs* 1693.56) (Table 3).

Survival outcomes

Overall, the 5-year disease-specific survival rate was 29.57%. The survival was observed significantly different in patients with different cancer locations (5-year disease-specific survival rate, L tumor *vs* M tumor *vs* U tumor *vs* T tumor: 33.11% *vs* 30.46% *vs* 25.66% *vs* 7.59%, $\chi^2 =$

Table 2 Univariate model of Cox and log normal regression with prognostic factors

	HR (95% CI)	
	Cox	Log normal
Sex		
Male	0.953 (0.843-1.078)	0.925 (0.818-1.046)
Female	1.00	1.00
Age at diagnosis	1.015 ¹ (1.009-1.020)	1.016 ¹ (1.011-1.021)
Past history		
Without	1.00	1.00
With	0.715 ¹ (0.631-0.831)	0.694 ¹ (0.612-0.787)
Family history		
Without	1.00	1.00
With	0.871 (0.752-1.009)	0.875 (0.754-1.014)
Cancer number		
Single	1.00	1.00
Multiple	0.870 (0.622-1.218)	0.924 (0.661-1.294)
Cancer location		
Lower third	1.00	1.00
Middle third	1.181 ¹ (1.017-1.373)	1.302 ¹ (1.233-1.374)
Upper third	1.436 ¹ (1.212-1.701)	1.695 ¹ (1.429-1.897)
Total stomach	2.464 ¹ (2.062-2.944)	2.207 ¹ (2.011-2.677)
Distant metastasis		
Absent	1.00	1.00
Present	2.554 ¹ (2.194-2.973)	2.596 ¹ (2.227-3.027)
Surgical curative degree		
Absolutely radical	1.00	1.00
Relatively radical	1.835 ¹ (1.593-2.114)	2.159 ¹ (2.020-2.308)
Palliative	4.236 ¹ (3.714-4.832)	4.661 ¹ (4.214-4.759)
Lymph node dissection		
> D2	1.00	1.00
D2	0.989 (0.859-1.138)	1.536 ¹ (1.458-1.619)
D1	1.056 (0.853-1.307)	2.359 ¹ (2.121-2.574)
< D1	3.310 ¹ (2.854-3.839)	3.624 ¹ (3.231-3.862)
Combined other organ resection		
Without	1.00	1.00
With	1.981 ¹ (1.749-2.245)	2.070 ¹ (1.825-2.348)
Histologic types		
Well differentiated	1.00	1.00
Middle differentiated	0.706 ¹ (0.592-0.843)	0.976 (0.918-1.039)
Poor differentiated	0.918 (0.814-1.036)	0.952 (0.897-1.011)
Borrmann classification (<i>n</i> (%))		
I	1.00	1.00
II	1.005 (0.892-1.340)	0.981 (0.894-1.019)
III	1.247 ¹ (1.173-1.638)	1.176 ¹ (1.074-1.293)
IV	2.512 ¹ (1.842-3.075)	2.610 ¹ (2.416-3.153)
Lauren classification (<i>n</i> (%))		
Intestinal type	1.00	1.00
Diffuse type	1.245 ¹ (1.082-1.184)	1.171 ¹ (1.015-1.384)
pT stage		
pT1	1.00	1.00
pT2	2.936 ¹ (2.299-3.751)	1.787 ¹ (1.666-1.916)
pT3	4.305 ¹ (3.357-5.522)	3.193 ¹ (3.066-3.321)
pT4	7.697 ¹ (5.759-10.287)	5.707 ¹ (5.579-5.833)
Total dissected nodes	0.993 ¹ (0.988-0.998)	0.994 ¹ (0.988-0.998)
pN stage		
pN0	1.00	1.00
pN1	1.555 ¹ (1.372-1.764)	1.633 ¹ (1.533-1.740)
pN2	2.510 ¹ (2.133-2.953)	2.667 ¹ (2.561-2.772)
pN3	3.669 ¹ (2.901-4.640)	4.355 ¹ (4.249-4.460)

¹Statistically significant (*P* < 0.05). HR: Hazard ratio; CI: Confidence interval.

190.27, *P* = 0.000) (Figure 1). In addition, the cases with distant metastasis received a poorer prognosis than those without distant metastasis (5-year disease-specific survival

Table 3 Multivariate model of Cox and log normal regression with prognostic factors (full model and final model)

	Cox HR (95% CI)		Log normal HR (95% CI)	
	Full model (AIC = 1508.49)	Final model (AIC = 2534.72)	Full model (AIC = 913.34)	Final model (AIC = 1693.56)
Sex				
Male	0.91 (0.801-1.034)		0.886 (0.781-1.005)	
Female	1.00			
Age at diagnosis	1.014 ¹ (1.009-1.02)	1.011 ¹ (1.006-1.017)	1.015 ¹ (1.010-1.021)	1.015 ¹ (1.009-1.020)
Past history				
Without	1.00	1.00	1.00	1.00
With	0.840 ¹ (0.738-0.955)	0.858 ¹ (0.755-0.975)	0.813 ¹ (0.716-0.914)	0.809 ¹ (0.713-0.919)
Family history				
Without	1.00		1.00	1.00
With	0.957 (0.8254-1.11)		0.967 (0.833-1.234)	
Cancer number				
Single	1.00		1.00	
Multiple	1.21 (0.861-1.701)		1.312 (1.935-1.840)	
Cancer location				
Lower third	1.00		1.00	1.00
Middle third	1.033 (0.885-1.205)		1.135 ¹ (1.073-1.199)	1.129 ¹ (1.069-1.194)
Upper third	1.406 ¹ (1.173-1.686)		1.288 ¹ (1.224-1.353)	1.277 ¹ (1.211-1.338)
Total stomach	1.466 ¹ (1.214-1.771)		1.462 ¹ (1.365-1.558)	1.439 ¹ (1.343-1.535)
Distant metastasis				
Absent	1.00		1.00	1.00
Present	1.21 ¹ (1.013-1.447)		1.205 ¹ (1.011-1.437)	1.198 ¹ (1.009-1.424)
Surgical curative degree				
Absolutely radical	1.00	1.00	1.00	1.00
Relatively radical	1.389 ¹ (1.197-1.611)	1.383 ¹ (1.194-1.601)	1.724 ¹ (1.537-1.934)	1.672 ¹ (1.538-1.817)
Palliative	3.889 ¹ (2.583-5.855)	2.687 ¹ (2.316-3.116)	2.972 ¹ (2.770-3.174)	2.796 ¹ (2.653-2.938)
Lymph node dissection				
> D2	1.00		1.00	
D2	0.908 (0.784-1.051)		0.967 (0.892-1.049)	
D1	0.901 (0.712-1.14)		0.935 (0.855-1.015)	
< D1	0.607 ¹ (0.395-0.935)		0.904 (0.784-1.024)	
Combined other organ resection				
Without	1.00		1.00	
With	1.406 ¹ (1.227-1.61)		1.447 ¹ (1.264-1.657)	
Histologic types				
Well differentiated	1.00		1.00	1.00
Middle differentiated	1.056 (0.878-1.271)		1.110 ¹ (1.042-1.183)	1.120 ¹ (1.051-1.193)
Poor differentiated	1.179 ¹ (1.035-1.343)		1.232 ¹ (1.160-1.304)	1.254 ¹ (1.182-1.327)
Borrmann classification				
I	1.00	1.00	1.00	1.00
II	1.142 (0.957-1.319)	1.201 (1.068-1.433)	1.018 (0.943-1.106)	1.015 (0.941-1.102)
III	1.315 ¹ (1.113-1.672)	1.394 ¹ (1.205-1.741)	1.246 ¹ (1.052-1.539)	1.241 ¹ (1.047-1.533)
IV	2.126 ¹ (1.758-3.119)	2.253 ¹ (1.827-3.284)	2.530 ¹ (2.376-2.713)	2.526 ¹ (2.372-2.708)
Lauren classification				
Intestinal type	1.00		1.00	1.00
Diffuse type	1.131 ¹ (1.012-1.358)		1.307 ¹ (1.154-1.528)	1.302 ¹ (1.148-1.523)
pT stage				
pT1	1.00	1.00	1.00	1.00
pT2	1.851 ¹ (1.431-2.394)	1.971 ¹ (1.528-2.542)	1.195 ¹ (1.102-1.297)	1.193 ¹ (1.100-1.294)
pT3	1.981 ¹ (1.511-2.598)	2.19 ¹ (1.678-2.858)	1.428 ¹ (1.328-1.527)	1.423 ¹ (1.324-1.522)
pT4	2.344 ¹ (1.699-3.235)	2.501 ¹ (1.821-3.435)	1.706 ¹ (1.557-1.855)	1.697 ¹ (1.549-1.847)
Total dissected nodes	0.987 ¹ (0.981-0.993)		0.988 ¹ (0.982-0.993)	
pN stage				
pN0	1.00	1.00	1.00	1.00
pN1	1.281 ¹ (1.123-1.461)	1.266 ¹ (1.11-1.444)	1.507 ¹ (1.393-1.620)	1.500 ¹ (1.387-1.622)
pN2	2.139 ¹ (1.783-2.566)	2.095 ¹ (1.749-2.51)	2.271 ¹ (2.151-2.391)	2.250 ¹ (2.130-2.370)
pN3	3.24 ¹ (2.446-4.292)	3.325 ¹ (2.52-4.386)	3.422 ¹ (3.242-3.602)	3.375 ¹ (3.196-3.554)

¹Statistically significant (< 0.05); HR: Hazard ratio; CI: Confidence interval; AIC: Akaike Information Criterion.

rate, 33.50% *vs* 7.56%, $\chi^2 = 372.21$, $P = 0.000$) (Figure 2). Furthermore, the cases with different histologic types were investigated with a different prognosis (5-year disease-spe-

cific survival rate, well differentiated tumors *vs* middle differentiated tumors *vs* poor differentiated tumors: 39.27% *vs* 29.67% *vs* 25.03%, $\chi^2 = 12.37$, $P = 0.002$) (Figure 3).

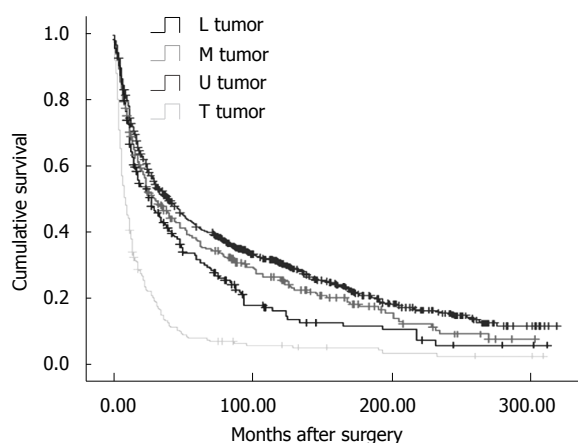


Figure 1 Disease-specific survival analysis according to cancer locations ($\chi^2 = 190.27$, $P = 0.000$, Log Rank test). L tumor: Lower third tumors; M tumor: Middle third tumors; U tumor: Upper third tumors; T tumor: Tumor occupied the total stomach.

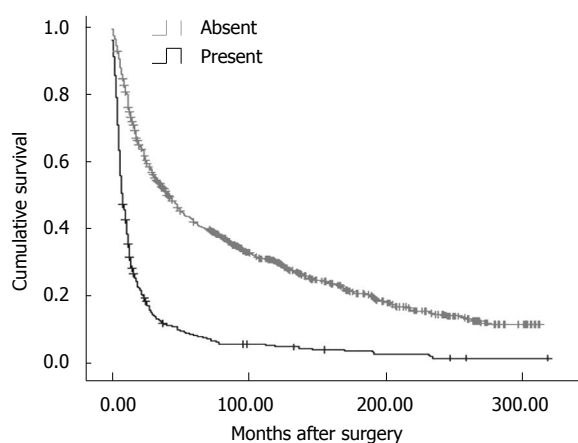


Figure 2 Disease-specific survival analysis according to distant metastasis status ($\chi^2 = 372.21$, $P = 0.000$, Log Rank test).

DISCUSSION

There were several studies that have investigated the factors influencing prognosis^[13,14]. The conclusions of the reports were controversial, though most of them used the Cox proportional hazard model to find the relation between survival time and patient characteristics, and clinical and pathological factors in patients with gastric cancer.

After evaluating the clinic-pathological factors of 738 patients, Kulig *et al*^[7] reported that patient age, depth of tumor infiltration, tumor location, and metastatic node ratio were identified as independent prognostic factors in a Cox proportional hazards model. In addition, Shiraishi *et al*^[15] reported that independent prognostic factors of gastric cancer were serosal invasion, extragastric lymph node metastasis and liver metastasis, but survival was not significantly associated with any of the patient factors or operation factors, including the extent of lymph node dissection. In our study, age at diagnosis, past history, surgical curative degree, Borrmann type, Lauren's classification, pT stage, and pN stage were significant prognostic factors in Cox mod-

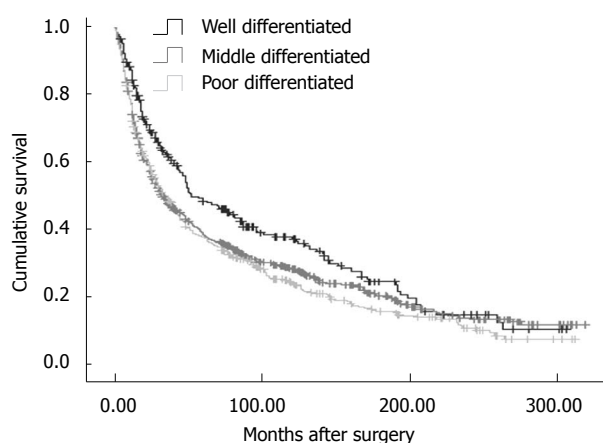


Figure 3 Disease-specific survival analysis according to histologic types ($\chi^2 = 12.37$, $P = 0.002$, Log Rank test).

els. There was a small difference between our study and other reports. In the final model of log-normal analysis, we investigated that cancer location, distant metastasis and histologic types were significantly related to the survival. The outcomes were also verified by disease-specific survival analysis. However, the association between above factors and survival were not observed. In log-normal analysis, Pourhoseingholi *et al*^[5] observed that distant metastasis, histology type and pT stage were significant prognostic factors after retrospectively studying 746 Iranian patients. Moreover, distant metastasis was a significant prognostic factor only in log-normal analysis, not in the Cox model.

Compared to the Cox model, the evaluation criteria in our study indicated log-normal regression was more powerful not only in the full model, but also in the final one. In the final model, the selected prognostic factors in the log-normal model were different compared to those in the Cox model. Furthermore, the data strongly supported the log-normal regression in the full and final models, and might lead to more precise results as an alternative for Cox.

In conclusion, according to the results of our study, age at diagnosis, past history, cancer location, distant metastasis status, surgical curative degree, combined other organ resection, histology types, Borrmann type, Lauren's classification, pT stage, total dissected nodes and pN stage were significant prognostic factors of gastric cancer. It is suggested that log-normal regression model can be a useful statistical model to evaluate prognostic factors instead of the Cox proportional hazard model.

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COMMENTS

Background

Most of studies used the Cox proportional hazard model to find the relation between survival time and covariates of patients with gastric cancer (GC). On the other hand, some studies reported that log-normal regression could estimate

the parameter more efficiently than the Cox model. However, the efficiency of log-normal regression was still controversial.

Research frontiers

In this retrospective study, the authors elucidated the factors affecting the survival of patients with GC using log-normal regression, and to compare these results with the Cox model.

Applications

It is suggested that log-normal regression model can be a useful statistical model to evaluate prognostic factors instead of the Cox proportional hazard model.

Peer review

Overall the study was well designed, performed, and analyzed. The very minor, but important parameters should be added in analysis.

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Diaphragm disease compared with cryptogenic multifocal ulcerous stenosing enteritis

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Abstract

As the use of drugs such as nonsteroidal anti-inflammatory drugs (NSAIDs) increases, so too do gastrointestinal ulcers, bleeding, perforation and obstruction. Diaphragm disease of the small intestine is formed by submucosal fibrosis and destruction of lamina muscularis due to chronic ulceration, which corresponds to the most severe stage of NSAID enteropathy. It may lead to stricture of the small intestine. If such ulcerations and strictures in the small intestine are multiple, differential diagnosis is between diaphragm disease and cryptogenic multifocal ulcerous stenosing enteritis (CMUSE), because the gross findings of diaphragm disease are similar to those of CMUSE. We report a rare case of diaphragm disease caused by NSAID. It has been finally confirmed by capsule endoscopy and the origin of chronic obscure gastrointestinal bleeding was found to be multiple ulcers and strictures in the small intestine. After operation, we diagnosed the patient with diaphragm disease rather than CMUSE.

INTRODUCTION

The complications of non-steroidal anti-inflammatory drugs (NSAIDs), aspirin, antiplatelet agents, and antithrombotic agents are known to include gastrointestinal ulceration, bleeding, perforation and obstruction^[1]. NSAID-induced mucosal injury can occur to the upper and lower gastrointestinal tract. The incidence of NSAID-induced enteropathy is not less than that of gastropathy. Diaphragm disease is the most severe stage of NSAID enteropathy. In ambulatory patients who took NSAIDs for > 3 mo because of arthritis, 70% had small intestinal ulcers and erosions by capsule endoscopy^[2]. The diaphragm is formed by chronic fibrosis and destruction of lamina muscularis with chronic ulceration, and causes obstruction of the lumen in the small bowel^[3]. However, diaphragm disease is a rare diagnosis.

Cryptogenic multifocal ulcerous stenosing enteritis (CMUSE) has multiple ulcerations and strictures in the small intestine; it is similar to diaphragm disease in terms of gross findings, and it is characterized by a chronic and

relapsing clinical course, and is more common in middle-aged patients.

We report a case of diaphragm disease in the small bowel that presented with obscure overt bleeding due to NSAID use, which was detected by capsule endoscopy. We review the differential diagnosis with CMUSE through histological findings and clinical course after surgery.

CASE REPORT

A 79-year-old woman was hospitalized for a low level of hematochezia. At admission, her hemoglobin level was 8.9 g/dL. She had also taken 20 mg piroxicam, 275 mg naproxen and 25 mg diclofenac daily for 4 years because of degenerative joint diseases. She had been hospitalized for iron deficiency anemia 5 years ago and there was no active bleeding focus upon esophagogastroduodenoscopy (EGD) and colonoscopy at that time. It was recommended that she undergo capsule endoscopy, however, she refused and was discharged.

After hospitalization, she had EGD and abdominal computed tomography (CT) to find the focus of her bleeding. No bleeding foci were revealed by EGD and abdominal CT. She had no more hematochezia after hospitalization. On day 3 of hospitalization, capsule endoscopy was performed. There were multiple, concentric circular ulcerations, with luminal narrowing in the jejunum and ileum, with many variable-sized erosions and bleeding stigmata in the ulcerations (Figure 1). The capsule in the small bowel was not excreted until 8 d after capsule endoscopy, even though she could have a meal. According to the results of capsule endoscopy, we need to diagnose differentially between NSAID-induced enteropathy and CMUSE, because of the gross similarities, such as multiple ulcerations and strictures in the small intestine. Even though the patient was an elderly woman and took NSAIDs, she was not diagnosed with NSAID-induced enteropathy because of the similar endoscopic findings to CMUSE. To confirm the diagnosis, histological examination was needed. She complained of chronic abdominal pain for 2 years, therefore, we could diagnose by capsule endoscopy that she had symptomatic multiple strictures.

To relieve the chronic abdominal pain caused by the multiple strictures in the small bowel, and to remove the retained capsule and evaluate the exact cause of the multiple ulcerations and strictures, we performed segmental resection of the ileum (Figure 2) instead of double balloon enteroscopy. Histological findings in the ileum (Figure 3) revealed typical multiple, circular ulcerations and a mucosal diaphragm, which suggested the most severe complications of chronic NSAID use. These mucosal diaphragms indicate chronic ulcers, submucosal fibrosis, reactive epithelial change, and chronic inflammation. After discharge, she had no more gastrointestinal bleeding and abdominal pain and took misoprostol at the outpatient clinic with close observation for > 1 year.

DISCUSSION

Diaphragm disease is the pathognomic characteristic of NSAID enteropathy, and was named by Bjarnason *et al*^[4].

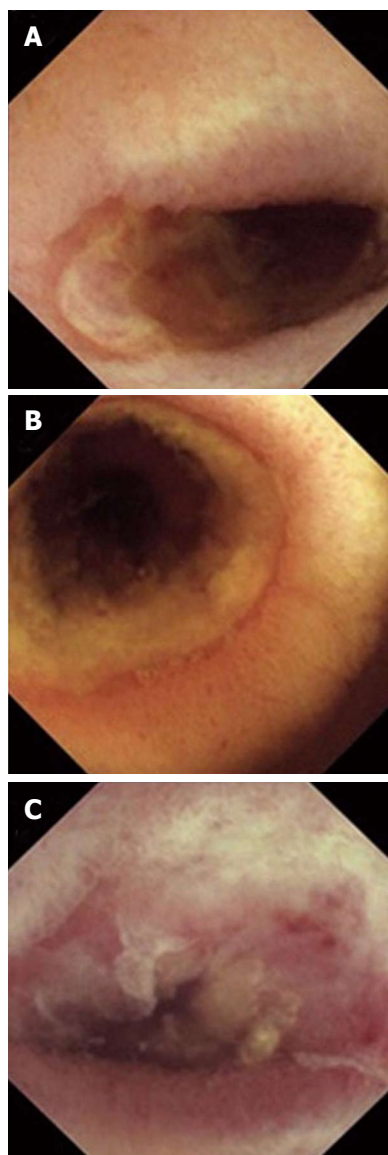


Figure 1 Capsule endoscopic findings. A: There were concentric ulcerations with luminal narrowing; B: There were many variable-sized erosions and bleeding stigmata in the ulcerations; C: There was a totally obstructed lesion in which the capsule was suspected to be retained.

They described the clinicopathological features of NSAID-induced stricture as diaphragm disease. The histopathological characteristics of diaphragm disease are: superficial ulceration at the apex of the villi; circumferential ring-like stricture; multiple, short segment annular strictures; transmural inflammation; and submucosal fibrosis^[5].

Several other authors have reported diaphragm disease in patients taking NSAIDs, by enteroscopy^[6] and after laparotomy^[5,7]. The first diagnosis of small intestinal diaphragm disease after use of NSAID through capsule endoscopy was reported by Yousfi *et al*^[3]. In their study with capsule endoscopy, there were multiple small-intestinal strictures where the capsule was retained. Thus, exploratory laparoscopy was required to remove the retained capsule, as in our case.

After long-term use of NSAIDs for > 20 years, the small intestine shows fibrotic constriction and thickened

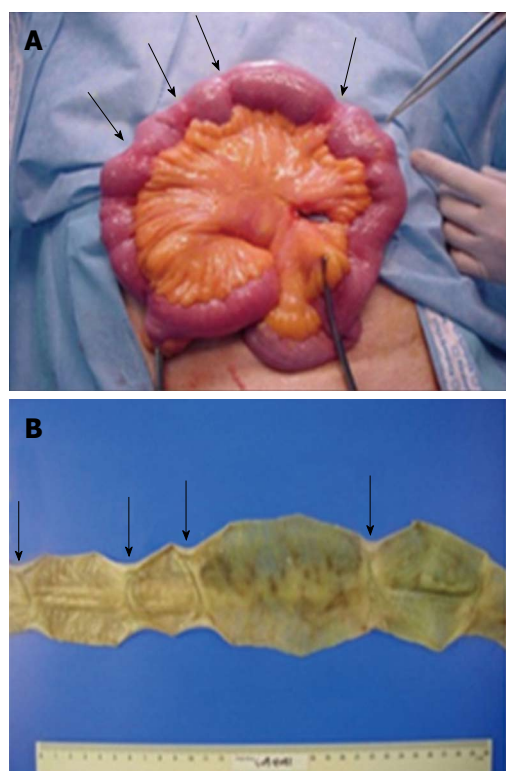


Figure 2 Specimen from segmental resection of the ileum. A: A capsule was located at 60 cm up from the terminal ileum. Forceps and hand point out the location in the ileum where the capsule was retained. There were multiple strictures in the ileum (black arrows); B: In longitudinal section, there were multiple thin, web-like mucosal septa that caused abrupt luminal narrowing in the small intestine (black arrows).

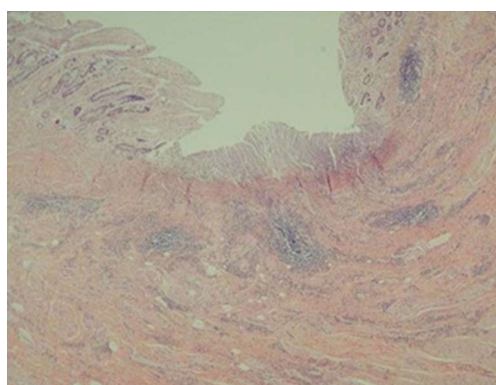


Figure 3 Histological findings of the ileum. The mucosal diaphragm reveals surface erosion or ulceration, submucosal fibrosis, reactive epithelial change, and chronic inflammation (hematoxylin and eosin stain, 40 x).

hyperemic mucosa that lead to obstruction through local damage and healing process^[8].

In NSAID-induced enteropathy, capsule endoscopy shows circumferential ulcerations, erosions and multifocal strictures^[3,9]. Capsule endoscopy is a useful option to establish the etiology of obscure overt gastrointestinal bleeding, especially in elderly patients. Diagnostic yield of capsule endoscopy for finding the focus of obscure gastrointestinal bleeding is reported to be 38%-93%^[10]. Diagnostic yield of capsule endoscopy for obscure gastrointestinal

Table 1 Differences between non-steroidal anti-inflammatory drug-induced enteropathy and cryptogenic multifocal ulcerous stenosing enteritis

	NSAID-induced enteropathy	CMUSE
Definition	Ulceration and stricture of small intestine induced by NSAIDs ^[19,20]	Unexplained small intestinal multiple stricture and ulceration ^[17,18]
Causes	NSAIDs	Unknown
Age	Old-aged people ^[26]	Middle-aged people ^[18]
Treatment	Stop NSAIDs, Prostaglandin (misoprostol) ^[21] , Sulfasalazine ^[22] , Metronidazole ^[23] , Glutamine ^[24] , Glucose/citrate ^[25]	Steroids ^[17]

NSAID: Non-steroidal anti-inflammatory drug; CMUSE: Cryptogenic multifocal ulcerous stenosing enteritis.

bleeding is not different for overt and occult bleeding^[11,12]. Diagnostic yields of CT angiography and double balloon enteroscopy in finding the focus of obscure gastrointestinal bleeding were 24% and 75.7%, respectively^[13,14].

The origin of gastrointestinal bleeding can be detected in a higher percentage of patients by capsule endoscopy than by CT angiography and double balloon enteroscopy^[10]. In our case, we performed capsule endoscopy to find overt obscure bleeding foci after abdominal CT scanning. There was no definite stricture or sign of significant obstruction by abdominal CT. However, the capsule became trapped in the bowel unexpectedly. The important complication of capsule endoscopy is capsule retention, for which the incidence is < 2%^[15]. Intestinal stricture might be suspected, especially in patients with chronic NSAID use, ischemic bowel disease, abdominal radiotherapy, and Crohn's disease. For these patients, capsule endoscopy can be performed after abdominal CT or small bowel series to find strictures^[10]. Stricture cannot be found completely by abdominal CT or small bowel series, therefore, an M2A patency capsule can be considered, which is biodegradable in the gastrointestinal tract in patients with suspected intestinal stricture^[16].

Our patient had multiple ulcerations and strictures in the small intestine, therefore, diaphragm disease was needed to be differentiated from CMUSE, even though the patient was an elderly woman who was taking NSAIDs. The characteristics of NSAID-induced enteropathy and CMUSE using previously published data are summarized in Table 1. CMUSE is defined as unexplained small intestinal multiple strictures and ulcerations of unknown origin. It is characterized as an atypical type of vasculitis^[17]. Its clinical features include unexplained stricture and ulceration of the small bowel, without systemic inflammation, which are found in young and middle-aged patients. CMUSE can relapse chronically or after surgery. The symptoms of CMUSE can be improved by steroid treatment^[17,18].

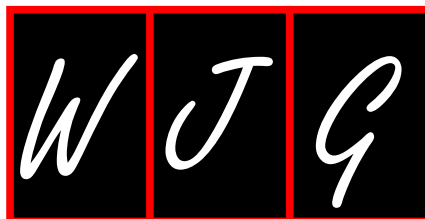
In conclusion, NSAID-induced diaphragm disease in the small bowel can be diagnosed efficiently by capsule endoscopy, and the gross endoscopic features of diaphragm disease are similar to those of CMUSE. We

also suggest that NSAID-induced enteropathy, such as diaphragm disease, should be suspected in NSAID users, especially in elderly patients.

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Time for the world to move beyond the percutaneous endoscopic gastrostomy

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Abstract

Percutaneous endoscopic gastrostomy (PEG) is a proven feeding tube, just as the nasogastric tube is proven to be able to deliver enteral nutrition. For long-term use, both patient and caregiver want neither. What is desired is the LOOPPEG® 3G tube, more secure than the PEG, and less risky to change than the nasogastric tube. Future clinical research should focus on this high-comfort low-risk tube.

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Key words: Tube feeding; Enteral nutrition; Dysphagia; Stroke

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TO THE EDITOR

I found "Survival of geriatric patients after percutaneous

endoscopic gastrostomy in Japan" by Yutaka Suzuki *et al*^[1] to be an interesting and timely article.

With an aged population and several centers working together, they were able to recruit a large sample and, consequently, produce robust results. The first lesson to be learnt is that collaboration can produce better results. The second lesson is that, for the Japanese population at least, the percutaneous endoscopic gastrostomy in geriatrics is proven. To the co-authors and their institutions, I offer my heartiest congratulations. My country, Singapore, is ageing rapidly and their experiences can offer valuable lessons.

I emphasize that my subsequent suggestion for future research should not be taken as criticisms of their work, which is an unqualified success. By way of introducing my comments, I pose two questions.

First, since elderly patients in other countries might react differently from Japanese patients, should we not do a similar study of the PEG in Singapore? My answer is no, for the following reason. The difference in year (or mo) is unlikely to be important to the geriatric patient, in whom compassion is more valued than cure.

Second, since the nasogastric tube might give a better survival than the PEG, should we not do a similar study on this feeding tube? Again, my answer is no, for the following reasons. Feeding tube and survival of the elderly have a correlation but not a cause-effect relationship. Both nasogastric tube and PEG can deliver the enteral nutrition, and the choice is determined more by the risk/comfort profile of the tube. Statistical significance does not mean clinical significance. Conversely, lack of the former does not mean that the PEG is not a clinically better tube. The relationship between nasogastric tube and PEG is predictable, independent of age and race, and unlikely to be affected by the study findings, however robust.

This relationship is illustrated in Figure 1. There are enough published data to show that the nasogastric tube is low in risk and low in comfort, whereas the PEG is very comfortable but also high in risk^[2]. For long-term use, both patients and caregivers want neither option! What

Risk	High	×	PEG
	Low	Nasogastric tube	✓
		Low	High
		Comfort	

Figure 1 Risk/Comfort Chart. The desired tube is the high-comfort low-risk option (✓). PEG: Percutaneous endoscopic gastrostomy.

they need is a very comfortable but low in risk option.

In my opinion, there is only one feeding tube which meets this profile. The LOOPPEG® 3G tube is comfortable because it bypasses the nose and low in risk because it cannot be dislodged^[3]. Also, it is less risky to change than the nasogastric tube. Consequently, the 3G tube can be made 15 Fr or smaller because tube blockage is a non-issue, having been negated by easy tube change. Thus, the trauma of changing the tube - physical, psychological and financial - is minimized.

However, no case series has been published. It may

take forever for a sizeable sample and robust results to come out from my part of the world. Hence, I hope our Japanese colleagues, having published a solid study, will take up the challenge to move beyond the PEG, research the 3G tube, and report their findings in this fine Journal.

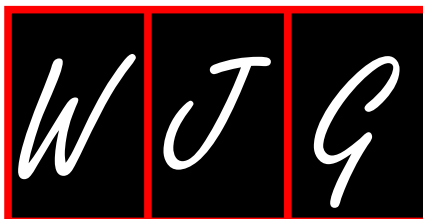
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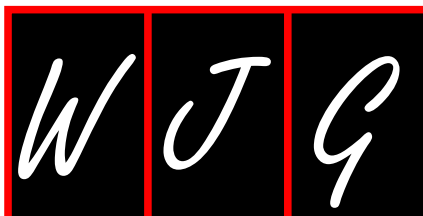
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Events Calendar 2011

January 14-15, 2011

AGA Clinical Congress of
Gastroenterology and Hepatology:
Best Practices in 2011 Miami, FL
33101, United States

January 20-22, 2011

Gastrointestinal Cancers Symposium
2011, San Francisco, CA 94143,
United States

January 27-28, 2011

Falk Workshop, Liver and
Immunology, Medical University,
Franz-Josef-Strauss-Allee 11, 93053
Regensburg, Germany

January 28-29, 2011

9. Gastro Forum München, Munich,
Germany

February 4-5, 2011

13th Duesseldorf International
Endoscopy Symposium,
Duesseldorf, Germany

February 13-27, 2011

Gastroenterology: New Zealand
CME Cruise Conference, Sydney,
NSW, Australia

February 17-20, 2011

APASL 2011-The 21st Conference of
the Asian Pacific Association for the
Study of the Liver
Bangkok, Thailand

February 22, 2011-March 04, 2011
Canadian Digestive Diseases Week
2011, Vancouver, BC, Canada

February 24-26, 2011

Inflammatory Bowel Diseases
2011-6th Congress of the European
Crohn's and Colitis Organisation,
Dublin, Ireland

February 24-26, 2011

2nd International Congress on
Abdominal Obesity, Buenos Aires,
Brazil

February 24-26, 2011

International Colorectal Disease
Symposium 2011, Hong Kong, China

February 26-March 1, 2011

Canadian Digestive Diseases Week,
Westin Bayshore, Vancouver, British
Columbia, Canada

February 28-March 1, 2011

Childhood & Adolescent Obesity:

A whole-system strategic approach,
Abu Dhabi, United Arab Emirates

March 3-5, 2011

42nd Annual Topics in Internal
Medicine, Gainesville, FL 32614,
United States

March 7-11, 2011

Infectious Diseases: Adult Issues
in the Outpatient and Inpatient
Settings, Sarasota, FL 34234,
United States

March 14-17, 2011

British Society of Gastroenterology
Annual Meeting 2011, Birmingham,
England, United Kingdom

March 17-19, 2011

41. Kongress der Deutschen
Gesellschaft für Endoskopie und
Bildgebende Verfahren e.V., Munich,
Germany

March 17-20, 2011

Mayo Clinic Gastroenterology &
Hepatology 2011, Jacksonville, FL
34234, United States

March 18, 2011

UC Davis Health Informatics:
Change Management and Health
Informatics, The Keys to Health
Reform, Sacramento, CA 94143,
United States

March 25-27, 2011

MedicRes IC 2011 Good Medical
Research, Istanbul, Turkey

March 26-27, 2011

26th Annual New Treatments in
Chronic Liver Disease, San Diego,
CA 94143, United States

April 6-7, 2011

IBS-A Global Perspective, Pfister
Hotel, 424 East Wisconsin Avenue,
Milwaukee, WI 53202, United States

April 7-9, 2011

International and Interdisciplinary
Conference Excellence in Female
Surgery, Florence, Italy

April 15-16, 2011

Falk Symposium 177, Endoscopy
Live Berlin 2011 Intestinal Disease
Meeting, Stauffenbergstr. 26, 10785
Berlin, Germany

April 18-22, 2011

Pediatric Emergency Medicine:
Detection, Diagnosis and Developing

Treatment Plans, Sarasota, FL 34234,
United States

April 20-23, 2011

9th International Gastric Cancer
Congress, COEX, World Trade
Center, Samseong-dong, Gangnam-
gu, Seoul 135-731, South Korea

April 25-27, 2011

The Second International Conference
of the Saudi Society of Pediatric
Gastroenterology, Hepatology &
Nutrition, Riyadh, Saudi Arabia

April 25-29, 2011

Neurology Updates for Primary
Care, Sarasota, FL 34230-6947,
United States

April 28-30, 2011

4th Central European Congress of
Surgery, Budapest, Hungary

May 7-10, 2011

Digestive Disease Week, Chicago, IL
60446, United States

May 12-13, 2011

2nd National Conference Clinical
Advances in Cystic Fibrosis, London,
England, United Kingdom

May 19-22, 2011

1st World Congress on Controversies
in the Management of Viral Hepatitis
(C-Hep), Palau de Congressos de
Catalunya, Av. Diagonal, 661-671
Barcelona 08028, Spain

May 21-24, 2011

22nd European Society of
Gastrointestinal and Abdominal
Radiology Annual Meeting and
Postgraduate Course, Venice, Italy

May 25-28, 2011

4th Congress of the Gastroenterology
Association of Bosnia and
Herzegovina with international
participation, Hotel Holiday Inn,
Sarajevo, Bosnia and Herzegovina

June 11-12, 2011

The International Digestive Disease
Forum 2011, Hong Kong, China

June 13-16, 2011

Surgery and Disillusion XXIV
SPIGC, II ESYS, Napoli, Italy

June 14-16, 2011

International Scientific Conference
on Probiotics and Prebiotics-
IPC2011, Kosice, Slovakia

June 22-25, 2011

ESMO Conference: 13th World
Congress on Gastrointestinal Cancer,
Barcelona, Spain

June 29-2, 2011

XI Congreso Interamericano
de Pediatría "Monterrey 2011",
Monterrey, Mexico

September 2-3, 2011 Falk Symposium

178, Diverticular Disease, A Fresh
Approach to a Neglected Disease,
Gürzenich Cologne,
Martinstr. 29-37, 50667 Cologne,
Germany

September 10-11, 2011

New Advances in Inflammatory
Bowel Disease, La Jolla, CA 92093,
United States

September 10-14, 2011

ICE 2011-International Congress of
Endoscopy, Los Angeles Convention
Center, 1201 South Figueroa Street
Los Angeles, CA 90015,
United States

September 30-October 1, 2011

Falk Symposium 179, Revisiting
IBD Management: Dogmas to be
Challenged, Sheraton Brussels
Hotel, Place Rogier 3, 1210 Brussels,
Belgium

October 19-29, 2011

Cardiology & Gastroenterology |
Tahiti 10 night CME Cruise,
Papeete, French Polynesia

October 22-26, 2011

19th United European
Gastroenterology Week,
Stockholm, Sweden

October 28-November 2, 2011

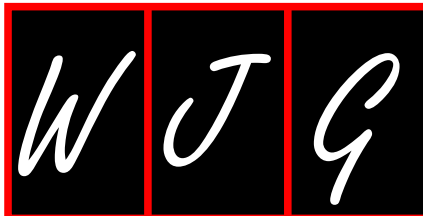
ACG Annual Scientific Meeting &
Postgraduate Course,
Washington, DC 20001,
United States

November 11-12, 2011

Falk Symposium 180, IBD 2011:
Progress and Future for Lifelong
Management, ANA Interconti Hotel,
1-12-33 Akasaka, Minato-ku,
Tokyo 107-0052, Japan

December 1-4, 2011

2011 Advances in Inflammatory
Bowel Diseases/Crohn's & Colitis
Foundation's Clinical & Research
Conference, Hollywood, FL 34234,
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GENERAL INFORMATION

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

In press

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

Organization as author

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

Both personal authors and an organization as author

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

No author given

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

Volume with supplement

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

Issue with no volume

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

No volume or issue

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

Books*Personal author(s)*

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

Chapter in a book (list all authors)

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

Author(s) and editor(s)

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

Conference proceedings

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

Conference paper

- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

Electronic journal (list all authors)

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

Patent (list all authors)

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

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

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

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