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- 5203 Classification of histological severity of *Helicobacter pylori*-associated gastritis by confocal laser endomicroscopy

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BRIEF ARTICLE

- 5211 Smad7 dependent expression signature highlights BMP2 and HK2 signaling in HSC transdifferentiation

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- 5225** Transient elastography: A non-invasive tool for assessing liver fibrosis in HIV/HCV patients

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- 5233** NKX2-3 and IRGM variants are associated with disease susceptibility to IBD in Eastern European patients

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- 5241** Clinical analysis of high serum IgE in autoimmune pancreatitis

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- 5247** Segmental gastrectomy with radical lymph node dissection for early gastric cancer

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- 5252** Predictive factors for lymph node metastasis in early gastric cancer

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- 5257** Staging systems for predicting survival of patients with hepatocellular carcinoma after surgery

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- 5263** Primary malignant liver mesenchymal tumor: A case report

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APPENDIX I Meetings
I-IV Instructions to authors

AIM AND SCOPE

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Terlipressin and hepatorenal syndrome: What is important for nephrologists and hepatologists

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Abstract

Hepatorenal syndrome (HRS) is a reversible form of functional renal failure that occurs with advanced hepatic cirrhosis and liver failure. Despite mounting research in HRS, its etiology and medical therapy has not been resolved. HRS encompasses 2 distinct types. Type 1 is characterized by the rapid development of renal failure that occurs within 2 wk and involves a doubling of initial serum creatinine. Type 2 has a more insidious onset and is often associated with ascites. Animal studies have shown that both forms, in particular type 1 HRS, are often precipitated by bacterial infections and circulatory changes. The prognosis for HRS remains very poor. Type 1 and 2 both have an expected survival time of 2 wk and 6 mo, respectively. Progression of liver cirrhosis and the resultant portal hypertension leads to the pooling of blood in the splanchnic vascular bed. The ensuing hyperdynamic circulation causes an ineffective circulatory volume which subsequently activates neurohormonal systems. Primarily the sympathetic nervous

system and the renin angiotensin system are activated, which, in the early stages of HRS, maintain adequate circulation. Both advanced cirrhosis and prolonged activation of neurohormonal mechanisms result in fatal complications. Locally produced nitric oxide may have the potential to induce a deleterious vasodilatory effect on the splanchnic circulation. Currently medical therapy is aimed at reducing splanchnic vasodilation to resolve the ineffective circulation and maintain good renal perfusion pressure. Terlipressin, a vasopressin analogue, has shown potential benefit in the treatment of HRS. It prolongs both survival time and has the ability to reverse HRS in the majority of patients. In this review we aim to focus on the pathogenesis of HRS and its treatment with terlipressin vs other drugs.

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Key words: Hepatorenal syndrome; Terlipressin; Kidney; Liver

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INTRODUCTION

Many studies have been carried out on hepatorenal syndrome (HRS); the pathophysiology and its management

however have not been completely resolved. HRS is a reversible form of functional renal failure that occurs predominantly with advanced liver disease arising from hepatic cirrhosis or severe liver injury from any condition such as severe alcoholic hepatitis or metastatic tumors^[1]. The important features of HRS are characterized by peripheral vasodilation with subsequent profound intrarenal vasoconstriction, leading to decreased glomerular filtration rate (GFR)^[2,3].

Currently, HRS encompasses 2 distinct types. Type 1 HRS often manifests itself rapidly; without appropriate treatment the mean survival time is approximately 2 wk^[4]. The distinguishing feature of type 1 HRS is rapid progressive renal failure that occurs within 2 wk and is associated with doubling of baseline serum creatinine or a 50% reduction in creatinine clearance^[5]. In more than 70% of cases there is an identifiable trigger for type 1 HRS^[6-9]. A large number of studies have shown that type 1 HRS can be precipitated by preceding spontaneous bacterial peritonitis infections, gastrointestinal bleeding and large-volume abdominal paracentesis without albumin replacement^[6,8]. Furthermore, type 2 HRS has a gradual onset with a steady decline in renal function. Interestingly, the hallmark for type 2 HRS is refractory ascites and often has no precipitating factors^[4]. The survival time is better in type 2 HRS at approximately 6 mo^[1,5]. Some would consider injudicious use of diuretics as a precipitating factor.

Importantly, the core feature of pathogenesis of HRS is peripheral arterial vasodilation, in particular in the splanchnic vasculature^[10]. This develops with advanced liver cirrhosis, which causes increased resistance to blood flow with high portal pressure. In turn, to ease the pressure within the hepatic portal system, locally acting vasoactive substances are released that cause vasodilation of the splanchnic vasculature^[10]. The overall resultant effect is circulatory dysfunction arising from a depleted intravascular volume that ultimately leads to poor renal perfusion and activation of compensatory mechanisms (renin angiotensin aldosterone system, sympathetic nervous system and vasopressin). These compensatory mechanisms with time become detrimental and result in sustained severe intrarenal arterial vasoconstriction with progressive physiological renal failure^[2]. The pooling of blood in the splanchnic vascular bed with the associated hypoperfusion of the kidneys and the ensuing intrarenal arterial vasoconstriction forms the basis for the development of HRS.

HRS has very poor prognosis with spontaneous recovery being unlikely^[2]. Treatment of HRS can be divided into medical and surgical, the latter being more beneficial. Current treatment modalities are used as a bridge to surgical intervention (liver transplant), although most patients do not survive long enough to receive a liver transplant^[2]. Pharmacotherapy is the initial treatment which buys time for a liver transplant but unfortunately there is no universally agreed first-line therapy. There are a number of pharmacological agents that have been investigated in the management of HRS and thus far most drugs aim to reverse the peripheral and splanchnic vasodilation. Usually

treatment is a combined therapy of vasoconstrictors with albumin to augment their efficacy^[11].

Vasoconstrictive drugs such as vasopressin analogues (ornipressin, terlipressin), octreotide and noradrenaline have been used in attempts to reduce the pooling of blood in the splanchnic vasculature and the peripheral arterial vasodilation^[12]. A few studies have investigated ornipressin combined with albumin or dopamine and they have been shown to reverse HRS^[13-15]. Globally the use of ornipressin has been abandoned in HRS because of the high risk of an adverse event, in particular ischemic events. Other studies have shown that with the use of potent vasoconstrictors such as ornipressin, the result can be ischemic mesenteric mucosa, myocardial ischemia, and associated ventricular arrhythmias^[16]. A safe alternative treatment is terlipressin (vasopressin analogue) which so far has shown promising results.

Several studies have confirmed that terlipressin combined with albumin achieves acceptable GFR and it almost normalizes the plasma creatinine levels in 42% to 77% of cases^[17-20]. The aim of the current review is to evaluate the recent developments made in the pathogenesis of HRS and the role of terlipressin, including its possible mechanism of its action.

PATHOGENESIS OF HRS

The etiopathogenesis of HRS has not been fully resolved and there are possible theories to explain it at a cellular and molecular level. The defining feature of HRS is profound vasoconstriction of the renal vasculature due to inadequate blood flow to the kidneys^[21-24]. The culmination of several factors leads to the development of HRS: (1) portal hypertension (PHT); (2) altered peripheral blood circulation; (3) activation of the sympathetic nervous system; and (4) the release of chemical mediators.

PHT AND NITRIC OXIDE

Over time, liver cirrhosis leads to structural changes at both a microscopic and macroscopic level within the hepatocytes. The pressure within the hepatic microcirculation becomes raised and the so-called sinusoidal PHT occurs^[25]. Furthermore, this is complemented by the ongoing changes taking place within the myofibroblasts, stellate cells and portal venules which all contribute towards the development of increased resistance to portal blood flow^[26,27]. Most research on animals has suggested 2 possible theories to explain the development of PHT: (1) "forward theory" - this theory puts forward that PHT arises as a direct consequence of increased resistance to portal inflow; and (2) "backward theory" which proposes that PHT occurs due to high portal blood inflow because of a hyperdynamic circulation^[28,29]. Furthermore, it is insinuated that this abnormally high portal blood inflow sustains the PHT^[30].

In spite of the etiology of PHT, some of the portal venous blood gets redirected *via* collateral vessels and this is partially to take pressure off the portal system^[31]. Gradu-

ally, with persistent PHT, local and systemic changes occur; neurohormonal systems are activated and locally produced vasoactive substances such as nitric oxide are released^[32]. Other locally acting vasodilatory substances released include carbon monoxide and prostacyclin^[33]. Nitric oxide however is widely believed to be one of the main culprits for initiating the splanchnic arterial vasodilation^[34].

In animal models nitric oxide has been shown to play an important role in vascular tone and splanchnic vasodilation^[35,36]. In other animal studies, it is postulated that the production of nitric oxide may be related to bacteria stimulating macrophages which in turn induce nitric oxide synthase (NOS)^[37-39]. NOS is an enzyme that forms nitric oxide from L-arginine, which is found throughout the body in numerous different types of cells. In addition, NOS has been shown to have 3 isoforms which are NOS I - neuronal NOS (nNOS), NOS II - inducible NOS (iNOS) and NOS III - endothelial NOS (eNOS)^[40-42].

Isoform nNOS is primarily found in the central nervous system and it has been shown to have a key role in controlling blood pressure. Several studies on rats have demonstrated that by inhibiting this isoenzyme it generates increased sympathetic activity with ensuing tachycardia, and hypertension^[43-45]. Conversely, iNOS is present in humans in several tissues including hepatocytes and alveolar macrophages; its release is induced by several cytokines including interleukin 1, interferon γ , tumor necrosis factor and lipopolysaccharides^[46,47]. Finally eNOS, as the name suggests, is predominantly found in endothelial cells in humans in both arterial and venous vessels^[48,49]. In the literature, eNOS has been shown to be involved in the peripheral arterial vasodilation that occurs in HRS and there are raised levels of eNOS in the circulation^[48]. Overall eNOS has an important role in maintaining sympathetic vascular tone and can be synthesized within the endothelium in response to stimuli.

HYPERKINETIC CIRCULATION AND COMPENSATORY MECHANISM

The hemodynamic changes that develop in cirrhosis in the splanchnic circulation have been studied extensively, and only slow progress has been made in determining its pathophysiology. A number of plausible theories have been postulated in the last 2 decades based on both *in vitro* and *in vivo* studies. Hyperdynamic circulation is a phenomena that happens over a period of time as a direct consequence of long standing PHT (Figure 1)^[50]. The hallmarks of this circulatory dysfunction are tachycardia, increased cardiac output and abnormally low peripheral vascular resistance with decreased arterial blood pressure^[51].

Hyperkinetic circulation develops in several steps: (1) splanchnic and peripheral vasodilation; (2) an increase in total blood volume with inadequate circulating volume; (3) increased cardiac output; and (4) the activation of a compensatory mechanism. Initially there is pooling of blood in the splanchnic vasculature due to PHT and this causes decreased circulatory volume.

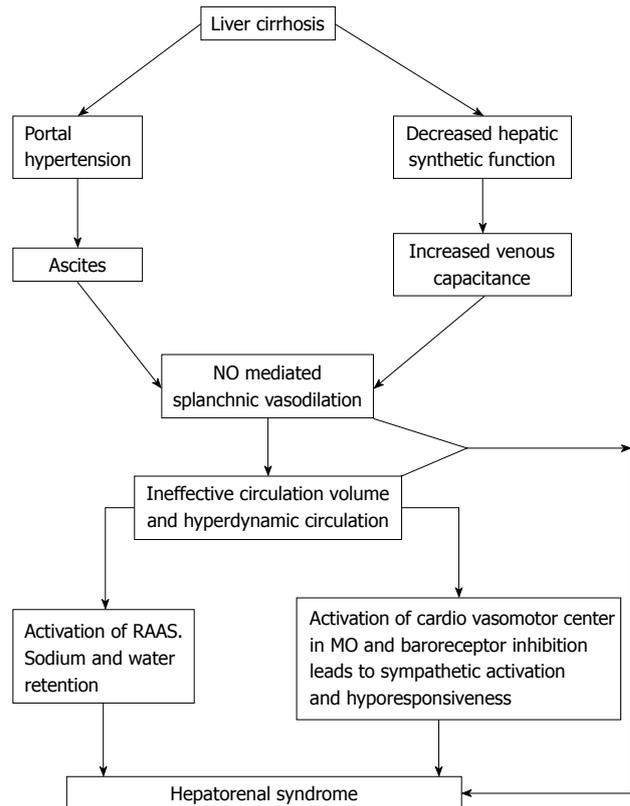


Figure 1 Flow chart showing the vicious cycle that develops with decompensated liver cirrhosis and the series of events that lead to hepatorenal syndrome. NO: Nitric oxide; RAAS: Renin angiotensinogen aldosterone system; MO: Medulla oblongata.

One of the earliest indicators of a hyperdynamic circulation is the redistribution of blood volume into the splanchnic circulation. This event has been demonstrated in Doppler ultrasonography studies in which patients with cirrhosis had remarkably high splanchnic blood flow when compared to normal subjects^[51]. The development of increased blood flow to splanchnic circulation and the pooling of blood produce a decreased circulating volume that triggers neurohormonal responses.

SYMPATHETIC NERVOUS SYSTEM, CARDIAC OUTPUT AND THE BARORECEPTORS REFLEX

A low circulating volume (low blood pressure) is detected by the baroreceptors or pressoreceptors located mainly in the internal carotid artery (carotid sinus) and ascending aorta. They are also found in small quantities in the wall of almost every large artery in the neck and thorax^[1]. These are pressure sensitive receptors which are physiologically inactivated when the aforementioned arteries become less stretched as a result of low blood pressure (Figure 1)^[52]. Consequently, the carotid and aortic baroreceptors signal conduction to the cardio and vasomotor regulatory centers in the medulla oblongata, *via* the glossopharyngeal and vagus nerves, respectively, is subdued. Thus, the cardio-

vasomotor regulatory centers become more active and sequentially induce the sympathetic nervous system to become active while suppressing parasympathetic (vagus nerve) stimulation to the heart. The sympathetic nervous system through the cardiac accelerator nerve increases the heart rate and cardiac output. Furthermore, the adrenal medulla, under the influence of the sympathetic nervous system, releases both adrenaline and noradrenaline. This eventually leads to an increase in mean arterial pressure through increased cardiac output and peripheral vascular resistance by acting on adrenergic receptors. The sympathetic response is further augmented by the activation of the RAAS and the release of vasopressin^[53]. Unfortunately, those complex neurohormonal compensatory responses to low blood pressure are temporary and the whole system that comprises the baroreceptors, RAAS and vasopressin becomes adapted and mal-responsive to the low circulating volume stimulus within 48-72 h^[4]. Consequently all the above outlined responses are reversed resulting in profound hypotension, renal hypoperfusion and worsening renal failure.

RENIN ANGIOTENSIN ALDOSTERONE SYSTEM

Arterial hypotension and reduced blood flow to the kidney results in decreased sodium delivery to the macula densa which in turn causes the release of renin from the juxtaglomerular apparatus^[54]. The renin release is the rate determining step for the activation of the RAAS. The activation of RAAS causes sodium and water reabsorption and vasoconstriction of the renal arteries (Figure 1)^[55]. These compensatory mechanisms maintain effective circulation in the early stages of the disease (compensated) but with time their effects eventually become deleterious and lead to the development of complications. These include ascites, hyperkinetic circulation, nitric oxide release, renal failure, and increased venous capacitance with decreased venous compliance. Essentially all these culminate to form the bases of HRS^[55].

Liver cirrhosis has been shown to be associated with activation of RAAS but also an increase in vasopressin secretion^[56]. The activation of RAAS may contribute to decreased renal perfusion^[56]. Importantly, albumin administration has been shown to be associated with a decrease in plasma renin level^[57]. In contrast, administration of vasopressin does not substantially change renal perfusion, though it induces splanchnic vasoconstriction^[57]. This may explain the potential benefit of administration of vasopressin and its analogues in HRS. The progression of PHT is associated with an increase in vasodilation of the splanchnic circulation and marked resistant to vasopressin. It is likely that further research is needed to address the interaction between RAAS and vasopressin.

In addition, the activation of the RAAS has an important role in hemodynamic regulation in the liver as well as proliferation of vascular smooth muscle cells and fibrosis

through 2 well coordinated complementary pathways: (1) vasoconstriction/proliferative pathway, incorporating the angiotensin converting enzyme (ACE), angiotensin (Ang) II-Ang II type 1 (AT1) receptor; and (2) a counter-regulatory vasodilatation/antiproliferative pathway, involving ACE2-Ang-(1-7)-Mas receptor^[58]. It is important to point out that the ACE, vasoconstriction/proliferation pathway induces contraction and proliferation of hepatic stellate cells, which lead to fibrosis^[58]. In contrast, activation of ACE2-Ang-(1-7) is not only associated with liver cirrhosis-induced splanchnic and systemic vasodilatation but also anti-fibrotic effects^[58].

Vilas-Boas *et al*^[59] suggested that the administration of a combination of propranolol and ACE inhibitor or AT1 receptor blocker may have potential benefit in cirrhotic patients. Furthermore, administration of propranolol *per se* has been shown to be associated with unfavorable consequences on the 2 main RAAS components, Ang II and Ang(1-7), in the splanchnic and peripheral circulation^[59]. In contrast, inhibition of RAAS by ACE inhibitors and AT1 receptor blockers has been shown to be associated with potential benefit in slowing progression of liver fibrosis and even cardiac and renal fibrosis^[60].

Interestingly, it has been hypothesized that the effect of Ang II dominates in advanced liver disease while the effect of Ang(1-7) dominates in moderate liver disease^[61]. Therefore, the RAAS can be viewed as a dual system that leads to vasoconstriction, fibrosis, vasodilatation and anti-fibrosis. However, further research is urgently needed to establish a therapeutic benefit of the dual function of the RAAS in targeting liver disease and preventing fibrosis in humans and, in particular, in the management of HRS.

DETRIMENTAL EFFECTS OF THE SYMPATHETIC NERVOUS SYSTEM AND RAAS

These wonderful compensatory mechanisms with prolonged activation result in even more increased sodium and water retention with a subsequent increase in total circulatory volume. RAAS, with its overall effect of salt and fluid retention contributes to the development of ascites usually in the presence of PHT. In addition, splanchnic vasodilation appears to be one of main culprits in the formation of ascites^[50]. Ascites develops when there is increased sinusoidal pressure which forces fluid to leak into the abdominal cavity^[1]. Ascites further fuels the constant activation of the RAAS and the sympathetic nervous system which fail to maintain effective circulating volume.

The lack of response to neurohormonal mechanisms in the latter stages of cirrhosis may be due to several factors: (1) nitric oxide-mediated pooling of blood in splanchnic vascular bed; (2) hyporesponsiveness of splanchnic vasodilation to neurohormonal mechanism; (3) ascites; and (4) downregulation of receptors.

Eventually the pooled blood in the splanchnic circulation cannot be utilized fully in the presence of ineffective

circulation. This is on account of the fact that the reservoir of blood in the splanchnic circulation continues to increase and is mediated by locally-produced nitric oxide. A recent study by Li *et al*^[62] demonstrated that nitric oxide caused changes in mesenteric venous capacitance and increased pooling of blood in rats with liver cirrhosis. In this study it was shown that the cirrhotic rats had a nitric oxide-mediated increase in venous capacitance and decrease in compliance. Nitric oxide is produced locally by eNOS which is activated by the high shear stress in the splanchnic vascular endothelium, which is caused by the increased splanchnic blood flow. In both animal and human studies, nitric oxide appears to be the main orchestrator of the splanchnic vasodilation that facilitates the pooling of blood^[63,64], *via* its direct action on the vascular smooth muscles.

Additionally, it is widely accepted that nitric oxide antagonizes the sympathetic and RAAS-driven vasoconstriction thus inducing vasodilatation of the splanchnic vascular bed. Accordingly, ineffective circulation continues to trigger neurohormonal responses, though in the latter stages of the disease there is hyporesponsiveness to these compensatory mechanisms. In the early stages of compensated liver cirrhosis, the neurohormonal activation is able to overcome the splanchnic vasodilation and maintain an acceptable circulating volume. However with decompensated liver cirrhosis; and increased PHT, the hyporesponsiveness is often an indicator of progression towards the end stage.

It is suggested that the hyporesponsiveness may be due to desensitization and downregulation of adrenergic receptors. In cirrhotic rats there appears to be β -adrenergic receptor hyporesponsiveness to catecholamines^[65]. This concept is not new; previous studies looking at heart failure have shown that prolonged activation of the neurohormonal response leads to a downregulation of β -adrenergic receptors^[66]. The hyporesponsiveness of the myocardium to catecholamine stimulation that is seen in cirrhosis is termed cirrhotic cardiomyopathy^[67].

FUNCTIONAL RENAL FAILURE

The renal system, through autoregulation, maintains a physiologically acceptable GFR over a range of blood pressures. Autoregulation consists of myogenic and neurohormonal responses. The development of a hyperkinetic circulation results in renal hypoperfusion despite increased total circulating volume. Initially with low blood pressure, the kidneys respond with smooth muscle contraction in the vessels (myogenic response), which helps to maintain the perfusion pressure^[1]. This response alone is not adequate, therefore the sympathetic nervous system and RAAS are activated and subsequently lead to renal vasoconstriction. The peripheral vasodilatation that occurs is perceived by the kidneys as a hypovolemia, that continues to promote renal vasoconstriction. The resultant effect is reduced GFR, oligo-anuria, raised plasma creatinine and the development of hepatorenal failure^[2].

Renal biopsies in HRS patients have shown remarkably normal renal histology architecture despite the dismal renal function. The findings have led to the term “reversible functional renal failure” being coined^[22]. The primary problem causing renal failure is liver cirrhosis and this functional renal failure can be reversed with liver transplantation. Kidney transplants from palliated patients with HRS into those with intrinsic renal failure, have remarkably been shown to have reversed to normal renal function^[68,69]. This further supports the concept of reversibility of functional renal failure in patients with HRS. The definitive treatment for HRS is liver transplantation; however with increasing shortages of organ donation and with long waiting lists, patients are more often than not succumbing to the dismal prognosis of HRS. Nevertheless treatment with vasopressin analogues, in particular terlipressin, has been shown to reverse the renal failure and can be used as a bridge to definitive treatment (liver transplant).

TERLIPRESSIN AS POTENTIAL TREATMENT FOR HRS

Terlipressin, an analogue of vasopressin, is used as potential treatment of HRS. In this review we focus on clinical trials and their strengths and weaknesses. It is worth mentioning that in the majority of these studies, terlipressin was used in combination with albumin. Furthermore, other trials compared the effect of terlipressin with noradrenaline. We included clinical trials with evidence-based medicine. Hence, the subsequent discussion will focus on the impact of terlipressin *vs* placebo and terlipressin *vs* noradrenaline with and without albumin.

Terlipressin and clinical trials

Terlipressin (without albumin) *vs* placebo: Hadengue *et al*^[70] carried out a double-blind, crossover, randomized study in 9 patients with type 1 HRS. The patients received terlipressin (2 mg/d for 2 d) and a placebo for 2 d in a randomized order. Terlipressin administration significantly increased creatinine clearance and urine output, but did not significantly change urinary sodium concentration. Urinary sodium excretion was not significantly different after placebo administration or terlipressin administration. Terlipressin administration significantly decreased plasma concentrations of renin and aldosterone but not atrial natriuretic peptide levels, and these biochemical changes were not seen in the placebo group. The study by Solanki *et al*^[19] was a randomized, controlled, single-blind trial. They assigned 24 consecutive patients with HRS to treatment with terlipressin 1 mg iv at 12 h intervals (group A, $n = 12$) or placebo at 12 h intervals (group B, $n = 12$). The end-point of the study was improvement in renal function defined as reversal of HRS and survival at 15 d. Terlipressin administration was shown to be associated with an improvement in parameters of renal function, mean arterial blood pressure and importantly reversal of HRS in 5 of the 12 patients in group A.

Table 1 Summary of effect of terlipressin associated with albumin on hepatorenal syndrome

Study	Main outcome
Sanyal <i>et al</i> ^[72] , 2008	Terlipressin administration with albumin shown to be associated with improvement in renal function and appeared superior to placebo in reversing type 1 HRS
Martín-Llahí <i>et al</i> ^[73] , 2008	Terlipressin administration with albumin shown to be associated with improvement in renal function in patient with liver cirrhosis and type 1 HRS, without significant impact on 3-mo survival
Neri <i>et al</i> ^[74] , 2008	Terlipressin administration with albumin shown to be associated with improvement in renal function in patients with type 1 HRS and also a high probability of survival
Uribe <i>et al</i> ^[77] , 2000	Terlipressin associated with albumin appeared to be a safe and effective treatment of HRS and decreased the frequent ischemic complications associated with terlipressin treatment alone. Terlipressin associated with albumin therapy was associated with marked improvement in renal function, reversal of HRS and improvement in circulatory function with an increase in mean arterial blood pressure

HRS: Hepatorenal syndrome.

Interestingly, Testro *et al*^[71] reviewed outcomes of 69 patients treated with terlipressin between 2001 and 2005. Their findings showed that 49 episodes (71%) of HRS were type 1, and 20 episodes (29%) were type 2. Forty-one (59.4%) patients responded to terlipressin. Twenty-one (30.4%) patients survived; 17 (81%) had type 1 HRS while 4 (19%) had type 2 HRS ($P = 0.27$). The only factor predicting transplant-free survival was type 1 HRS. No patients with type 2 HRS survived without transplantation ($P = 0.02$). These trials clearly showed the potential benefit of administration of terlipressin in individuals with HRS. However, Terlipressin administration was associated with minimal reversible ischemic events e.g. crampy abdominal pain and cardiac arrhythmias. We suggest that randomized clinical trials are now warranted.

Terlipressin (with albumin) vs placebo: Interestingly, concomitant administration of terlipressin and albumin is shown to be associated with better clinical outcomes. A summary of studies that used terlipressin (with albumin) vs placebo is provided in Table 1.

Terlipressin vs noradrenaline: The use of noradrenaline, a cheap and widely available drug, in the management of HRS was shown to be as effective as terlipressin but associated with increased risk of ischemic events. Data from an unblinded, pilot study suggested that noradrenaline was as effective and safe as terlipressin in patients with HRS. Twenty-two consecutive cirrhotic patients with HRS (9 with type 1 HRS; 13 with type 2 HRS) were randomly assigned to treatment with noradrenaline (0.1–0.7 $\mu\text{g}/\text{kg}$ per minute) and albumin (10 patients) or with terlipressin (1–2 mg/4 h) and albumin (12 patients). Treatment was administered until HRS reversal or for a maximum of 2 wk. Reversal of HRS was observed in 7 of the 10 patients (70%) treated with noradrenaline and in 10 of the 12 patients (83%) treated with terlipressin. Treatment led, in both groups, to a significant improvement in renal and circulatory function; no patient developed signs of myocardial ischemia^[75]. Sharma *et al*^[76] reported similar beneficial results in treating HRS with noradrenaline, however, they also reported that 2 patients had ventricular ectopies with noradrenaline. We suggest that further studies

are urgently needed to evaluate the use of noradrenaline as potential treatment for HRS.

Terlipressin and meta-analyses

Several meta-analyses have been conducted to determine the effect of terlipressin in HRS with regard to the duration of treatment, infusion of albumin and comparison with noradrenaline. Dobre *et al*^[77] concluded in their meta-analysis that terlipressin administration was associated with improvement in HRS reversal and that noradrenaline has the same effect as terlipressin in improving surrogate markers of HRS. Sagi *et al*^[11] showed that the risk ratio for reversal in type 1 HRS with terlipressin therapy was 3.66 [95% confidence interval (CI): 2.15–6.23]. Recurrence of HRS was low (8%). Serious side effects requiring discontinuation of therapy were seen only in 6.8% of patients on terlipressin therapy. There was a trend towards improved transplant-free survival at 90 d in the Terlipressin group (relative risk 1.86, 95% CI: 1.0–3.4, $P = 0.05$). The conclusion of their meta-analysis was that terlipressin is effective in reversing HRS type 1 and recurrence of HRS is rare with at least 14 d of therapy and associated with an increased survival. Importantly, Fabrizi *et al*^[78] showed in their meta-analysis that discontinuation of terlipressin therapy was associated with a significant increase in the number of relapses. Furthermore, Fabrizi *et al*^[79], in another meta-analysis, showed that terlipressin was more effective in reversing HRS than placebo without apparent impact of terlipressin on survival in HRS patients. This may again suggest the need for large clinical trials addressing the impact of terlipressin in HRS patient survival. Interestingly, administration of albumin with terlipressin showed a reduction in mortality in type 1 HRS^[10]. Therefore, the current evidence suggests that terlipressin can have a potential benefit in treating HRS and that an improvement in survival can be achieved with its concomitant administration with albumin.

CONCLUSION

HRS continues to be a challenging task to manage following chronic liver cirrhosis. The grave prognosis and the short survival times have fuelled great interest in clinical

trials; its reversibility creates scope for prolonging both survival and quality of life. The current literature reviewed has further re-enforced terlipressin as a potential first-line treatment in HRS. Terlipressin has so far shown to increase survival rates and reverse functional renal failure. The increased neurohormonal response, especially of the RAAS, has been decreased with the administration of terlipressin. This subsequently improves circulatory dysfunction and lowers plasma creatinine levels near to baseline values. The effects of nitric oxide, which is a factor in the deleterious neurohormonal response, appears to be overcome by the administration of terlipressin through unknown mechanisms.

In addition, terlipressin has few adverse side effects, which allows patients to continue with treatment in order to achieve desirable effects. At present however, we acknowledge that there are a limited number of randomized, controlled studies carried out on terlipressin and therefore there is a real need for large multi-centered trials to be carried out. We recommend that terlipressin, with concomitant administration of albumin, may be the first line treatment in the management of HRS.

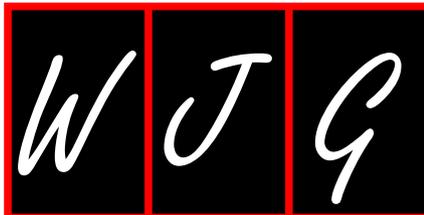
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Growth factor- and cytokine-driven pathways governing liver stemness and differentiation

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Abstract

Liver is unique in its capacity to regenerate in response to injury or tissue loss. Hepatocytes and other liver cells are able to proliferate and repopulate the liver. However, when this response is impaired, the contribution of hepatic progenitors becomes very relevant. Here, we present an update of recent studies on growth factors and cytokine-driven intracellular pathways that govern liver stem/progenitor cell expansion and differentiation, and the relevance of these signals in liver development, regeneration and carcinogenesis. Tyrosine kinase receptor signaling, in particular, c-Met, epidermal growth factor receptors or fibroblast growth factor receptors, contribute to proliferation, survival and differentiation of liver stem/progenitor cells. Different evidence suggests a dual role for the transforming growth factor (TGF)- β signaling pathway in liver stemness and differentiation. On the one hand, TGF- β

mediates progression of differentiation from a progenitor stage, but on the other hand, it contributes to the expansion of liver stem cells. Hedgehog family ligands are necessary to promote hepatoblast proliferation but need to be shut off to permit subsequent hepatoblast differentiation. In the same line, the Wnt family and β -catenin/T-cell factor pathway is clearly involved in the maintenance of liver stemness phenotype, and its repression is necessary for liver differentiation during development. Collectively, data indicate that liver stem/progenitor cells follow their own rules and regulations. The same signals that are essential for their activation, expansion and differentiation are good candidates to contribute, under adequate conditions, to the paradigm of transformation from a pro-regenerative to a pro-tumorigenic role. From a clinical perspective, this is a fundamental issue for liver stem/progenitor cell-based therapies.

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Key words: Hepatocyte growth factor; Epidermal growth factor; Fibroblast growth factor; Transforming growth factor- β ; Hedgehog and β -catenin; Liver; Stem cell

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INTRODUCTION

Liver is unique in its capacity to regenerate in response

to injury or tissue loss. Following two-thirds partial hepatectomy, hepatocytes exit the G0 phase of the cell cycle and synchronously re-enter the cell cycle to regenerate the liver mass completely in 6-7 d in rodents, or 3-4 mo in humans^[1-4]. Liver stem/progenitor cells do not seem to be required for this process. However, when this response is impaired, as in the case of a hepatocyte-selective proliferative defect or acute liver failure, the contribution of liver progenitors becomes much more relevant^[5,6]. A population of small cells with a low cytoplasmic/nuclear ratio that arose from a small number of portal cells, not from hepatocytes, were first observed in rodents and became known as “oval cells”^[7,8]. Although several lines of evidence suggest that oval cells derive from the biliary compartment, other origins have been also suggested^[4].

Significant work in the past few years has focused on the signaling pathways, as well as cell-cell interactions, that control the initial proliferation/expansion and the terminal differentiation of liver stem/progenitor cells. Oval cells express MET, the receptor of the hepatocyte growth factor (HGF). The superabundance of HGF-producing cells in the immediate vicinity of oval cell proliferation and differentiation suggests that this growth factor is involved in all aspects of stem cell behavior, proliferation, migration, and differentiation, through a paracrine mechanism^[9]. Oval cells also express receptors for epidermal growth factor (EGF)-like ligands, and *in vivo* infusion of a combination of HGF and EGF enhance the mitogenic response of oval cells after administration of 2-acetylaminofluorene^[10], which reveals the relevance of both growth factors in liver stem/progenitor cell biology. Additionally, different studies have revealed that oval cells also respond to other growth factors in an autocrine/paracrine manner^[11]. The transforming growth factor (TGF)- β family of cytokines play a relevant role in the maintenance of embryonic stem cell identity, and it has been shown that the specification of pancreas and liver progenitors is restricted by the TGF- β pathway^[12]. All these growth factors and cytokines might modulate not only proliferation of liver stem/progenitor cells, but also cell death, as well as contributing to their terminal differentiation.

This review gives an update on recent relevant studies of the growth factors and cytokine-driven intracellular pathways that govern liver stem/progenitor cell expansion and differentiation, and the relevance of these signals in liver development, regeneration and carcinogenesis.

TYROSINE KINASE RECEPTOR-MEDIATED SIGNALING PATHWAYS

HGF

HGF was firstly identified in the 1980s as a potent mitogen for hepatocytes^[13-15]. A factor secreted by fibroblasts and smooth muscle cells was discovered separately, which promoted epithelial cell scattering^[16]. Later studies unraveled that HGF and scatter factor were indistinguishable^[17,18]. HGF is a growth factor that induces a wide range of biological activities, including stimulation of

proliferation, migration, morphogenesis, and survival of a variety of cell types^[19-24], which plays a major role in tissue formation and homeostasis. HGF acts through binding to its tyrosine kinase receptor, Met. Ligand-receptor binding results in autophosphorylation of the receptor in specific tyrosine residues located in the C-terminal domain, and subsequent phosphorylation/activation of multiple adapter and signal transducing proteins, such as growth factor receptor-bound protein 2 (Grb2)/Sos, Ras-mitogen-activated protein kinase, Grb2-associated binding protein 1 (Gab1), phosphoinositide 3-kinase (PI3K), phospholipase C- γ , p38, and signal transducer and activator of transcription (STAT)-3, among others, which mediate the biological activities of HGF/c-Met^[25,26]. For decades, HGF has been recognized as a growth factor involved in the hepatocyte proliferative response during liver regeneration (a recent review on the role of HGF in liver regeneration can be found in^[3]), but an unequivocal demonstration of an essential role of the HGF/c-Met signaling in liver regeneration has only been provided recently. Thus, liver specific c-Met and HGF conditional knock-out mice show an impairment of the regenerative response^[27-29]. Hepatocytes that lack a functional c-Met display reduced basal survival and a higher sensitivity to Fas-induced liver damage, both *in vivo* and *in vitro*. Moreover, after toxic liver injury induced by exposure to CCl₄, c-met^{-/-} livers showed delayed healing from necrotic injury^[28]. Complete abolition of the cell cycle has also been demonstrated when c-Met is deleted after partial hepatectomy, by using RNA interference techniques^[30]. In addition to the effects on proliferation, these authors have described an alteration in expression of apoptosis-related genes, particularly, increased expression of pro-apoptotic genes, and decreased expression of anti-apoptotic genes, and enhanced activation of caspase 3. Altogether, these studies provide clear evidences of a role for this ligand/receptor system in promoting hepatocyte proliferation, survival, and tissue remodeling during liver regeneration.

HGF/c-Met signaling is also essential during fetal liver development. Both HGF- and c-Met-deficient embryos show abnormally small livers and liver-to-body weight ratios and massive hepatocyte apoptosis^[31-33]. Recent studies from Dr. Maina's laboratory have demonstrated HGF/c-Met survival properties in primary embryonic hepatocytes, as shown by the ability of HGF to impair Fas-induced apoptosis by acting through PI3K and AKT to prevent FLICE inhibitory protein degradation^[34]. Additionally, in the context of the adult liver, numerous works have reported an important contribution of the pro-survival activity of HGF in protecting liver during fibrosis and other hepatic dysfunction^[35-40], thus expanding the scenarios in which the anti-apoptotic activity of HGF plays an active role.

Although hepatocytes have long been considered the prime target of the actions of HGF, there is accumulating evidence of an important role for HGF/c-Met signaling on liver stem/progenitor cell function and behavior. Liver stem/progenitor cells express c-met^[41]. Furthermore,

during oval cell activation induced by N-acetyl-2-amino-fluorene/partial hepatectomy (AAF/PH) in rats, HGF expression increases coincidentally with oval cell proliferation, mainly on the periportal regions where oval cells are located^[9,41]. These data suggest that the HGF/c-Met system regulates some aspects of liver stem/progenitor cell biology. In support of this, *in vivo* infusion of HGF during AAF/PH-induced liver regeneration stimulates oval cell expansion into the liver lobules^[10]. Similar results have been obtained by *in vivo* transfer of HGF cDNA into liver subjected to the Solt-Farber regime^[42]. HGF-dependent mitogenic activity has also been shown in rat and mouse oval cell lines *in vitro* by either adenovirus-mediated transfer of the HGF gene or addition of exogenous HGF^[43-46]. The molecular mechanisms that mediate the mitogenic effects of HGF in liver progenitors appear to be cell-type specific, because PI3K/AKT activation^[43] and nuclear factor- κ B activation, downstream of p38 and extracellular signal-regulated kinase (ERK) MAPKs^[44], are involved. Additionally, bi-potential hepatoblast cell lines (precursors of both hepatocytes and cholangiocytes) have been established from transgenic animals expressing a constitutively active human Met^[47]. However, HGF is much more than a mitogen for liver stem/progenitor cells. HGF effectively protects WB-F344 cell from apoptosis induced by tumor necrosis factor- α in a dose-dependent manner^[44]. More recently, using a novel *in vitro* model of genetically modified oval cells that harbor an inactivated Met tyrosine kinase, we have demonstrated that loss of Met increases sensitivity to apoptosis caused by serum deprivation or treatment with TGF- β ^[46]. By virtue of these results, we hypothesize that Met-driven anti-apoptotic activity plays an important role supporting the expansion of liver progenitors following liver injury, by helping them to overcome the local tissue injuries and inhibitory signals. Therefore, the HGF/c-Met signaling pathway might be a major survival pathway in liver that operates during liver development, homeostasis, and regeneration (both hepatocyte and oval cell-mediated).

The role of HGF as a morphogen is already established^[48]. Morphogenesis is a complex invasive growth program that plays a fundamental role in normal development^[49,50]. Not surprisingly, morphogenic properties of HGF are exhibited in embryonic and postnatal mouse non-parenchymal epithelial cell-derived cell lines. In these cells, HGF induces a morphogenic response that includes cell scattering and ductal branching in collagen gels. These changes are not observed by treatment with other liver growth factors including EGF, TGF- β , acidic fibroblast growth factor (aFGF) and insulin, and are not inhibited by TGF- β ^[51]. A similar response has also been described in pancreatic oval cells *in vitro*; a cell population closely related to its hepatic counterpart^[52]. Recently, HGF has been directly involved in promoting motility and invasiveness of human liver progenitor cells through Matrigel; an effect that is partially mediated by matrix-metalloproteinase-mediated extracellular matrix (ECM) proteolytic degradation and activation of the MAPK/ERK pathway^[53].

Another important biological activity of HGF in liver progenitor cells that cannot be overlooked is its modulatory effect on the differentiation capacity of these cells. HGF has been reported to be required not only for an efficient proliferation and survival, but for hepatocytic differentiation of embryonic hepatic stem cells *in vitro*^[54-57]. Furthermore, virtually all the strategies for *in vitro* differentiation of embryonic and adult stem/progenitor cells of different origin into hepatocytes include HGF as a hepatic-inducing factor (a thorough compilation of *in vitro* differentiation methods is found in^[58]). Successful differentiation is generally achieved by step by step addition of growth factors, cytokines, and hormones, trying to emulate the sequence of events taking place during *in vivo* hepatogenesis. The requirement of HGF in this process relies on the specific role played by this growth factor at different liver developmental stages. During the commitment phase, HGF might antagonize differentiation of bi-potential hepatoblasts along the cholangiocytic lineage, which results in support of growth and differentiation of fetal hepatocytes^[59]. In fact, results from Suzuki *et al*^[57] have demonstrated that HGF can initiate differentiation of albumin-negative liver stem cells into albumin-positive hepatic precursors at the same time that allows their expansion and decreases expression of cholangiocyte-lineage markers, such as CK19 or γ -glutamyl transferase, but it cannot induce latter markers of hepatocyte differentiation, such as glucose-6-phosphatase or tryptophan-2,3-dioxygenase.

Later, after birth, the expression of both HGF and c-Met significantly increases in the liver, and activation of this pathway crucially assists during complete functional hepatic maturation^[41,60]. We have also described that HGF combined with TGF- β helps to maintain the expression of hepatocyte differentiation markers in rat fetal hepatocytes in culture^[61,62]. In rat primary neonatal hepatocytes, HGF promotes scattering, but this effect is not associated with a dedifferentiation process, as shown by an increase in the expression of hepatic differentiation markers using HGF treatment^[63,64]. Although a role for HGF in hepatocyte differentiation seems to be beyond reasonable doubt, it should be pointed out that HGF has also been directly implicated in transdifferentiation of hepatocytes to biliary epithelial cells^[65]. These data highlight the enormous complexity in terms of signaling networks and molecular mechanisms associated with regulation of phenotypic transitions in liver epithelial cells.

All these results provide sufficient evidence to support a crucial role for an HGF/c-Met-induced signaling pathway in liver stem/progenitor cell biology. What it is not totally clear, however, is its mode of action. HGF is mainly produced by mesenchymal cells, and c-Met is expressed in epithelial cells, therefore, this ligand-receptor system is generally considered to act in a paracrine fashion^[66]. Consistent with this, the main producers of HGF in the liver are the stellate cells^[67,68], although sinusoidal endothelial cells also express HGF^[69]. c-Met is expressed in hepatocytes, biliary epithelial cells, and liver progenitor cells^[41,54,70,71]. As men-

tioned above, in rat models of oval cell activation *in vivo*, HGF mRNA has been identified in the desmin-positive stellate cells that surround the ductal structures of oval cells, or interspersed with the oval cells, whereas c-Met expression is detected in oval cells^[9,41]. These results have prompted the conclusion that the HGF/c-Met system operates in oval cells *via* a paracrine mechanism. However, *in vitro* studies carried out in our laboratory in oval cell lines have shown an autocrine regulatory mechanism for HGF/c-Met involved in protection against apoptosis^[46]. Whether the autocrine regulation plays a role *in vivo* has not been explored, but these data suggest that oval cells might respond to both autocrine and paracrine Met signaling in a context-dependent fashion.

EGF receptor ligands

Another tyrosine kinase receptor family that regulates liver pathophysiology is the EGF receptor (EGFR) family. This receptor is part of a complex signaling system that includes multiple ligands, namely TGF- α , EGF, heparin-binding EGF, amphiregulin, betacellulin, epiregulin, epigen, and crypto; and four transmembrane receptors: EGFR (Her1/ErbB-1), ErbB-2 (Her2/neu), ErbB-3 (Her3), and ErbB-4 (Her4). Complexity of this pathway relies on differential ligand binding affinity to the receptors, as well as formation of receptor homo- and heterodimers, all of which leads to activation of distinct intracellular signaling cascade and diverse biological activities. Among all the ligands, TGF- α and EGF are the most widely studied. Both TGF- α and EGF bind and activate the same receptor, EGFR. Ligand binding results in dimerization and autophosphorylation of EGFR in tyrosine residues of the cytoplasmic domain. This leads to recruitment of adapter proteins, such as Grb2 and Shc, and subsequent activation of multiple downstream pathways, including PI3K, Ras-MAPK, c-Jun N-terminal kinase, p38, protein kinase C and STAT-3, which mediate cell proliferation, migration, differentiation and evasion from apoptosis^[72-76]. TGF- α and EGF are well-known regulators of hepatocyte proliferation. Infusion of either one of the two factors initiates DNA synthesis in liver of adult rats^[77,78], and when added exogenously, they stimulate growth of primary hepatocytes at all developmental stages: fetal, neonatal, and adult^[79-82]. Together with HGF, EGFR ligands represent the only complete mitogens in adult hepatocytes in serum-free medium, and the most important growth factors involved in the proliferative response during liver regeneration^[3]. Demonstration of a critical role for EGFR in hepatocyte proliferation during the initial phases of liver regeneration has recently been provided by generating mice with a liver-specific EGFR deficiency^[83]. In addition to the regulatory role in proliferation, and similarly to Met, EGFR is a major survival pathway in the liver^[84]. EGF-mediated EGFR activation is able to abolish completely the apoptotic response induced by TGF- β in fetal rat hepatocytes^[62] or by Fas receptor stimulation in mouse hepatocytes^[85]. Furthermore, EGFR ligands appear to

be important modulators of hepatocyte differentiation as well. Morphological and gene expression studies from our laboratory and collaborators have shown that EGF, acting in cooperation with other cytokines and hormones, maintains primary fetal and neonatal hepatocyte differentiation^[64,86,87].

Expression studies have suggested that ErbB1-triggered signaling also plays a role in stem/progenitor-cell-mediated liver regeneration. Indeed, both TGF- α and EGFR are transcriptionally upregulated during the period of active proliferation and differentiation of progenitor cells in the rat liver subjected to the 2-AAF/PH protocol^[88], and they appear to drive the early proliferation of the progenitor cell compartment^[89,10]. Although both HGF and EGF promote the expansion of oval cells *in vivo*, some differences are observed. HGF increased number of both ductal and Ito cells at a similar rate, whereas infusion of EGF mostly increases ductal cells. Our laboratory and others have also shown that EGF and TGF- α are mitogens in mouse and rat oval cells *in vitro*^[11,46,90].

The effects of this signaling pathway on liver stem/progenitor cells are not restricted to mitogenesis. *In vivo* infusion with either EGF or HGF not only amplifies liver progenitor expansion following liver injury but also decreases apoptosis^[10]. We also have evidence of an important role for EGFR-mediated signaling in regulating oval cell survival *in vitro*. Thus, inhibition of EGFR *via* treatment with a synthetic inhibitor increases basal apoptosis (in the absence of serum and exogenous stimuli) and strongly amplifies TGF- β -induced apoptosis (our unpublished results). EGFR-mediated mitogenic, morphogenic, and differentiation activities have also been reported. EGF, combined with TGF- β , triggers a scattering response in mouse oval cell lines *in vitro*^[11]. In addition to this, EGF is often included as a hepatogenic factor in strategies to induce *in vitro* differentiation of stem/progenitor cells into hepatocyte-like cells^[58]. Consistently, T β T-FH cell lines - a cell population of fetal hepatocytes that has suffered an epithelial mesenchymal transition (EMT) and a dedifferentiation process after TGF- β treatment - recover the original epithelial phenotype and gain cytokeratin-19 expression by treatment with EGF and DMSO, which suggests conversion to hepatoblast-like cells^[91].

It should be noted that we have seen autocrine regulation for EGFR-dependent signaling in oval cell lines (our unpublished results). Different to the HGF/c-Met system, an EGFR-ligand-mediated autocrine mechanism has been suggested, based on the detection of EGFR ligand transcripts in oval cells during liver regeneration^[88]. *In vivo* and *in vitro* studies have shown that choline-deficient ethionine-supplemented diet-treated mouse livers express cytokines such as lymphotoxin- β , interferon- γ , and interleukin (IL)-6^[92,93]. Collectively, these data strongly support that autocrine regulatory mechanisms are important in liver progenitor cells. The significance of the c-Met and EGFR autocrine loops in oval cells is not yet totally understood. Certainly, autocrine signaling has been mostly associated with malignancy. This seems to apply to stem/progenitor

cells as well, because tumorigenic conversion of mouse oval cell has been associated with growth factor production and alteration in growth factor responsiveness^[11]. More specifically, an HGF/c-Met autocrine loop has been identified in spontaneously transformed WB-F344 rat liver stem-like cells, which contributes to drive autonomous cell proliferation^[94]. Spontaneously transformed oval cells express TGF- α . These cells form tumors when injected into nude mice, a capacity that is significantly reduced by transfection with TGF- α antisense gene^[95]. A cross-talk between Met and EGFR has also been proposed. Thus, rat liver-epithelial-cell-derived tumor cell lines that constitutively express TGF- α display increased levels of both c-met gene and protein, as well as an amplified response to HGF^[96]. However, 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC)-treated mouse liver-derived oval cell lines, which show autocrine activation of Met and EGFR-dependent pathways, do not show any sign of transformation^[46] (and our unpublished results). Whether this is due to a matter of time, dose, or lack of critical partners for the neoplastic transformation, it is not yet known. For now, awaiting further conclusive experiments, a direct link between the establishment of functional c-Met and EGFR-dependent autocrine loops and neoplastic transformation cannot be firmly established in liver progenitor cells.

All the data summarized above highlight not only a relevant role of Met and EGFR-triggered signaling pathways in regulating the liver progenitor cell compartment, but a striking parallelism between the two pathways, both of which mediate growth, survival, migration and hepatocytic differentiation (Figure 1). Further studies will clarify which of these biological activities are totally overlapping and which are not. In this sense, Met and EGFR mutant mice and cell models should provide very useful and invaluable tools in this regard.

FGFs

The FGFs are a family of growth factors with high affinity for heparan sulfate proteoglycans, which bind to transmembrane tyrosine kinase FGF receptors (FGFRs). The role of these growth factors in hepatic fate specification of pre-hepatic endoderm cells during liver development is well known. There are a number of excellent reviews on this subject, some of which are cited here^[97-99]. Activation of adult stem/progenitor cells is believed to use similar, if not identical, genetic programs as the embryonic progenitors, therefore, FGF is among the main targets to be analyzed in rodent models of oval cell expansion. Indeed, aFGF (also known as FGF-1) is upregulated at the stage of oval cell progression^[89,100], being expressed by both oval cells and Ito cells. FGFR1 and FGFR2 are also expressed at high levels during the period of active proliferation and differentiation of oval cells, but exhibit a different pattern. Although FGFR1 is mainly expressed in oval cells, FGFR2 is expressed in both oval and Ito cells^[101]. These results suggest a differential role for these two receptors during liver stem/progenitor-cell-mediated regeneration, as well as the establishment of both autocrine and para-

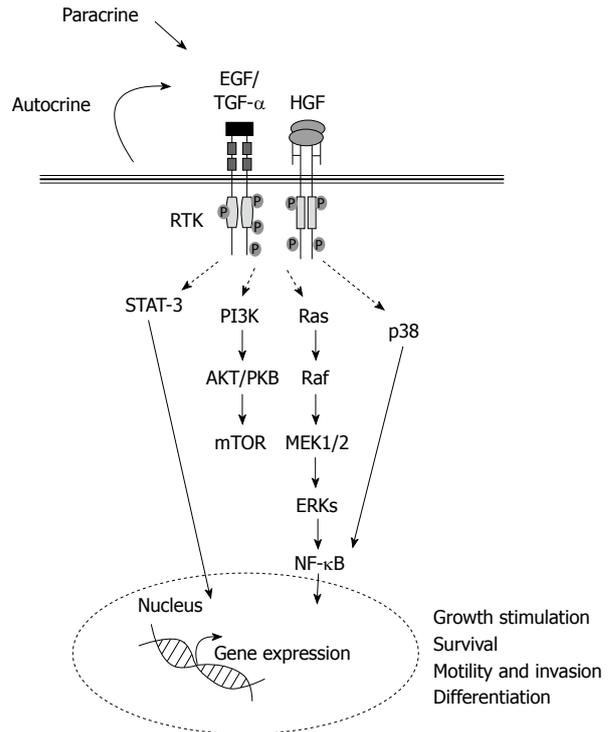


Figure 1 Schematic illustration of the major signaling pathways and biological activities induced by hepatocyte growth factor and epidermal growth factor receptor ligands in liver progenitor cells. HGF: Hepatocyte growth factor; EGF: Epidermal growth factor; TGF: Transforming growth factor; STAT: Signal transducer and activator of transcription; PI3K: Phosphoinositide 3-kinase; NF- κ B: Nuclear factor κ B; mTOR: Mammalian target of rapamycin; MEK: Mitogen-activated protein kinase kinase; ERKs: Extracellular-signal-regulated kinases.

crine signaling. In addition to these *in vivo* observations, *in vitro* studies have shown that aFGF is able to push Met murine hepatocytes-bi-potential precursors isolated from transgenic livers, which express a constitutively active human Met - to progress from a very early state of differentiation to a more mature state, associated with the expression of liver functions^[47]. Moreover, FGF1-pretreated cells are resistant to the TGF- β dedifferentiation effect^[102]. Essentially, FGFs have proved to be effective in mediating early hepatic differentiation, and therefore are included in most *in vitro* differentiation protocols^[58].

TGF- β FAMILY

The TGF- β family of cytokines regulates hepatocyte proliferation and death, and plays relevant roles during liver regeneration^[103]. However, TGF- β and other pro-inflammatory cytokines are important inducers of fibrocarcinogenesis, due to their ability to induce myofibroblast differentiation and ECM deposition^[104,105]. Recent evidence has shown that TGF- β might also regulate liver stemness and phenotype^[106].

TGF- β active form acts as a dimer, and signals by bringing together two receptors with serine-threonine kinase activity, which are known as type I and type II receptors (Figure 2). After TGF- β binding, the type II receptor

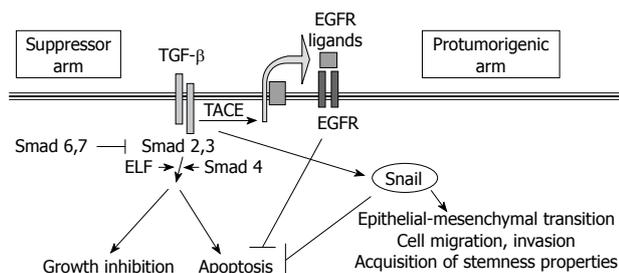


Figure 2 Overview of the major signaling pathways, and their cellular effects, induced by transforming growth factor- β in liver cells. TGF: Transforming growth factor; EGFR: Epidermal growth factor receptor; ELF: Embryonic liver fodrin; TACE: Tumor necrosis factor-converting enzyme.

phosphorylates and activates the type I receptor, which is responsible for phosphorylation of the receptor-regulated Smad family of transcription factors (R-Smads), i.e. Smad 2 and 3 in the case of TGF- β 1, β 2 and β 3^[107]. After phosphorylation, Smad 2 or 3 forms a complex with Smad 4 and shuttles to the nucleus, where it possesses DNA-binding activity, although it must associate with other DNA-binding co-factors to achieve high-affinity binding. Indeed, through combination with different transcription factors, the same TGF- β stimulus can induce or repress many different target genes. Activation of the Smad transcriptional activity can be counteracted by the presence of other members of the Smad family that play inhibitory effects (inhibitory Smads), such as Smad 6 and Smad 7, which compete with Smad 2 and 3 for binding either to the receptor complex or to Smad 4.

The most relevant Smad-mediated cell responses to TGF- β are growth inhibition and apoptosis. TGF- β inhibits proliferation in adult^[108,109], as well as fetal or regenerating hepatocytes^[82,109], and it is a well-known inducer of hepatocyte cell death^[110,111]. The inhibitory effects of TGF- β on liver stem/progenitor cell growth and survival are somewhat unclear. TGF- β overexpression results in impairment of oval cell expansion induced by DDC^[112]. Consistently, we have shown that treatment with TGF- β inhibits growth and induces apoptosis in DDC-derived oval cell lines *in vitro*^[46]. However, when compared to adult hepatocytes, other authors have reported that the majority of the adult liver progenitor cells are more resistant to endogenously produced TGF- β anti-proliferative and pro-apoptotic effects *in vitro*^[113], which indicates a differential sensitivity to TGF- β between liver progenitors and mature hepatocytes. Indeed, several mechanisms have been proposed that would explain this differential response. On the one hand, the ratio between R-Smads and inhibitory Smads might be different in oval cells. In this sense, Nguyen *et al.*^[114] have recently reported that oval cell lines show higher levels of Smad 6 than do adult hepatocytes. On the other hand, oval cells might show over-activation of survival signals, such as the MAPK/ERK pathway^[115] that might be related to the autocrine production of growth/survival factors, such as HGF^[46]. It is worth noting that, when combined with growth factors such as EGF or HGF, TGF- β might contribute to cellular scat-

tering and morphological differentiation of hepatoblasts and liver stem cells^[87,116,117]. In this same line of evidence, hepatocytes are undifferentiated and liver architecture is lost in Smad 2+/- and Smad 3+/- mice, as well as in ELF (a β -spectrin that is crucial for the propagation of the TGF- β signal) mutants^[118-121]. Defects in Smad 2+/- and Smad 3+/- mutants are restored by HGF treatment. Although mechanisms by which TGF- β signals can be supplanted by HGF are unknown, data seem to support cooperation between two independent pathways, that converge on β 1-integrin expression, rather than direct pathway crosstalk^[119]. Emerging new data have reinforced the idea that TGF- β is important for stem cell transitioning to a progenitor cell phenotype, and ultimately, its conversion to a fully differentiated phenotype. Indeed, TGF- β signaling, and particularly ELF, appears to play a crucial role in hepatocyte proliferation and transitional phenotype during human liver regeneration, and its loss is associated with activation of liver progenitor cells^[106]. It has also been shown recently that TGF- β might be a determinant in the appearance of progenitor/stem cells in hepatocarcinogenesis. The examination of human hepatocellular carcinoma (HCC) has revealed that cells that are labeled with stem-cell markers have unexpectedly lost the TGF- β receptor II and ELF, and show marked activation of the IL-6 pathway, a major stem-cell signaling pathway^[121,122]. These data support that absence of TGF- β -driven epithelial differentiation favors carcinogenesis.

However, TGF- β is a pleiotropic cytokine inducing several, and sometimes contradictory, signals in epithelial cells. Indeed, in addition to the well-known Smad-mediated transcriptional responses that predominantly address tumor suppressor actions, TGF- β induces other Smad-dependent or independent effects that contribute to tumor progression^[107]. Among these, related to the topic of this review, one of the more relevant is the capacity to induce EMT processes. EMT is a physiological process during embryogenesis, in which an epithelial cell loses expression of adhesion molecules, such as E-cadherin, and other components responsible for cell polarity. Instead, they express mesenchymal components of the cytoskeleton and acquire motility and scattering properties^[123]. A closely related phenotypic conversion is also detected in fibrosis and neoplasia and is associated with disease progression^[124]. Members of the TGF- β family can initiate and maintain EMT in a variety of biological systems and pathophysiological situations, through activation of major signaling pathways and transcriptional regulators integrated in extensive signaling networks^[125,126]. In culture, hepatocytes and hepatoma cells undergo EMT in response to TGF- β ^[127-130], which support a potentially crucial role for TGF- β in the development and progression of hepatic fibrogenesis and cancer. The mechanisms that allow cells to escape from the apoptotic effects of TGF- β and undergo EMT are not completely understood. However, recent results have indicated that, in some epithelial cells, including fetal rat hepatocytes and hepatoma cells,

TGF- β might induce both pro- and anti-apoptotic signals and their balance defines the cell fate^[129,131-133]. In fact, certain evidence indicates a crosstalk between the genetic programs that control TGF- β -induced growth arrest/apoptosis and those that regulate EMT, because once the cell has adopted a mesenchymal phenotype, it does not respond to TGF- β suppressor effects^[128,134,135]. Thus, TGF- β might regulate its own signaling to switch from tumor suppression to tumor progression. Indeed, it is interesting to point out that transcription factors of the Snail family, repressors of the E-cadherin gene, are required for cell survival during EMT^[136,137].

In recent works from our group, we have demonstrated that transdifferentiation of liver cells from an epithelial to a mesenchymal phenotype, such as that mediated by TGF- β , induces dedifferentiation and allows enrichment in a population of cells with putative liver progenitor properties^[91,128,138]. The phenotypic characteristics observed (elongated phenotype, strong expression of Thy-1, vimentin or α -smooth muscle actin) are also highly reminiscent of myofibroblasts^[139]. These findings are in agreement with the recently proven fact that EMT not only endows cells with migratory and invasive properties, but also induces stem cell properties^[123]. Furthermore, additional works have proved the capacity of TGF- β to induce/maintain a stemness phenotype in other tissues^[140]. Preliminary results have indicated that human fetal hepatocytes respond to TGF- β downregulation of E-cadherin and upregulation of Snail, thus acquiring a fibroblastic-like morphology and a liver progenitor cell phenotype (unpublished observations from our group in collaboration with Dr. N. Fausto, University of Washington, Seattle, USA).

These findings might have implications for regenerative biology of the liver and open new perspectives for the *in vitro* isolation of putative liver stem/progenitor cells to be used in basic and translational research in the liver. Moreover, a recent study has also suggested that TGF- β treatment of HCC cells might induce the selection of cells expressing high levels of CD133, a putative stem-cell marker in diverse hematopoietic and non-hematopoietic tissues and cancers^[141], through a mechanism partially dependent on the Smads pathway, and that involves epigenetic regulation of the CD133 promoter. These results indicate that TGF- β might also play a role in transdifferentiating liver tumor cells to liver cancer stem cells.

In the embryo, progenitors to pancreatic β cells and hepatocyte lineages arise from neighboring domains of ventral foregut endoderm. It has been recently found that the specification of pancreas and liver progenitors is restricted by the TGF- β pathway^[12]. It has been speculated that TGF- β signaling restrains lateral endoderm specification until the cells move sufficiently far from the heart and into a bone morphogenetic protein signaling domain, with the latter then becoming the dominant Smad 4-dependent pathway, which leads to pancreatic induction. TGF- β signaling appears to be strongly inhibitory to the pancreatic lineage and modestly inhibitory to the liver lineage, which suggests that TGF- β also plays a relevant role in maintain-

ing the stemness phenotype of endodermal precursors during liver development.

All these results suggest a dual role for the TGF- β signaling pathway in liver stemness and differentiation. On the one hand, TGF- β mediates progression of differentiation from a stem or progenitor stage, but on the other hand, it contributes to the expansion of liver stem cells. Further work is necessary to understand better the relevance of both effects in liver development, regeneration and carcinogenesis.

HEDGEHOG FAMILY LIGANDS

Hedgehog (Hh) family ligands are widely acknowledged morphogens that regulate tissue remodeling during embryogenesis^[142,143]. In particular, Indian hedgehog and Sonic hedgehog ligands, and their receptor, Patched, are expressed at different stages of liver organogenesis, and available data point to dynamic signal activation and temporarily restricted effects on hepatoblast regulation. Thus, Hh signaling is necessary to promote hepatoblast proliferation but it needs to be shut off to permit subsequent hepatoblast differentiation^[143-148]. Hh signaling is also involved in the maintenance of a hepatic progenitor reservoir throughout life, both in humans and mice. Blockade of Hh activity in hepatic progenitors *in vitro* decreases survival, whereas stimulation of Hh activity inhibits endogenous apoptosis. Both autocrine and paracrine modes of action are suggested, based on simultaneous expression of Hh ligands and receptors in liver progenitor cells^[149]. Additional observations suggest that Hh pathway activation is a common feature of various types of chronic liver injury associated with mobilization of hepatic progenitor populations. Participation of the Hh pathway has been demonstrated in the ductular reaction that is elicited by chronic alcohol-induced liver injury in mice and humans^[150]; non-alcoholic steatohepatitis in humans^[151]; methionine choline-deficient ethionine-supplemented diet^[152] and fatty liver damage^[153] in mice. Hh ligands are released by hepatocytes and myofibroblasts, and lead to enhanced viability and proliferation of bile ductular cells and hepatic progenitors, thus promoting the ductular response and fibrogenesis. Myofibroblasts, but not hepatocytes, also respond to Hh ligands with an increase in viability^[152,154-157]. Either Hh paracrine signaling between myofibroblast and hepatic progenitors or autocrine signaling, or both, promote EMT in hepatic progenitors, which ultimately contributes to liver fibrosis^[157-159].

The way in which Hh signaling interacts with other pathways to control the fate of hepatic progenitor populations during liver repair after damage or neoplasia is still not well understood. Nonetheless, some interesting pieces of information are emerging. Similar to that which has been described in embryogenesis^[160], a functional crosstalk between the TGF- β and Hh signaling pathways has been proposed in the context of adult liver progenitor expansion during liver injury. In ethanol-fed mice, TGF- β induces production of Hh ligands in hepatocytes,

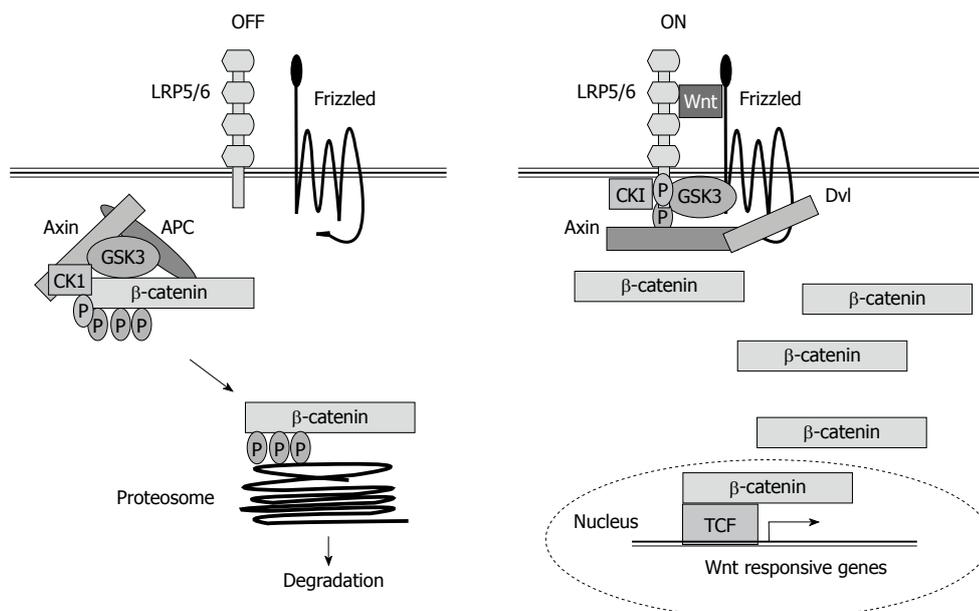


Figure 3 Wnt/β-catenin signaling. Left figure shows how β-catenin is pushed to degradation in the absence of Wnt ligand. Right figure shows how in the presence of Wnt, β-catenin regulates gene expression. TCF: T-cell factor; LRP: Low density lipoprotein receptor-related protein; APC: Adenomatous polyposis coli; CK1: Casein kinase 1; GSK: Glycogen synthase kinase.

which subsequently promotes survival and expansion of ductular/oval cell populations. This supports the concept that enhanced exposure to TGF-β contributes to the accumulation of cells with a ductular phenotype, which are protected from TGF-β-mediated apoptosis^[155,161]. Reciprocally, Hh-induced EMT might depend, at least partially, on induction of TGF-β^[159]. Further research is required to delineate the Hh-TGF-β interaction.

These findings suggest a role for the Hh pathway as a major mediator in the communication network established between myofibroblast and liver progenitors, which promotes progenitor accumulation and contributes to hepatic fibrosis pathogenesis through EMT induction.

WINGLESS/β-CATENIN PATHWAY

Proteins of the wingless (Wnt) family are secreted signaling molecules that regulate multiple processes in animal development and control tissue homeostasis. The Wnt signaling pathway is highly conserved throughout evolution and plays essential roles in controlling cell proliferation, cell to cell adhesion, and motility^[162]. In the liver, it plays many crucial roles during hepatic development and regeneration, and its dysregulation is evident in aberrant growth during hepatocarcinogenesis^[163]. Wnt signaling is itself inherently complex^[164]. On the one hand, both the ligands and receptors involved in Wnt signal transduction belong to large multi-gene families, which allows for a large number of possible ligand-receptor interactions. On the other hand, Wnt-receptor interactions can elicit a variety of intracellular responses, the best-known of which results in the activation of β-catenin/T-cell factor (TCF) transcriptional complexes. In the absence of signals, β-catenin accumulates in adherens junctions and free β-catenin levels

are very low because the tumor suppressor adenomatous polyposis coli forms a trimer complex with glycogen synthase kinase-3-β and axin/conductin, which interacts with and phosphorylates β-catenin, thus targeting it for degradation to the proteasome (Figure 3). Wnts bind a two-part receptor: a seven transmembrane Frizzled and low-density lipoprotein-related protein (LRP)5/6, both being required for canonical signaling. Ligand binding mediates phosphorylation of the cytoplasmic tail of LRP5/6, which creates an axin-binding site. Axin recruitment inactivates the destruction complex. This stabilizes β-catenin, which enters into the nuclei where it displaces Groucho from TCF, nucleating formation of a multiprotein activator complex, and activating Wnt target genes^[165] (Figure 3). Furthermore, β-catenin is at the crossroads of growth factor and cytokine signaling. Indeed, certain evidence indicates that TGF-β might induce nuclear β-catenin accumulation, through induction of platelet-derived growth factor signaling^[166]. β-catenin expression leads to elevated EGFR levels in hepatocytes and immunohistological analysis shows high correlation between the expression of nuclear/cytoplasmic β-catenin and EGFR in most hepatoblastomas^[167]. β-catenin also participates in homotypic cell-cell interactions through its association with E-cadherin. Thus, nuclear β-catenin accumulation in HCC cells might contribute to impaired E-cadherin expression, which mediates the EMT process, migration and survival. It is also known that β-catenin and Met form a complex on hepatocyte membranes. Upon HGF stimulation, the complex is dissociated, in a β-catenin tyrosine phosphorylation-dependent but Wnt-independent manner, which results in β-catenin nuclear translocation^[168]. In addition, a role for β-catenin as a downstream effector of HGF in HGF-induced hepatomegaly has been demonstrated^[169].

It has been recently suggested that oval cells respond to Wnt ligands *in vitro* with an increase in amino-terminus dephosphorylated β -catenin and cell cycle entry^[170], and that canonical Wnt/ β -catenin/TCF signaling plays a key role in the normal activation and proliferation of adult hepatic stem cells^[171,172]. In this same line of evidence, repression of Wnt/ β -catenin signaling in the anterior endoderm is essential for liver and pancreas specification^[173], which indicates that turning Wnt signaling off is essential for liver differentiation. An opposite situation might be found during hepatocarcinogenesis, where reactivation of the Wnt/ β -catenin pathway, or accumulation of nuclear β -catenin due to other alterations might contribute to the expansion of liver tumor stem cells. Indeed, recent reports have highlighted the relevance of Wnt/ β -catenin signaling in the activation of tumorigenic liver progenitor cells^[174] and the acquisition of hepatic stem-cell markers^[175] in HCC. Accumulation of nuclear β -catenin has been shown to induce an early liver progenitor phenotype in HCC, which correlates with tumor recurrence^[176].

In summary, Wnt family and β -catenin/TCF pathways are clearly involved in the maintenance of the liver stemness phenotype, and its repression is necessary for liver differentiation during development. Its overactivation during liver tumorigenesis might contribute to the acquisition of a liver cancer stem cell phenotype.

CONCLUSION

For the past 10-15 years, significant progress has been made in elucidating the cellular and molecular mechanisms that contribute to control of liver stem/progenitor cell behavior. Its complexity and multifaceted nature is evident. Among the diverse signaling pathways at play, the major growth factors, cytokines, and other ligand/receptor systems known to play an important role in liver development, homeostasis and regeneration, certainly occupy a central position. Many of the classical responses elicited by these factors are conserved. However, differences in the downstream mechanisms following ligand-receptor engagement, or signal interaction and crosstalk, as well as specific alterations in intracellular mediators, are being identified as contributing factors to the differential response of liver stem/progenitor cells compared with their mature counterparts. In addition, besides delivery of signals by the surrounding microenvironment, accumulating observations are pointing to co-existence of paracrine and autocrine modes of response as general regulatory mechanisms on this cell population. Collectively, these data indicate that liver stem/progenitor cells follow their own rules and regulations. It is also clear that the same signals that are essential for their activation, expansion, and differentiation, are good candidates to contribute, under adequate conditions, to the paradigm of transformation from a pro-regenerative to a pro-tumorigenic role. Unquestionably, from a clinical perspective, this is a fundamental issue for liver/stem progenitor cell-based therapies. Despite the fact that additional efforts are required to delineate per-

fectly how the functional switch takes place, the studies summarized here are steps in the right direction.

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Paediatric and adult colonic manometry: A tool to help unravel the pathophysiology of constipation

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Abstract

Colonic motility subserves large bowel functions, including absorption, storage, propulsion and defaecation. Colonic motor dysfunction remains the leading hypothesis to explain symptom generation in chronic constipation, a heterogeneous condition which is extremely prevalent in the general population, and has huge socioeconomic impact and individual suffering. Physiological testing plays a crucial role in patient management, as it is now accepted that symptom-based assessment, although important, is unsatisfactory as the sole means of directing therapy. Colonic manometry provides a direct method for studying motor activities of the large bowel, and this review provides a contemporary understanding of how this technique has enhanced our knowledge of normal

colonic motor physiology, as well as helping to elucidate pathophysiological mechanisms underlying constipation. Methodological approaches, including available catheter types, placement technique and recording protocols, are covered, along with a detailed description of recorded colonic motor activities. This review also critically examines the role of colonic manometry in current clinical practice, and how manometric assessment may aid diagnosis, classification and guide therapeutic intervention in the constipated individual. Most importantly, this review considers both adult and paediatric patients. Limitations of the procedure and a look to the future are also addressed.

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INTRODUCTION

Constipation is a common condition, with approximately 15% of adults and 9% of children reporting symptoms^[1-4]. The direct and indirect costs are substantial; in the USA alone, an estimated \$US1.7 billion/year is spent on adults^[5] and a further \$US3.9 billion/year on childhood constipation^[6]. While anatomical malformation (e.g. anal stenosis, imperforate anus), metabolic and gastrointestinal causes (e.g. hypothyroidism, celiac disease, and cystic fibrosis),

intestinal nerve or muscle disorders (e.g. Hirschsprung disease, chronic idiopathic intestinal pseudo-obstruction), childbirth or pelvic surgery are known to cause constipation, for many patients, their condition is regarded as “idiopathic”. Indeed, in children, it has been reported that less than 10% of those suffering from constipation have a recognizable underlying organic cause^[7,8]. Defects in the nerves and pacemaker cells (e.g. decreased ICC density^[9]) could be responsible in a proportion of cases, but as yet, techniques are not sufficiently developed to clearly identify such altered morphology, rendering any attribution to patho-aetiological significance (cause, effect, or epiphenomenon) speculative^[8,10,11].

Given that both aetiology and pathophysiology are unclear in many cases, it is perhaps therefore not surprising that up to one-third of adults and children who seek medical help will fail non-surgical therapy^[12,13]. Patients refractory to such interventions are debilitated, with physical functioning, mental health, general health and bodily pain all scoring poorly on quality of life questionnaires, compared to the non-constipated population^[14]; indeed, the impact is comparable to other chronic conditions, such as inflammatory bowel disease in adults^[15] and cancer in children^[16]. In refractory cases, surgery, including subtotal or total colectomy, repair of anatomical anomalies believed to impede defaecation^[17,18], appendicostomies^[19], and more recently sacral nerve stimulation^[20] may be considered. However surgical procedures are not without risk, with reported post-operative morbidity often high, and functional outcomes suboptimal^[17,21,22]; this, in turn, equates to poor quality of life^[23].

Improving therapies for functional bowel disorders is a fundamental goal for all researchers and clinicians working in this field, and to achieve this objective, a better understanding of pathophysiologies that may underpin such disorders is essential. In chronic constipation, altered colonic motor function remains the leading hypothesis to explain symptom generation, and this may be true not only for constipation associated with delayed colonic transit^[24], but also for constipation allied to an evacuatory disorder^[25]. In clinical practice, routine investigation of colonic motor function is achieved by use of transit studies (typically radio-opaque markers^[24,26]), while defecatory function typically is assessed using evacuation proctography or balloon expulsion. Diagnostic manometry, which provides a direct assessment of those contractile activities subserving intestinal functions, is well developed for other parts of the gastrointestinal (GI) tract, notably the oesophagus and anorectum, but its diagnostic potential in the colon remains less certain. This is due to a number of factors including the relative inaccessibility of the proximal large bowel, the technical constraints of current manometric recording systems, and inadequate understanding of normal colonic motor physiology, which is fundamental to confidently diagnosing motor abnormalities in disease states. This review examines the equipment and protocols used to record colonic motor patterns *in vivo* in humans, with particular focus on the diagnostic relevance of data

obtained, and the ability of colonic manometry to guide treatment. Current limitations and future direction for the procedure are also covered.

COLONIC MANOMETRY

Manometric studies of true colonic (as opposed to recto-sigmoid) motor function have been reported upon since the late 1980s^[27]. However, the colon remains the least well understood section of the GI tract, particularly its proximal portions. For constipation, around 20 studies in adults, and fewer in paediatric populations, have been published. As such, colonic manometry is still largely used as a research tool in adults, with relatively few authors advocating diagnostic use^[28,29]. Nevertheless, a recent American Neurogastroenterology and Motility Society consensus statement has recommended this test for the assessment of severely constipated patients (both adult and paediatric) who are unresponsive to medical therapy, and who have evidence of slow colonic transit in the absence of an evacuatory disorder^[30]. Furthermore, in children, colonic manometry has been proposed to discriminate normal colonic motility from colonic neuromuscular disorders^[31]. It may also help to clarify the pathophysiology of persistent lower GI symptoms after surgery for Hirschsprung disease, evaluate colonic involvement in a child diagnosed with idiopathic intestinal pseudo-obstruction syndrome, assess function of a diverted colon prior to possible re-anastomosis, and to assess colonic motor activity prior to intestinal transplantation to determine if the colon should be kept at the time of transplant^[32]. What is certainly true is that colonic manometric procedures lack standardisation, with a variety of catheter types, placement techniques and protocols currently used.

It must also be remembered that colonic manometry is an invasive procedure, and as such should only be performed in those patients with symptoms severe enough to have a marked impact on their quality of life and social well-being. Extensive conventional treatment should be offered before testing colonic motility.

Catheter types

In general, there are two broad types of catheters used: (1) water-perfused; and (2) solid-state. As yet, there have been no studies which directly compare the two types. Preference for one over the other is guided by existing equipment, desired application, study design, and particularly cost.

Water-perfused manometry catheters: Water-perfused manometry is used in children and has been the preferred choice in the vast majority of studies in adults. Catheters are made of flexible PVC^[27,33] or extruded lengths of silicone rubber^[34]. The latter is highly flexible, and is desirable for patient tolerability if an oral route is used for intubation (see below). The catheters incorporate between 4 and 16 recording ports or side-holes, with an inter-side-hole distance of between 1 and 15 cm^[24,35]. Each recording port

consists of an open lumen, which is connected to a pneumohydraulic infusion pump that ensures constant flow of water. The basic premise for recording is that contractions of the colonic wall occlude the manometric ports, thus impeding flow of perfusate (degassed water). Resistance to flow is transmitted as pressure change to external transducers, and the degree of resistance depends upon the amplitude and duration of the contraction. Such catheters are relatively inexpensive and highly versatile with regard to configuration (number, position and orientation of side-holes); in addition, silicone catheters are autoclaveable, and therefore can be re-used many times without fear of contamination. However, due to the requirement of being attached to the manometry system, and need for constant water infusion, studies are always performed in the laboratory setting. This confines the subject to a bed for the length of the recording period with minimal mobility allowed, thus creating a somewhat unphysiological environment. In addition, the volume of water introduced into the lumen is considerable (> 3 litres) if recording from multiple side-holes for prolonged periods of time. Whilst the colon does have the ability to absorb up to 6 litres of fluid a day^[36], the effects of introduction of this amount of fluid upon colonic motility remains unknown.

Solid state manometry catheters: So-called 'solid-state' assemblies traditionally consist of strain gauges embedded into a flexible PVC catheter. Each strain gauge is attached to an amplification/recording system *via* fine connective wiring^[35]. Until recently, solid-state catheters have typically had between 6 and 10 sensors spaced at 7-15 cm intervals^[24]; however, recent technological advances now allow in excess of 20 sensors. Recorded pressure signals can be stored on portable digital recorders enabling the subject to be ambulant^[29,37]. However, the cost of these catheters is considerable in comparison to water-perfused catheters, and there has been a tendency in the past for recording channels to break^[38,39]. Nevertheless, with further technological improvements, and recent developments in fibre-optic technology, which has seen the emergence of an optical manometry system (see Future directions below), such limitations should be overcome^[40,41].

Placement techniques

In human subjects, gaining access to the colon can generally be achieved through two routes: *antegrade* placement *via* the nose or mouth, or *retrograde* placement *via* the anus. Colonic catheters can alternatively be placed through a variety of stomas, a method used particularly in children^[42-44] but also in adults^[45].

Retrograde placement: This provides the easiest access to the colon, and is by far the most commonly used procedure in both adults and children^[33,37,46,47]. In adults, catheters are placed with the aid of a colonoscope and can be positioned in the desired location. To date, most studies utilising this method have located the tip of the catheter at the hepatic flexure or mid-transverse colon, meaning

that recordings are only achieved from sites distal to this. However, the Sydney group have achieved true pancolonic recordings over the past few years by securing the tip of the catheter to ascending colonic/caecal mucosal folds using endoclips^[20,29,48,49]; this has the advantage of helping to prevent catheter displacement or excretion during defecation^[50,51].

In children, the retrograde placement of colonic manometry catheters has also utilised colonoscopic procedures^[46]; however, in recent years colonic catheters have also been successfully placed using fluoroscopic guidance alone, both through stomas and *via* the rectum^[44]. However, this technique may be associated with prolonged exposure to radiation, in some cases up to 27 min^[44].

One of the major advantages of retrograde catheter intubation is subject tolerability. Once the catheter has been sited, there is little or no discomfort. However, in addition to concerns over catheter displacement, there are other potential disadvantages, most notably the requirement for bowel preparation and usually some form of anaesthesia or sedation. The removal of faeces from the colon has recently been shown to result in an increase in the frequency of high amplitude propagating contractions^[52,53], and also to disrupt the spatiotemporal organisation of propagating sequences (PSs)^[53]. However, the colonic responses to physiological stimuli, such as a meal and morning waking, remain unchanged^[53]. Nevertheless, it could be argued that bowel preparation is advantageous, in that the 'starting point' for each study, provided that bowel preparation is performed in an equivalent manner, is standardised.

Antegrade placement: This is a less common method for recording colonic motility and is restricted to adult studies^[25,34,39,54]. The catheter is fed through the nasal cavity or mouth, and once through the pylorus (often achieved under fluoroscopic guidance), a balloon on the tip of the catheter is inflated with air or water to facilitate transit through the small and large bowel^[25,34]. The main advantage of this procedure is that it obviates the need for bowel preparation, and thus the study is performed under essentially normal basal physiological conditions. The procedure is, however, time-consuming in comparison to retrograde catheter placement. Even in healthy controls, it may take up to 36 h to intubate the distal descending colon^[34,35]. Furthermore, with the catheter *in situ* for a prolonged period of time, subject tolerability becomes an issue with nasal/oral/pharyngeal discomfort and nausea commonly reported. Finally, while antegrade placement can be used to study colonic motility in health and in patients with relatively normal colonic transit^[25], its use in patients with slow transit constipation (STC) is problematic. As antegrade catheter placement relies on peristalsis to promote the catheter tip through the gut, the process can be greatly prolonged in patients with a disorder characterised by delayed gut transit (the primary clinical indication for this investigation^[30]), especially when small bowel motility may also be abnormal^[55].

Placement through a stoma: Intubation *via* appendicostomy, caecostomy, ileostomy or colostomy has been used to successfully investigate children with STC^[19,44,56]. In such subjects, after a preceding colonic washout, the in-dwelling device (e.g. Chait caecostomy button) is removed. Two techniques can then be adapted: (1) following sedation, the catheter can be advanced through the stoma with the aid of a guidewire, and positioned under fluoroscopic guidance^[44]; and (2) a 10F feeding tube can be positioned through the stoma through which a Bisacodyl solution (2–4 mg) can be instilled directly into the caecum. A manometry catheter can then be introduced through the feeding tube and advanced in an antegrade direction along the colon. The Bisacodyl induces propulsive activity, and a balloon on the tip of the catheter can be inflated with water to aid propulsion through the large bowel^[42,43].

RECORDED COLONIC MOTOR ACTIVITIES

Non-propagating motor activity

Non-propagating activity makes up the majority of a colonic manometric recording, consisting of apparently random pressure waves recorded at single or multiple recording sites, often alternating with phases of motor quiescence. Pressure waves may be sub-classified on the basis of duration, and are considered to be of either long duration (the majority) or short duration (often superimposed on long duration pressure waves). The presence of two types of phasic contraction in the colon is unique, compared with the remainder of the GI tract^[57]. The functionality of non-propagating activity is outlined below.

Propagating motor activity

Propagating pressure waves are categorised into PSs (also termed propagating contractions) and high amplitude PSs (HAPSs; also termed high amplitude propagating contractions; Figure 1); the latter are recognised as the motor correlate of mass intraluminal movement and are involved in defaecation (Figure 2)^[59,62]. Both PSs and HAPSs can be further qualified by the terms antegrade (aboral) or retrograde (oral), depending upon the direction of propagation. However, criteria used to define these events are inconsistent^[35]. A general classification includes an array of 3 or more pressure waves recorded from adjacent recording sites, with a trough to peak amplitude ≥ 5 mmHg per pressure wave, in which the conduction velocity between wave onsets is between 0.2 and 12 cm/s^[34,50]. The definition of what constitutes a HAPS is based on a threshold value for amplitude of one or more of the component pressure waves^[35]; this varies markedly in the literature from > 50 to 136 mmHg^[34,50,63–67]. Consequently, the range of published frequencies is wide^[35]; in many cases, the chosen threshold value appears to be arbitrary. Some, however, are based on proven functional characteristics^[34].

PSs are identified throughout the large bowel, although they originate with greater frequency in the proximal compared to the distal colon^[37,38,58,59,68,69]. The majority of ascending colonic PSs do not migrate beyond the

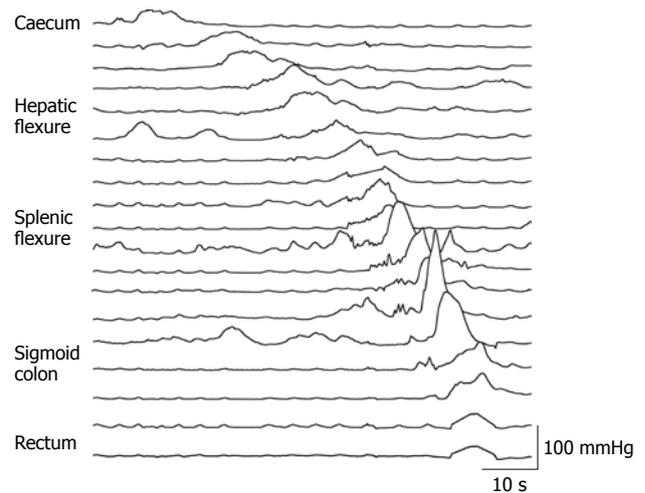


Figure 1 The high amplitude propagating sequence was first described in 1988^[27]. The majority of these propagating events originate in the proximal colon and extend to the sigmoid colon. The amplitude of the component pressure waves increase as the motor patterns reaches the descending colon^[58].

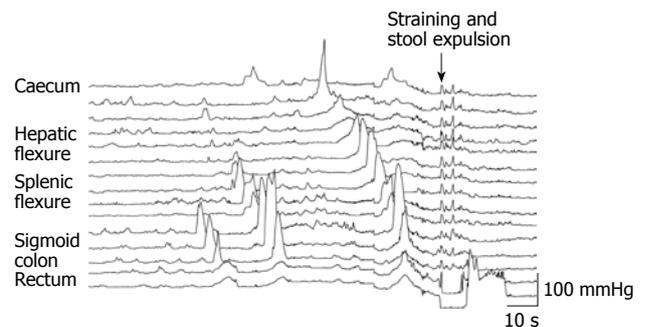


Figure 2 High amplitude propagating sequences are commonly associated with defaecation in healthy controls. Note the series of three high amplitude propagating sequences (HAPSs) prior to stool expulsion. The first originates at the distal descending colon, and with each subsequent HAPS, the site of origin moves to a more proximal location with the final HAPS extending the entire length of the colon^[34].

splenic flexure, and conduction velocity of PSs increases as the PS moves distally from the proximal colon, as does the amplitude of the propagating pressure waves^[50,58,59,70].

Given their functional significance, HAPSs have garnered most interest in terms of pathological implication, and indeed decreased HAPS frequency is widely accepted as one of the principal hallmarks of STC (see below^[27,29]). However, focus on propagated pressure waves alone, as is the case in many published reports, has perhaps led to their clinical impact being over-stressed, particularly given that they occur only a minority of the time during a colonic manometric recording; the organisation of other, more common motor activities may be of similar (or even greater) importance.

Organised colonic motor patterns

Akin to the interdigestive migrating motor complex of the upper GI tract^[71], the colon exhibits periodic bursts of regular phasic pressure wave activity, termed either colonic

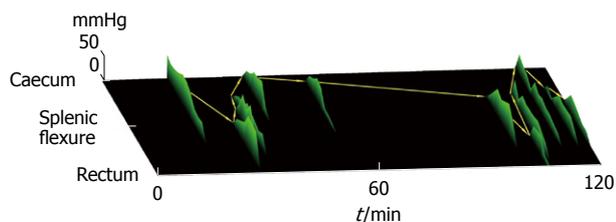


Figure 3 Two hour spatiotemporal maps of colonic propagating sequences in a female healthy control. In this map each individual ridge represents an antegrade propagating sequence. The start of each ridge indicates the site of origin and the time of day the propagating sequence occurred. The length of the ridge indicates the extent of propagation. The heights of the ridge indicate the amplitude of the component pressure waves. The yellow arrows link the site of origin of sequential propagating sequences. While no single propagating sequence spans the entire colon collectively, a linked series of propagating sequences can do so^[76].

motor complexes^[38,39,58] or rectal motor complexes (MC)^[35,72], depending upon their site of origin. MCs predominate in the sigmoid or rectum, where they have also been termed “periodic rectal motor activity”^[37,73,74]. The functional significance of these events is unclear, although it has been suggested that they provide a “brake” around the rectosigmoid junction^[73], and reflect enteric neuromotor integrity, given that they occur in extrinsically denervated colon preparations^[75].

In addition to MCs, sequential PSs have been shown to be linked in organized spatiotemporal patterns throughout the colon^[76]. Many of these PSs form series in which three or more consecutive PSs demonstrate a regional shift in the colonic region from which they originate, i.e. each PS in a linked series will originate in a progressively more proximal or distal colonic location. Whilst most single PSs do not span the length the colon, collectively, a series of linked PSs can do so. It is likely that such linkage is important for the transport of content over longer lengths of the colon (Figure 3)^[76].

COLONIC MANOMETRY PROTOCOLS

Paediatric studies

Despite the variety of placement techniques and catheter types, once the catheter is positioned, there is commonality to the actual recording protocol. In children, clinical studies generally do not last more than 4–5 h^[77], but 24 h studies have been used in the research setting to provide more detailed information on motility characteristics^[42,43]. Paediatric colonic manometry catheters typically contain 6–8 recording side holes, evenly spaced at 7.5, 10 or 15 cm intervals^[42,43,77]. The paediatric colonic motility test includes at least 1 h of fasting and 1 h postprandial after finishing a high calorie meal. During the test, the child is required to remain in bed and it is important to have a trained observer at the bedside. If HAPSs are not recorded during the fasted or postprandial period, then drug stimulation with Bisacodyl (0.2 mg/kg, max 10 mg, diluted with 0.9% NaCl) is administered. HAPSs induced by Bisacodyl usually occur within a few minutes and are identical to spontaneous

HAPSs. A cramping sensation and the urge to defaecate often accompany the presence of HAPSs^[47]. If the paediatric test extends to 24 h, then the nocturnal frequency of motor patterns and the colonic response to waking are also measured^[42,43,77].

Adult studies

In published adult colonic manometry studies, similar protocols are followed, although the catheter length is generally longer, containing up 16 sensors (water-perfused) spaced at 7.5 cm intervals^[25,34]. Recordings are typically of 24 h duration. All studies examine two or more of the following: (1) fasting; (2) meal responses; (3) nocturnal suppression; (4) morning waking; and (5) response to chemical stimuli^[24,35].

Normative data

For a clinical diagnosis, data collected from patients is compared to that obtained from healthy controls. In the adult population, recruitment of volunteers is generally not problematic, allowing normal ranges to be developed for various parameters of the motility recording (though it must again be stated that the size of published normative data sets remains inadequate).

By contrast, colonic motility recordings in truly healthy paediatric control subjects are lacking for obvious ethical reasons. Di Lorenzo *et al.*^[78] attempted colonic manometry in 32 “healthy” paediatric patients, though they were not strictly healthy controls, as they had diagnoses ranging from functional faecal retention ($n = 15$) and non-ulcer dyspepsia ($n = 10$), to Munchausen by proxy ($n = 7$). Other paediatric studies in adolescents with STC have used healthy young adults as the control group; whether this is appropriate is unknown^[42,43].

OBSERVATIONS FROM COLONIC MANOMETRY STUDIES

Both propagating and non-propagating motor patterns may be temporally associated with propulsion and mixing of colonic content^[59,60,79], signifying that these are important determinants of normal physiology in health and of pathophysiology in patient groups. In adult and paediatric patients with chronic constipation, a number of findings have been made which suggest pathological significance, including: (1) a lack of the normal^[37,58,80] increase in colonic motor activity after a high calorie meal^[29,43,46,49,80–86] (Figure 4); (2) a lack of the normal^[29,50,51,58] suppression of colonic motor activity at night, and a suppressed or absent increase in colonic activity in response to morning waking^[25,29,43,80] (Figure 4); (3) a decrease in frequency of HAPSs^[27–29,39,47,49,80,83,85–88], although normal daily frequencies have also been reported in some constipated subjects^[25,43] (Figure 4); (4) increased non-propagating activity in the left colon^[89]; (5) absence^[25] of the characteristic spatiotemporal patterning of PSs preceding normal spontaneous defecation^[34]; (6) diminished co-ordination between

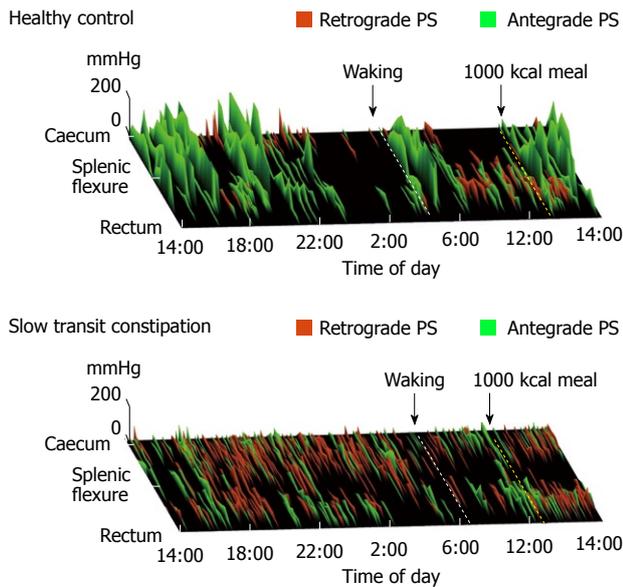


Figure 4 Twenty-four hour spatiotemporal maps^[80] of colonic propagating sequences in a female healthy control and a female patient with slow transit constipation. Within each map the ridges represent antegrade (green) and retrograde (red) propagating sequences (PS). The antegrade PSs originate at the oral end of the green ridge and retrograde PSs originate at the anal end of the red ridges. The start of each antegrade and retrograde ridge indicates the site of origin and the time of day the PS occurred. The length of the ridge indicates the extent of propagation. The height of the ridge indicates the amplitude of the component pressure waves. The yellow-hatched line indicates when the 1000 kcal lunch was given, the white-hatched line indicates the time of morning waking. In health the frequency of propagating sequences are reduced during sleep and increase upon morning waking and in response to a high calorie meal. The map in the STC patients is characterized by an increased frequency of short extent PSs and a lack of high amplitude propagating sequences. There is an absent meal response (no increase in PSs) and an absent nocturnal suppression of PSs.

sequential pan-colonic PSs^[76,80]; (7) a blunting of the normal^[49] increase in PS or HAPS frequency in response to rectal or colonic infusion of Bisacodyl has been shown in a proportion of individuals^[47,49,85], although in the majority of patients a normal response is recorded^[49,83,85,90-92]; (8) a blunting of the normal increase in colonic HAPS frequency to intravenous injection of the cholinergic agonist edrophonium chloride^[92]; (9) a blunting of the normal proximal colonic increase in motor activity in response to a rectal infusion of chenodeoxycholic acid^[93]; (10) an increase in the frequency of HAPSs in response to sacral nerve stimulation in patients with STC^[20]; and (11) a significant increase in the frequency of rectosigmoid motor complex activity^[73,74].

CAN COLONIC MANOMETRY FINDINGS HELP TO DISTINGUISH SUBTYPES OF CONSTIPATION?

Constipation can be conceptualized into two broad overlapping categories: STC, and disorders of evacuation^[1,94-96]. In some cases, this distinction among subgroups, based on aberrant physiological measurement, has proven ben-

eficial in planning treatment and in predicting therapeutic outcome^[96-99]. For example, identification of dyssynergic defaecation by anorectal manometry and balloon expulsion testing, in the absence of delayed colonic transit, is predictive of a high success rate from biofeedback^[97,98]. Likewise, in carefully selected patients with severe STC, where the transit delay is restricted to the colon^[17,22,100,101], and there is no evidence of evacuatory dysfunction, surgery such as colectomy with ileorectal anastomosis may be effective. In children this group is successfully managed with an appendix stoma and antegrade enemas^[19].

In terms of colonic manometric investigation, specific biomarkers or biosignatures that may help to define constipation subtypes (and thus provide therapeutic targets) have, as yet, not been fully established. In adults, only three studies have addressed the validity of manometric findings between “recognised” subgroups^[102-104]. The first concluded that intraluminal measurements could not be used to discriminate between subgroups of patients with either STC or an evacuation disorder^[102]. The second study examined three subgroups of constipated patients with either STC, an evacuation disorder, or ‘normal transit’ constipation, and found that fasting and postprandial motor parameters were not useful for discriminating amongst these subtypes, although colonic compliance was^[103]. Bassotti *et al.*^[104] noted that no colonic motor patterns were able to differentiate between constipated patients with or without delayed transit.

A further study in patients with constipation secondary to antidepressants revealed minimal motility differences compared to patients with idiopathic constipation^[85]. Finally, Hervé *et al.*^[83] took the approach that manometric findings themselves should be used as the basis for subclassification. In a study of 40 adults with STC, they identified 4 subgroups: group 1 displayed no HAPS or a colonic response to a high calorie meal; group 2 showed increased sigmoid motor activity; group 3 had a reduced frequency of HAPSs; and group 4 displayed normal colonic motility. However the clinical impact of such findings, in terms of guiding successful management, remained undetermined. Nevertheless, through sufficiently large scale studies, a classification system incorporating findings from pancolonic manometric investigations, rather than being based on traditional studies of colonic transit and evacuatory function alone, may be merited. Current stratification, where the colon is seen to be responsible for transit, and the anorectum solely responsible for evacuation, is likely a gross oversimplification.

CAN COLONIC MANOMETRY HELP TO GUIDE TREATMENT AND IMPROVE OUTCOMES?

The primary indicators of abnormal colonic motor function in constipation (see above) are reduced HAPS frequency and a diminished or absent response to eating, morning waking or chemical stimulation. The colonic re-

response to ingestion of a meal is likely to involve the CNS and neurohormonal pathways; a suppressed response has been proposed as indicative of colonic myopathy and an absent response as a possible neuropathy^[29]. Similarly, diurnal variation in colonic motor activity is likely to be mediated by the CNS, and therefore a diminished or absent response to sleep or morning waking supports a neuropathic cause in such patients^[29]. With regard to chemical stimuli, a failed response may indicate an abnormality within the myenteric plexus^[105], cholinergic pathways^[92] or recto-colonic neural pathways^[93].

Adult studies

In adults, very few interventional studies have been based upon evidence gained from colonic manometric investigation. In 3 patients with severe constipation who had failed conservative therapy, Bassotti *et al*^[28] demonstrated globally reduced colonic motility, a minimal meal response and no response to Edrophonium. Based upon these data, 2 patients underwent a total colectomy and 1 a hemicolectomy, with “fairly good results at follow-up” reported. No long-term data were provided.

In a larger study, Rao *et al*^[29] performed 24 h colonic manometry in 21 patients with STC. Utilising the response to ingestion of a meal, response to morning waking, and HAPS frequency as diagnostic criteria, patients were classified as having a neuropathy ($n = 10$) if they had an absence of two or more, a myopathy ($n = 5$) if they had a reduced response to two or more, or being normal ($n = 6$). Those with a suspected neuropathy were offered a colectomy (performed in 7/10, with “improved” bowel symptoms reported; no follow-up duration specified). Those with a myopathy were offered a regime of biofeedback and laxatives, and reported “modest improvement” at 1 year.

Paediatric studies

In children, colonic manometry studies are far more likely to guide treatment options. In a study by Pensabene *et al*^[106], results of colonic manometry testing resulted in a recommendation to change therapy (mostly surgical) in 93% of the patients with intractable organic or functional constipation. Importantly, 88% of the 98 parents believed that the therapeutic suggestions made had been helpful in improving their child's health^[106].

Di Lorenzo *et al*^[107] studied 46 children with constipation and/or faecal incontinence after surgery for Hirschsprung disease. Four groups were established based upon results from colonic manometry: (1) HAPSs propagating from the proximal colon through the neorectum to the anal sphincter, which was associated with faecal incontinence ($n = 18$); (2) an absence of HAPSs and lack of colonic meal response, which was predominantly associated with constipation ($n = 15$); (3) a normal manometric study, with a hypertensive anal sphincter, which was invariably associated with constipation ($n = 4$); and (4) a normal manometric study, but the child presented with fear of defaecation and retentive posturing, which was predominantly associated with constipation and soiling ($n = 9$).

Those in group one were treated with anticholinergics and Loperamide. In group two, resection of the abnormal section of colon was recommended. In the third group, four-quadrant intrasphincteric botulinum toxin injections were recommended, and in the fourth group, a programme of behaviour modification and stool softeners were used^[107]. Based upon these treatments, the authors reported an improvement in global health and emotional health scores as well as an improvement in the number of bowel movements and resolution of abdominal pain^[107].

Also in paediatric patients, colonic manometry is reported to have value in determining poor outcomes for the surgical treatment of intractable constipation using an appendicostomy or a caecostomy with antegrade irrigation of the colon^[47]. For example, those children with a poor outcome also displayed an absence of colonic response to Bisacodyl. However, the fact that 50% of children with no production of HAPS still had good outcomes to antegrade irrigation suggests that the Bisacodyl response is by no means a solid predictor^[47].

CURRENT LIMITATIONS

While colonic manometry studies in both children and adults have helped to define some of the physiological and pathophysiological aspects of colonic motor function, there are still no published quantitative data on propagating or non-propagating activity that clearly differentiates healthy subjects from constipated patients^[30]. Furthermore, at least in children, morphological changes reflecting possible myogenic or neurogenic disorders in muscle tissue do not correlate with particular features of colonic manometric recordings^[108] or anorectal manometry^[109]. It also remains unclear whether data derived from adult studies can be extrapolated to children and *vice versa*. No manometric studies using the same equipment and protocols have compared childhood and adult constipation. Indeed, because a normal frequency of HAPSs has been identified in children with STC (contradicting most reported findings in adults), childhood constipation may represent a different entity^[43]. The impact of sensory, as opposed to motor dysfunction on the development of constipation is gaining increasing recognition^[110,111]. Nevertheless, the two are inextricably linked, and future studies should look to explore both domains concurrently, by the best methods available, rather than consider certain functional bowel conditions as principally motor disorders (e.g. constipation), and others as sensory disorders (e.g. the irritable bowel syndrome).

With variations in protocols, catheter types, numbers of recording sites, spacing between recording sites, placement techniques and definitions of recorded activities, it is perhaps not surprising that consistent findings have not been reported in the literature^[24,35]. Furthermore (and as stated above^[24]), almost all studies that detail “colonic” manometry have, in reality, recorded colonic motor patterns distal to the mid-transverse colon. Support for the use of true pancolonic manometry resides in the fact that

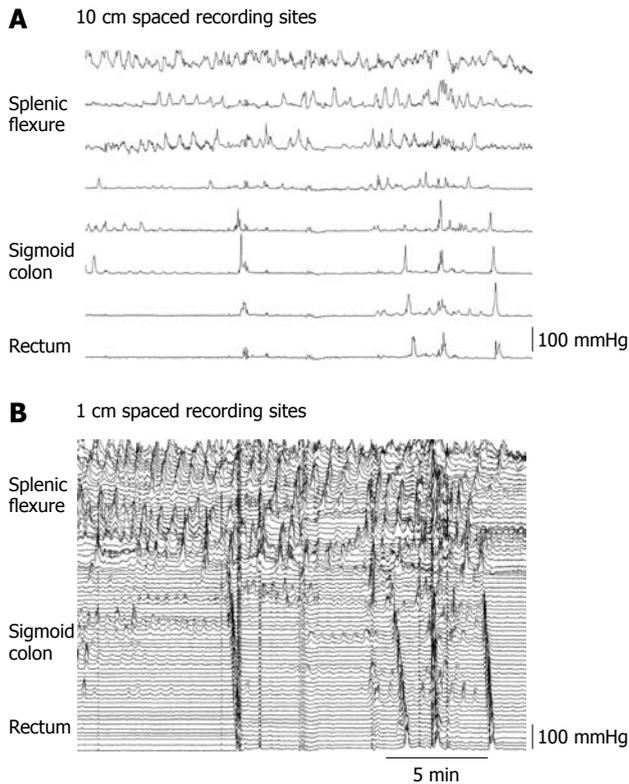


Figure 5 Manometric traces of colonic motor activity recorded by a fibre-optic manometry catheter with 90 sensors spaced at 1 cm intervals. A: To represent common sensor spacing for current published colonic recordings, the data set, obtained through “high resolution” manometry, is sub-sampled to present every 10th channel (10 cm spacing, top); B: The complete data set, captured at 1 cm intervals, is displayed at the bottom. Note that at 10 cm spacing, the most proximal three channels reveal what appears to be non-propagating pressure waves. However, when the full data set is viewed (B), a series of short-extent retrograde propagating events are detected. These events are missed when spatial resolution is poor. Modified from^[41].

PS and HAPS are not distributed evenly throughout the colon, and predominantly originate in the ascending and proximal transverse colon, and that the entire colon appears to function in a coordinated fashion^[76,112]. ‘Partial’ colonic recordings thus provide an incomplete picture of colonic (patho)physiology.

FUTURE DIRECTIONS

In the oesophagus and the anorectum, manometry is an established diagnostic tool. In comparison to the colon, these regions afford easier access and therefore have been subjected to far more research and clinical investigation. More recently, development of high resolution manometry (HRM) has further enhanced diagnostic potential, particularly in the oesophagus^[113], most notably with regard to standardisation of recording procedures. With the advent of fibre-optic manometry^[40,114], HRM recordings are now feasible throughout the entire colon. Catheters incorporating up to 120 sensors spaced at 1 cm intervals have already demonstrated that the vast majority of PSs propagating over short distances are missed by recording sites spaced > 7 cm apart^[40,41] (Figure 5). If such technology

is able to identify those elusive biomarkers that can help to reliably distinguish constipation subtypes and guide management, then this provides the opportunity to take colonic manometry out of the research arena and into clinical practice. Such progress is only possible through appropriately designed and powered studies, utilising equivalent hardware and software, both in adults and children. The revolution that has been seen with oesophageal HRM, such that traditional manometry is now regarded as obsolete, can serve as a template for the clinical potential of pancolonic manometric investigation.

CONCLUSION

Pancolonic manometric investigation provides a unique window onto motor functions of the large bowel, and through its use we now have a greater understanding of normal colonic physiology and also the pathophysiology of constipation in both adults and children. Although a recent consensus statement^[30] advocates use of colonic manometry in patients with “significant motility disorders”, the technique is still not refined enough for widespread clinical use, and no prospective and controlled studies have been performed evaluating the clinical value of this tool. Nevertheless, technological advances offer the potential of adding colonic manometry to the available diagnostic armamentarium in broader clinical practice. To achieve such a goal, there is a fundamental requirement for standardisation of methodologies and recording protocols, further development of automated analysis software, and a vital need for generating larger normative data sets, which will enable diagnostic yield to improve. This will be achieved through the coordinated efforts of those dedicated to this field. Further clinical exploration of this technique affords the possibility of a more directed therapeutic approach in patients with chronic constipation. Colonic manometric studies, performed in large numbers of constipated patients, will hopefully establish biomarkers that can distinguish existing (largely predetermined) constipation subtypes (i.e. STC, evacuation disorders), or aid a more contemporary phenotypic classification.

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Transient elastography in chronic hepatitis B: An Asian perspective

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Abstract

Transient elastography (TE) is a new non-invasive tool for assessing liver stiffness, which is correlated with the histologic stage of liver fibrosis. Many studies have reported a good accuracy of TE in predicting significant fibrosis and an optimal accuracy in predicting cirrhosis. Furthermore, the potential role of TE in screening the general population has also been proven. TE thus helps physicians to decide treatment strategies, predict prognosis, and monitor disease progression in patients with chronic liver disease and to screen the general population to identify high risk patients with potential liver disease. However, most data on the clinical roles of TE have been gathered in European patients with chronic hepatitis C (CHC), because TE was first developed in France. Accordingly, much data on the usefulness of TE in patients with CHC has accumulated. Recently, however, vigorous efforts have been made to apply TE

to patients with chronic hepatitis B (CHB), and TE has also proved to have acceptable accuracy in diagnosing liver fibrosis and cirrhosis in these patients. Thus, we focused on TE in the Asian population with CHB in comparison with the European population with CHC and found that the diagnostic performance and cutoff values were different between the 2 populations possibly as a result of several different confounders between Asian and European populations (the etiology of chronic liver disease, histologic features, major fluctuation in alanine aminotransferase levels, and the prevalence of high body mass index and metabolic syndrome). Therefore, further studies tailored to the Asian population with CHB should be performed before the widespread application of TE in Asian populations with CHB.

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Key words: Asia; Chronic hepatitis B; Fibroscan; Hepatitis B virus; Liver stiffness measurement; Transient elastography

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INTRODUCTION

Transient elastography (TE) using FibroScan® (EchoSens, Paris, France) is a newly introduced non-invasive tool, that generates an elastic wave using a vibrator applied to the thoracic wall at the level of the right lobe of the liver and measures the propagation velocity of the wave,

which is directly associated with liver stiffness (LS)^[1]. To date, the clinical utility of TE has been widely reviewed, and it is regarded as having considerable accuracy for predicting liver cirrhosis in patients with chronic liver disease (CLD) of diverse etiologies^[2-5]. TE is quick, highly reproducible, and completely harmless to patients. In addition, it can be learned and performed easily after a short training period (by nurses or technicians) without consuming the time of clinicians. For these reasons, TE has become popular in clinical practice as a tool for aiding in the diagnosis and follow-up of liver disease.

Because TE was first developed in France, most studies on its benefits have been explored in European countries where chronic hepatitis C (CHC) is prevalent. Accordingly, extensive data on the clinical roles of TE in assessing liver fibrosis in patients with CHC have been gathered. Recently, several meta-analysis studies reported that TE is a reliable non-invasive tool to detect advanced liver fibrosis and liver cirrhosis^[6-8]. However, most studies included in the meta-analysis investigated European populations with CHC. Data from Europe cannot be extrapolated to the Asian population, as subsequent trials of TE in Asian countries where hepatitis B virus (HBV) infection is more prevalent than hepatitis C virus (HCV), displayed divergent results. In this Topic Highlight, we will focus on TE in the Asian population with chronic hepatitis B (CHB).

METHODOLOGICAL CONSIDERATION OF TE IN THE ASIAN POPULATION

LS values are defined as the median of 10 valid measurements and at least 60% of TE shots should be successful for each examination according to the manufacturer's recommendations. Accordingly, to date, only the results of TE examinations satisfying the above criteria have been considered as reliable and have been included for the analysis in reported studies.

Another important parameter for confirming the validity of LS values is the interquartile range (IQR), which is defined as the values between which 50% of observations fall. The lower boundary is the 25th percentile (lower quartile), the upper boundary is the 75th percentile (upper quartile). Generally, the IQR/median LS value ratio (IQR/M) should not exceed 30% if the reliability of LS values is to be preserved. However, recently, Lucidarme *et al*^[9] proposed new criteria for reliable LS values, using the IQR/M based on the data from more than 250 French patients with CHC. They found, in a multivariate analysis, the fibrosis stage (F0-2 *vs* F3-4) and IQR/M were significantly associated with significant discordances between TE and liver biopsy (LB), with an optimal discriminant cutoff value of 0.21. They thus concluded that the IQR/M can overestimate liver fibrosis using TE, irrespective of success rate, when the significance discordance was defined as a discordance of at least 2 stages of fibrosis between LS values by TE examination and the METAVIR scoring system. From these results, they suggested a novel algorithm for clinical

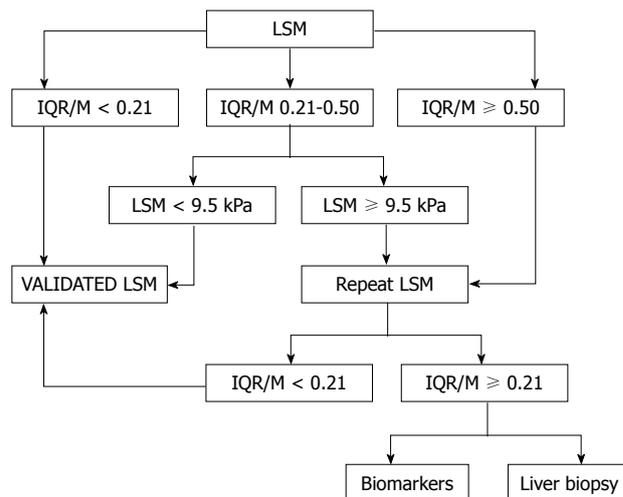


Figure 1 Suggested algorithm for clinical practice as first-line assessment of hepatic fibrosis in patients with chronic hepatitis C. IQR/M: Interquartile range/median liver stiffness value ratio; LSM: Liver stiffness measurement.

cal practice as first-line assessment of liver fibrosis in patients with CHC (Figure 1).

Because the IQR/M was confirmed in only one European study with CHC showing relatively high body mass index (BMI) ($25 \pm 4.1 \text{ kg/m}^2$), its application to the Asian population with CHB (who generally show a lower BMI) is difficult and requires further validation. Although the data are preliminary, we have attempted to validate the IQR/M for our cohort of 156 patients with CHB (mean age 38.8 years, male 75.0%, mean BMI 23.2 kg/m^2) who underwent LB and TE prior to starting antiviral treatment. In this study, we selected the cutoff LS values of Marcellin *et al*^[10] (7.2 kPa for \geq F2, 8.1 kPa \geq F3, and 11.0 kPa for F4) as the reference values between 2 external studies that investigated the performance of TE and then set up the optimal cutoff LS values for each fibrosis stage in patients with CHB^[10,11]. We identified 28 (18.0%) patients showing significant discordance between TE and LB. However, the IQR/M was not significantly different between patients with discordance and those with non-discordance (0.125 ± 0.083 *vs* 0.129 ± 0.079 , $P = 0.831$), and the success rate also failed to show a significant difference.

Interestingly, the mean IQR/M of our study population was greatly reduced compared to that of subjects in Lucidarme *et al*^[9] (0.30 in patients with discordance and 0.22 in those with non-discordance) and the proportion of patients with an IQR/M > 0.03 ($n = 7$, 4.5%) was very small. The reasons are not clear why the IQR/M in our study was reduced in comparison with that in the previous study, and was not selected as a discriminant factor to predict discordance. However, we think that the optimal cutoff value of the IQR/M will be lower than that from patients with CHC even if the IQR/M can be validated in the future for the Asian population with CHB, or that the IQR/M is not a predictor of discordance in the Asian population with CHB due to other potential confounders that overwhelm the influence of the IQR/M, such as the inhomogeneous histological features of CHB which often

Table 1 Normal liver stiffness values of transient elastography

	Asian study			European study			
	Kim <i>et al.</i> ^[14]	Fung <i>et al.</i> ^[19]	Corpechot <i>et al.</i> ^[15]	Roulot <i>et al.</i> ^[13]	Sirli <i>et al.</i> ^[16]	Colombo <i>et al.</i> ^[17]	Colombo <i>et al.</i> ^[18]
Type	Full article	Full article	Letter	Full article	Full article	Abstract	Abstract
No. of subjects	69	28	71	429	144	327	746
Population	Liver and kidney donors	Liver donors	Healthy volunteers	Medical check-up	Healthy volunteers	Blood donors	Blood donors
Liver stiffness (kPa)	4.6 (mean)	4.6 (median)	4.8 (median)	5.5 (mean)	4.8 (mean)	4.9 (mean)	4.4 (median)
95th percentile (kPa)	4.7	-	-	8.6	-	7.8	6.7
BMI (kg/m ²)	22.6 (mean)	-	22.5 (median)	25.8 (mean)	-	-	-
Effects on TE							
Age	No	-	No	No	No	No	No
Gender	M = F	-	M > F	M > F	M > F	M = F	M > F
High BMI	No	-	No	Increased TE values	No	Increased TE values	No
Metabolic syndrome	-	-	-	Increased TE values	-	-	-
Fatty liver	-	-	-	-	-	Increased TE values	Increased TE values

BMI: Body mass index; TE: Transient elastography.

makes liver texture inherently macronodular. This would result in LS values that vary depending on the area of the liver and necroinflammatory activity, which has been demonstrated to raise LS values. Therefore, the validation of the IQR/M in the Asian population with CHB requires further studies using increased sample sizes to allow sufficient cases with a spectrum of IQR/M values.

Several issues still remain to be resolved regarding the Asian population with CHB: How many valid measurements do we need to maintain the performance of TE^[12]? What is the optimal success rate of the TE measurement to accurately exclude unreliable LS values? Can the IQR/M alone be applied to increase the performance of TE without a sufficient number of valid measurements and an adequate success rate?

WHAT ARE THE NORMAL LS VALUES FOR THE ASIAN POPULATION

Before discussing data on TE in the Asian population with CHB, it is important to first confirm that TE can reliably identify patients with CLD from the normal population. If TE cannot, the clinical meaning of further analysis on the performance of TE in grading the severity of CLD would be significantly lessened. Despite the importance of this, to date, most studies on TE have focused on patients with CLD.

The concept of “what are normal LS values assessed by TE?” is a critical issue that should be addressed to determine whether TE can be used for screening the general population and for subsequent selection of high-risk patients who require periodic follow-up and adequate treatment measures. Indeed, concerns regarding normal LS values are increasing, and several studies (including 2 Asian studies) have proposed normal LS values despite variations in study design^[13-19].

In a study by Corpechot *et al.*^[15], the authors found that the normal LS values in the healthy population were significantly higher in men than in women and that the

median LS value was 4.8 kPa (range, 2.5-6.9 kPa). Roulot *et al.*^[13] examined a large cohort of 429 apparently healthy subjects to establish normal LS values [5.81 ± 1.54 kPa (range, 3.8-8.0 kPa) in men *vs* 5.23 ± 1.59 kPa (range, 3.3-7.8 kPa) in women, *P* < 0.01]. Another study conducted in Romania demonstrated that the mean values of TE in 144 normal subjects were 4.8 ± 1.3 kPa (range, 2.3-8.8 kPa) and that the normal LS values were significantly different between genders^[16]. Colombo *et al.*^[17] also assessed the LS values of 327 voluntary blood donors and found that the mean LS value was 4.9 kPa (95% CI: 4.6-5.1 kPa) and the normal LS values showed no significant differences between genders. However, Colombo *et al.*^[18] in their follow-up study that enrolled more than 1000 healthy blood donors reported that the normal LS value was 4.4 kPa (95th percentile, 6.7 kPa) and that the male gender presents with increased LS values.

All the aforementioned studies were conducted in Europe. However, normal LS values in the Asian population are now available. Fung *et al.*^[19] reported a mean LS value in 28 healthy living-related liver donors of 4.6 kPa (range, 2.0-7.1 kPa), and all subjects had LS values of < 7.2 kPa, which indicated that they had no significant fibrosis. We have previously reported that the normal range of LS values was 3.9-5.3 kPa, which was calculated from 69 strictly selected living liver and kidney donors^[14].

Table 1 indicates the results of all studies on normal LS values. The upper normal range of LS values was consistently lower than the range generally used for identifying significant liver disease (7-8 kPa) in the majority of previous studies^[20-22]. These data demonstrated that TE can perform reliably in identifying high-risk subpopulations without an overlap between the normal and abnormal ranges of LS values. Interestingly, the mean LS values in Asian studies appear lower in comparison with European studies, and the effects of gender on the performance of TE are variable among studies. The discrepancy cannot be fully explained, because the complete histological data of the normal subjects were largely unavailable except a small

Table 2 Failure rate of transient elastography measurement

	Asian study				European study		
	Kim <i>et al.</i> ^[14]	Chan <i>et al.</i> ^[24]	Masuzaki <i>et al.</i> ^[25]	Wong <i>et al.</i> ^[26]	Ziol <i>et al.</i> ^[2]	Marcellin <i>et al.</i> ^[10]	Maimone <i>et al.</i> ^[27]
Etiology	HBV	HBV	HCV	HBV	HCV	HBV	HBV
Total patients (n)	74	1136	876	487	327	202	230
Excluded patients (n)	5	30	10	34	76	29	10
Excluded patients due to TE failure (n)	1	30	10	17	23	14	10
TE failure rate (%)	1.4	2.6	1.1	3.5	7	6.9	4.3
Enrolled patients (n)	69	1106	866	453	251	173	220
Age (yr)	38.9 (mean)	47 (mean)	66.2 (mean)	37 (median)	47.5 (mean)	40.1 (mean)	45.2 (mean)
Male, n (%)	35 (50.7)	-	398 (46.0)	270 (60.0)	155 (61.8)	115 (66.5)	99 (45.0)
BMI (kg/m ²)	22.6 (mean)	-	22.5 (mean)	22.4 (median)	23.9 (mean)	24.5 (mean)	-
Failure criteria							
Success rate	< 60%	< 60%	< 60%	< 60%	< 60%	< 50%	< 60%
The number of VMs	< 10 VMs	< 10 VMs	< 8 VMs	< 10 VMs	< 10 VMs	< 7 VMs	< 10 VMs

HBV: Hepatitis B virus; HCV: Hepatitis C virus; TE: Transient elastography; BMI: Body mass index; VM: Valid measurement.

number of liver donors in the studies by our group^[14] and Fung *et al.*^[19]. Lower mean BMI, younger age, and lower prevalence of metabolic syndrome in the Asian studies can explain, at least in part, the lower mean LS values observed. Another reasons are that other confounders of TE performance, such as high alanine aminotransferase (ALT) levels and fatty liver, were not sufficiently excluded^[17,18] and that the hepatic imaging studies and/or cardiologic evaluation were not fully completed in European studies^[13,16]. These reasons may have increased the normal range of LS values in the European studies.

More carefully designed studies with a large number of subjects are thus still required to fully assess the normal LS values for both Western and Asian populations. However, it should be remembered that the actual normal range of LS values cannot be precisely defined without a definition of a “normal liver”, sufficient histological evaluation of normal subjects, and further stratified analysis with lifestyle factors between genders (such as alcohol consumption). If these issues are resolved, we can identify the true normal LS value and use this as a reference for future studies.

INFLUENCE OF BMI ON THE PERFORMANCE OF TE IN THE ASIAN POPULATION

Previous work has demonstrated that BMI can affect the performance of TE. This can be explained in 2 ways. First, BMI influences the failure rate of TE, and second, BMI acts to increase LS values. Although previous studies have reported that the success rate of TE decreases in subjects displaying higher BMI^[13,23], TE failure may not be significant, because these patients were largely excluded from the analysis. However, in another point of view, this effect of high BMI on TE failure can be a significant pitfall of TE, as the majority of patients with high BMI have an increased chance of suffering from fatty liver and, if TE examination fails, they miss the opportunity to receive

rapid and non-invasive methods to exclude significant fibrosis. From the knowledge of the varying failure rates between Asian and European study populations, we can discern the possible influence of BMI on TE failure rate according to the study population.

Table 2 summarizes the failure rates of previous studies conducted in Asian and European populations. Overall, TE failure rates and BMI both appear to be lower in Asian compared to European studies, indicating that the lower BMI found in Asian populations is possibly associated with a lower TE failure rate.

In spite of debate, several European studies have reported that a high BMI (which might cause hepatic steatosis) could potentially increase LS values^[13,17], although research to date has not determined whether steatosis itself increases LS value in patients with chronic viral hepatitis^[28-30]. For the Asian population, the effects of high BMI on TE performance have not been fully validated, because most Asian studies on TE lack sufficient numbers of patients with high BMI (> 30 kg/m²). In our previous study, BMI did not influence LS values, although our study population was younger and showed lower BMI values than European studies^[14]. This potential effect of high BMI on TE performance should therefore be further investigated for the Asian population.

INFLUENCE OF METABOLIC SYNDROME ON THE PERFORMANCE OF TE IN THE ASIAN POPULATION

Recently, the effects of metabolic syndrome (MS) on TE have been examined in a French study^[13]. Here, BMI > 30 kg/m² was more frequent among subjects with MS than among normal subjects (49.1% *vs* 8.9%, respectively, *P* < 0.001). The mean LS value was higher in subjects with MS compared to controls (6.51 ± 1.64 kPa *vs* 5.33 ± 1.51 kPa, *P* < 0.001). In a multivariate analysis, LS values were still significantly different between subjects with and without MS, irrespective of BMI and other variables. Because MS

has been demonstrated to increase LS values significantly, and hepatic steatosis which can result in histological progression to cirrhosis and hepatocellular carcinoma is strongly associated with MS^[31-33], a potential role of TE in detecting MS was proposed. However, 88% of the subjects with MS had LS values within the defined normal range. This result indicated that not only could TE not precisely perform in the diagnosis of MS, but also that hepatic steatosis differentially affected by MS may have influenced LS values differently for different individuals. One drawback of the study^[13] was a lack of ultrasonographic evaluation of hepatic steatosis. It is thus unclear whether the increased LS values in the subjects with MS were dependent on MS itself or on hepatic steatosis associated with MS. Other studies in Italy^[17,18] attempted to overcome this drawback by including ultrasonographic evaluation of the healthy blood donors and concluded that the severity of hepatic steatosis was independently related to LS values.

The association between MS or hepatic steatosis and LS values was investigated primarily in healthy subjects, because the effects of MS or hepatic steatosis on TE can be attenuated if the study population presented with background fibrotic liver (the most significant factor for high LS values). Therefore, it is difficult to identify the main factors that increase LS values among MS, hepatic steatosis, associated steatofibrosis, and background fibrosis, if the study enrolls patients already presenting with CLD.

As mentioned above, only one published European study reporting the effects of MS on TE in healthy individuals is currently available. Furthermore, no available European and Asian data address the effects of MS on TE performance in patients with chronic viral hepatitis. Considering the different clinicopathological course of hepatic steatosis in patients with CHC and CHB and the varied distribution of body fat according to race, further studies on the effects of MS and hepatic steatosis should be performed with the Asian populations.

INFLUENCE OF ALT ON THE PERFORMANCE OF TE IN THE ASIAN POPULATION WITH CHB

The most important confounding factor of TE is serum ALT levels. Hepatic inflammation, as reflected by higher ALT levels, tends to increase LS values^[11,20,34]. Even minor changes in ALT levels have been shown to influence LS values^[35]. Because HBV, unlike HCV, frequently exhibits acute ALT flares^[36,37], the interpretation of LS values becomes increasingly difficult in the setting of CHB when major fluctuations of necrosis and inflammatory activity occur^[24,38]. It thus becomes more relevant to consider ALT levels when examining TE in the Asian population with CHB.

Considering the significant effects of high ALT levels, several Asian studies with CHB patients attempted to establish varying cutoff LS values according to ALT levels. Chan *et al.*^[11] proposed ALT-based algorithms when interpreting LS results, and established different optimal cutoff

values according to ALT levels (one group with normal ALT *vs* the other group with ALT > upper limit of normal (ULN) and $\leq 5 \times$ ULN). In our previous study, we also stratified the study population according to ALT levels and calculated the optimal cutoff values for each group^[34]. For patients with normal ALT levels, 6.0, 7.5 and 10.1 kPa were selected as the optimal cutoff values for \geq F2, \geq F3, and F4, respectively, whereas 8.9, 11.0, and 15.5 kPa were selected in those with ALT > ULN and $\leq 2 \times$ ULN. Considering this unreliability of TE performance in patients with high ALT levels, more recent studies began to exclude patients displaying ALT > $5 \times$ ULN for analysis^[24]. In addition, the optimal time interval for TE to recover its reliability in patients who experience acute exacerbation of CHB was recently reported^[38].

Although it seems reasonable to use different cutoff values according to ALT levels, large-scale validation of these LS values has not been performed for Asian patients with CHB. Furthermore, some issues still remain unresolved, such as how we stratify patients with CHB according to ALT levels to establish the cutoff values, and who should be excluded for TE examination because of unreliability of TE among patients with high ALT levels.

DIAGNOSTIC PERFORMANCE OF TE IN THE ASIAN POPULATION WITH CHB

Few studies have investigated the performance of TE in the Asian population with CHB^[4,11,39-43]. The characteristics of studies and the identified performance of TE to predict significant fibrosis and cirrhosis are summarized in Tables 3 and 4 (Marcellin *et al.*^[10] is listed for comparison with other Asian studies). The listed Asian studies were selected if they evaluated TE in Asian populations with CHB, they used LB as a reference standard, and they assessed the diagnostic accuracy of TE [using area under the receiver operating characteristic curve (AU-ROC)] for F ≥ 2 or F = 4 fibrosis stage and/or diagnostic indexes (sensitivity, specificity, positive predictive value, or negative predictive value based on some cutoff LS values). Most Asian studies were conducted in Korea and China (Hong Kong) and some studies were available in abstract form from Korea, Singapore, and Thailand.

The AUROCs for predicting F ≥ 2 fibrosis and F = 4 fibrosis stage in patients with CHC were reported as 0.79-0.83 and 0.97-0.95, respectively in the studies by Zioli *et al.*^[2] and Castera *et al.*^[44]. However, the AUROCs in Asian studies seems to be lower than those reported in European studies (0.76-0.88 for F ≥ 2 and 0.80-0.93 for F4, Table 4), although TE diagnosed cirrhosis more accurately than significant fibrosis in Asian studies.

Overall, TE is accepted as a promising and accurate tool for the early detection of cirrhosis irrespective of the etiology of CLD, although the optimal cutoff values remain debatable. The range of the optimal cutoff values for diagnosing HBV-related cirrhosis in the Asian population were between 9.0 and 10.1 kPa based on the full-length articles^[4,11,39] (Table 4) and the range for cirrhosis was less than 11.0 kPa, which is consistently lower than in

Table 3 Characteristics of studies evaluating the performance of transient elastography for the diagnosis of liver fibrosis in patients with chronic hepatitis B

	Type	Country	Total sample (n)	Sample size (n)	Excluded due to failure		Age (yr)	Male (%)	BMI (kg/m ²)	LB length (mm)	Staging
					TE (reason)	LB (reason)					
Kim <i>et al</i> ^[41]	Original	Korea	194	103	0 (SR < 60%, < 10 VMs)	4 (< 10 mm, < 10 PTs)	40.0	80.2	23.8	16.7	METAVIR
Chan <i>et al</i> ^[111]	Original	China	186	161	1 (SR < 60%, < 10 VMs)	22 (< 15 mm, < 6 PTs)	45.0	76.0	24.0	19.0	METAVIR
Kim <i>et al</i> ^[36]	Original	Korea	130	130	0 (SR < 60%, < 10 VMs)	0 (< 10 mm, < 6 PTs)	42.5	79.2	25.3	14.5	METAVIR
Marcellin <i>et al</i> ^[10]	Original	France	202	173	14 (SR < 50%, < 7 VMs)	15 (< 10 PTs)	40.1	66.5	24.5	16.6	METAVIR
Chang <i>et al</i> ^[40]	Abstract	Singapore	35	33	2 (obesity, narrow ICS)	0 (-)	43.0	-	25.6	-	Ishak
Tanwandee <i>et al</i> ^[41]	Abstract	Thailand	104	104	0 (-)	0 (-)	44.0	63.0	23.6	-	METAVIR
Choi <i>et al</i> ^[42]	Abstract	Korea	48	48	0 (-)	0 (-)	41.7	58.3	23.3	-	-
Chang <i>et al</i> ^[43]	Abstract	Singapore	88	84	3 (-)	1 (-)	49.0	71.6	-	-	-

TE: Transient elastography; VM: Valid measurement; LB: Liver biopsy; BMI: Body mass index; SR: Success rate; PT: Portal tract; ICS: Intercostal space.

Table 4 Histologic distribution and the performance of transient elastography for the diagnosis of liver fibrosis in patients with chronic hepatitis B

	n (%)					METAVIR and other scoring system (≥ F2/F4)							
	F0	F1	F2	F3	F4	AUROC	Cutoff (kPa)	Se (%)	Sp (%)	PPV (%)	NPV (%)	LR (+)	LR (-)
Kim <i>et al</i> ^[41]	0	9 (9.9)	33 (36.3)	10 (11.0)	39 (42.9)	-/0.803	-/9.7	-/82	-/62	-/63	-/76	-/4.97	-/0.13
Chan <i>et al</i> ^[111]	10 (6.2)	27 (16.8)	47 (29.2)	37 (23.0)	40 (24.8)	-/0.93	-/9	-/98	-/75	-/57	-/98	-/1	-/0.01
Kim <i>et al</i> ^[36]	0	10 (7.7)	37 (28.5)	16 (12.3)	67 (51.5)	-/0.84	-/10.1	-/76	-/81	-/76.1	-/80.9	-/-	-/-
Marcellin <i>et al</i> ^[10]	16 (9.2)	70 (40.5)	44 (25.4)	29 (16.8)	14 (8.1)	0.81/0.93	7.2/11	70/98	83/75	80/57	73/98	4/1	-/0.01
Chang <i>et al</i> ^[40]	7 (20.0)	16 (45.7)	F2-3 (5, 14.3)	-	7 (20.0)	-/-	11.8/-	90/-	78/-	-/-	-/-	-/-	-/-
Tanwandee <i>et al</i> ^[41]	-	-	-	-	-	0.757/-	6.9/7.3	70/93	79/61	82/31	66/98	-/-	-/-
Choi <i>et al</i> ^[42]	-	-	-	-	-	0.88/0.86	7.7/10.4	88/79	88/83	-/-	-/-	-/-	-/-
Chang <i>et al</i> ^[43]	-14.8	-30.7	-14.8	-21.6	-17.1	0.801/-	8.8/-	-/-	-/-	-/-	-/-	-/-	-/-

AUROC: Area under the receive operating characteristic curve; Se: Sensitivity; Sp: Specificity; PPV: Positive predictive value; NPV: Negative predictive value; LR: Likelihood ratio.

patients with CHC^[45,46]. These findings can be explained in several ways. The histopathological characteristics of CHC (including portal lymphoid follicles, bile duct damage, lobular activity, and steatosis) may contribute to the variations in cutoff values compared with those in patients with CHB^[47]. Another explanation is that the total fibrotic material in CHB may be lower than that in CHC, because CHB tends to make the liver macronodular and heterogeneous^[48]. Other researchers have proposed that the different types and extent of liver inflammatory infiltrate within the liver may account for the different cutoff LS values between CHB and CHC^[20].

The performance of TE in prediction of cirrhosis is acceptable for the Asian population with CHB, but increased performance in prediction of significant fibrosis and subsequent precise staging, particularly for patients with CHB who are candidates for antiviral treatment, is needed and should be pursued through future studies. This is particularly important, because the decision to start antiviral treatment and the type of antiviral agents to be used may be affected by fibrosis stage.

CONCLUSION

Because of limitations of LB, prohibiting its routine use for the evaluation of liver fibrosis in patients with CHB,

interest in the use of noninvasive TE has increased. Ideally, TE can be used to screen the general population to detect high-risk patients with potential liver disease, to identify patients with significant fibrosis who could benefit from the initiation of antiviral treatment, to select patients with cirrhosis who are at a high risk of developing HCC^[25], and to identify patients with cirrhosis and portal hypertension. To date, although numerous European studies have demonstrated that this is possible, data on TE for the Asian population are scarce.

We are now fully armed with nuggets of knowledge that the etiologies of CLD, BMI, MS, cardiac function, cholestasis, hepatic steatosis, and ALT levels can influence the performance of TE, and also that several confounders vary between Asian and European populations, for example, the etiology of CLD, major fluctuation in ALT levels, and the prevalence of high BMI and MS. However, because almost all information on TE has thus far originated from European data, for the Asian population with CHB, TE is not popular clinically. Therefore, further studies tailored to the Asian population with CHB will restore the confidence of Asian clinicians to utilize TE.

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Consequences of *Helicobacter pylori* infection in children

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Abstract

Although evidence is emerging that the prevalence of *Helicobacter pylori* (*H. pylori*) is declining in all age groups, the understanding of its disease spectrum continues to evolve. If untreated, *H. pylori* infection is lifelong. Although *H. pylori* typically colonizes the human stomach for many decades without adverse consequences, children infected with *H. pylori* can manifest gastrointestinal diseases. Controversy persists regarding testing (and treating) for *H. pylori* infection in children with recurrent abdominal pain, chronic idiopathic thrombocytopenia, and poor growth. There is evidence of the role of *H. pylori* in childhood iron deficiency anemia, but the results are not conclusive. The possibility of an inverse relationship between *H. pylori* and gastroesophageal reflux disease, as well as childhood asthma, remains a controversial question. A better understanding of the *H. pylori* disease spectrum in childhood should lead to clearer recommendations about testing for and treating *H. pylori* infection in children who are more likely to develop clinical sequelae.

INTRODUCTION

Helicobacter pylori (*H. pylori*) is one of the most common chronic bacterial infections world-wide, and it is currently estimated that approximately half of the world's population is infected with the bacterium^[1,2]. However, the prevalence of *H. pylori* is not homogeneous world-wide^[1,3]. In western countries, the prevalence of infection has been decreasing during the past few decades^[4-6]. *H. pylori* infection is acquired early in life (almost always before the age of 10 years), and in the absence of antibiotic therapy, it generally persists for life^[1].

It is widely accepted that *H. pylori* infection is the main etiological factor for gastritis and peptic ulcer^[3]. Its eradication is associated with healing of these diseases and significant reduction of ulcer recurrence and rebleeding^[7,8]. Several studies have demonstrated that inflammation caused by *H. pylori* infection might contribute to the development of adenocarcinoma of the stomach; moreover, it has been involved in the development of low-grade B-cell lymphoma of gastric mucosa-associated lymphoid tissue

type (MALT)^[3,9]. Recently, a potential role of *H. pylori* infection in other digestive diseases (gastroesophageal reflux disease; GERD) as well as several extra-intestinal pathologies [iron deficiency anemia (IDA), growth retardation, idiopathic thrombocytopenic purpura (ITP), asthma and allergic disorders] has been suggested^[10]. The postulated role of *H. pylori* in the pathogenesis of extra-intestinal manifestations is based on the facts that: (1) local inflammation has systemic effects; (2) *H. pylori* gastric infection is a chronic process that lasts for several decades; and (3) persistent infection induces a chronic inflammatory and immune response that is able to induce lesions both locally and remote to the primary site of infection^[11].

The aim of this report is to provide a critical review of the available literature about digestive and extradigestive manifestations of *H. pylori* infection in children. Pertinent articles have been identified through a MEDLINE search. Studies published in English during the past two decades have been identified and reviewed.

GASTRITIS AND PEPTIC ULCERS

During childhood, *H. pylori* is associated with predominant antral gastritis, and duodenal ulcers^[12-14]. Successful eradication of *H. pylori* markedly reduces the rate of recurrence of duodenal ulcers in affected children^[2,15,16]. Gastric ulcers are much less common in children than they are in adults^[17].

A pooled analysis of early reports (1983-1994) has demonstrated that the rate ratio of antral gastritis for children with *H. pylori* infection (compared with uninfected subjects) ranged from 1.9 to 71.0 (median, 4.6)^[17]. The prevalence of *H. pylori* in children with duodenal ulcer was high (range, 33%-100%; median, 92%) compared with children with gastric ulcer (range, 11%-75%; median, 25%)^[17]. Thus, there was strong evidence for an association between *H. pylori* infection and antral gastritis and duodenal ulcer in children; there was weak evidence for an association with gastric ulcer. Nevertheless, a subsequent retrospective study (1995-2001) from Japan has confirmed that the prevalence of *H. pylori* was very high in antral (nodular) gastritis and duodenal ulcer (98.5% and 83%, respectively), but it has also demonstrated that *H. pylori* was a definite risk factor for the development of gastric ulcer, although the prevalence of infection did not reach 50%^[18]. *H. pylori* was significantly linked to duodenal and gastric ulcers in the age group 10-16 years, but not ≤ 9 years.

More recently, a decreasing proportion of *H. pylori*-positive peptic ulcers in adults has been observed, along with a decrease in the prevalence rate of the infection^[19]. In children, there have been few data published in the literature to investigate the trend of *H. pylori* prevalence in peptic ulcer^[20-23]. In a prospective European multicenter pilot study on the incidence of gastric and duodenal ulcer disease in children, Kalach *et al.*^[20] have found that ulcers occurred in 10.6% of cases, with *H. pylori* infection in only 26.7% of these. From January 2001 to December 2002, information on 518 children was collected from the pe-

diatric European register for treatment of *H. pylori*^[21]. At endoscopy, 454 children had *H. pylori*-associated gastritis and 64 had an ulcer (12.3%). However, this series included children from Russia and they had a significantly higher prevalence of peptic ulcer (35% *vs* 6.7% in the remainder of European children, $P < 0.0001$; OR: 7.5; 95% CI: 4-13). Thus the prevalence of *H. pylori*-positive ulcers in children differed between countries, and this was not completely explained by the prevalence of the infection in the population studied^[22]. In a retrospective review (1998-2006) of 619 Chinese children who had undergone upper endoscopy for investigation of upper gastrointestinal symptoms, Tam *et al.*^[23] have found that 43 (6.9%) had peptic ulcer. Of these 43 patients, 37 and six had duodenal and gastric ulcer, respectively. The prevalence of *H. pylori* infection was 56.8% (21/37) in duodenal ulcer and 33.3% (2/6) in gastric ulcer. When they arbitrarily divided the study period into two, 1998-2001 and > 2002 , no significant difference in the prevalence of *H. pylori* infection between the two periods was found.

GASTRIC MALIGNANCIES

In relation to *H. pylori*-associated gastric malignancies in children, there have been a few cases of gastric MALT lymphoma^[14,24,25], but there have been no reports of adenocarcinoma.

There is evidence to support an association between long-standing *H. pylori* infection, gastric atrophy, and intestinal metaplasia with the development of intestinal-type and undifferentiated adenocarcinomas in adults^[3]. It has been suggested that chronic gastritis, gastric atrophy, intestinal metaplasia and gastric cancer develop progressively, stepwise over decades, in predisposed individuals infected by *H. pylori*^[26]. However, gastric atrophy and intestinal metaplasia have indeed been described in children living in countries with high gastric cancer incidence^[27], and they are sometimes found in very young subjects^[28-30]. These findings provide support to the hypothesis that host genetic factors that affect the inflammatory and immune response to *H. pylori* infection might determine why some individuals infected with this bacterium develop precancerous lesions and gastric carcinoma while others do not^[31,32]. Thus, it is probable that the prevalence of gastric atrophy and intestinal metaplasia varies according to the geographic/genetic origins as well as environmental factors^[27-30,33-40], as shown in Table 1. Yet, sampling problems exist. In fact, the non-systematic search during pediatric gastroscopy for these histological states might mask their true prevalence^[32]. Most reported studies of the histological features of *H. pylori* infection in children have used either random biopsies^[41] or a small number of targeted biopsies^[29,34,42,43], taken primarily from the antrum^[29,44]. In most studies, the identification of atrophy has been focused on the presence of intestinal metaplasia or has been ill defined^[29].

In clinical practice, the updated Sydney system is widely used for grading gastric histopathological findings (density

Table 1 Prevalence of gastric atrophy in children

Author (yr)/country	Updated Sydney System	Mean age (range, yr)	No. of patients		Gastric atrophy and/or intestinal metaplasia (%)	
			<i>H. pylori</i> +	<i>H. pylori</i> -	<i>H. pylori</i> +	<i>H. pylori</i> -
Whitney <i>et al</i> ^[28] (2000)/USA	Yes	10.7 (1-21)	42	0	Antral: 16.6/0 Fundic: 2.3/0	-/-
Kolho <i>et al</i> ^[33] (2000)/Finland	Not reported	9.5 (2-16)	71	0	0/0	-/-
Campbell <i>et al</i> ^[34] (2001)/Gambia	Yes	1.4 (-/-)	21	16	0/0	0/0
Guiraldes <i>et al</i> ^[35] (2002)/Chile	No	12.2 (5-17)	59	14	0/0	0/0
Oztürk <i>et al</i> ^[36] (2003)/Turkey	Yes	12.2 (6-16)	18	9	Antral: 72.2/77.7	11.1/0
Guarner <i>et al</i> ^[29] (2003)/USA	Yes	- (1-17)	19	45	Antral: 52.6/15.7 Fundic: 0/5.2	22.2/0 0/0
Usta <i>et al</i> ^[37] (2004)/Turkey	Yes	11.8 (4-17)	175	0	2.2/1.1	-/-
Levine <i>et al</i> ^[38] (2004)/Israel	Not reported	14.2 (-/-)	55	40	0/0	2.5/0
Ricuarte <i>et al</i> ^[27] (2005)/Colombia, Korea	No	12.0 (4-18)	97	18	16.4	1
		14.0 (8-18)	10	48	0	0
Kato <i>et al</i> ^[39] (2006)/Japan	Yes	11.3 (1-16)	131	65	Antral: 51.9/4.6 Fundic: 34.8/0	10.8/4.6 8.3/4.2
Tutar <i>et al</i> ^[30] (2009)/Turkey	Yes	1.3 (0.1-2.0)	40	112	2.5/0	0/0
Kalach <i>et al</i> ^[40] (2009)/France	Yes	5.3 (0.1-17.7)	66	553	0/0	0.2/0.2

¹Atrophic mucosa: 31% as intestinal metaplasia; 63% as pseudopyloric metaplasia; 6% as both. *H. pylori*: *Helicobacter pylori*.

of *H. pylori* organisms, acute and chronic inflammation, atrophy and intestinal metaplasia)^[45]. Although this system has been validated in adult patients, interobserver variability is still a problem, primarily in the evaluation of mucosal atrophy^[46,47]. Thus, further validation of atrophy parameters needs to be obtained for pediatric biopsy samples^[29]. In contrast, metaplastic epithelium is easily detected by the pathologist, owing to the characteristic goblet cells^[32].

In adults, five gastric biopsy samples are recommended (two antral, two corporeal and one from the angulus)^[45], but no consensus is available about the optimal number and site location of gastric biopsies in children. Clinical practices in this domain are very heterogeneous, which could in part account for the different prevalence figures of atrophic gastritis in children^[32]. Of note, in a study of 173 children from countries with high gastric cancer incidence, Ricuarte *et al*^[27] emphasized the importance of biopsy site location for identifying the presence of corpus atrophy. In children, atrophy is only identified in biopsies taken near the normal antrum-corporum junction, which is consistent with the notion that atrophy progresses as an advancing antrum-corporum border^[27]. Therefore, identification and characterization of the natural history of *H. pylori* gastritis requires, in addition to biopsies that target the antrum and the cardia, targeted biopsies to include the lesser and greater curvature of the corpus, starting just proximal to the anatomical junction of the antrum and corpus. Unfortunately, the sites recommended by the updated Sydney system can identify corpus atrophy only when it is extensive.

Studies from the 1990s have established that the development of low-grade gastric MALT lymphoma is strongly associated with chronic *H. pylori* gastritis. In two large series of adult patients, *H. pylori* was detected by histological examination in 92% and 100% of those with gastric MALT lymphoma^[48,49]. Recognition of the responsiveness of MALT lymphoma to antibiotic therapy aimed at eradication of *H. pylori* has changed the approach to its manage-

ment. Remission rates in the literature range from 60% to 80%, although recurrence can be expected in 5% of cases^[50-53]. MALT lymphoma occurs commonly in middle and old age; only a small number of cases have been reported in both immunocompetent and immunocompromised children^[14,24,25]. Individual case reports have described the regression of MALT lymphoma after *H. pylori* eradication therapy alone^[24,25].

FUNCTIONAL DYSPESIA

The role of *H. pylori* infection as a cause of non-ulcer or functional dyspepsia has been one of the most debated controversies in the medical community since the discovery of this bacterium.

Dyspepsia is very common in children with chronic or recurrent abdominal pain (RAP), with as many as 80% reporting this symptom^[54]. The relation between RAP in childhood and *H. pylori* infection is not clear^[17]. Pediatric studies are limited by the lack of a clear definition for RAP or by the use of nonspecific criteria for the diagnosis of chronic abdominal pain^[54]. A pooled analysis of early reports (1983-1994) has demonstrated that prevalence rates of infection in children with RAP were inconsistent (range, 0%-81%; median, 22%), with lower rates (range, 0%-9%; median, 6%), in children who met Apley's criteria (i.e. at least three discrete episodes of abdominal pain of sufficient severity to interrupt normal daily activities or performance occurring over a period of ≥ 3 mo)^[17].

In adults, several controlled trials have shown a vague connection between *H. pylori* colonization and dyspeptic symptoms^[55]. In children, controlled randomized treatment studies have been scant. The results of two uncontrolled trials have suggested improvement of clinical symptoms after treatment of *H. pylori* infection^[56,57]. However, the double-blind, randomized placebo-controlled trial by Ashorn *et al*^[58] has suggested that RAP is not an indication

for a test and treatment strategy for *H. pylori* infection in children. In fact, in that study, at 52 wk, dyspeptic symptoms improved to the same extent in the treatment group and in children who received placebo, irrespective of the healing of gastritis, which was more commonly achieved along with eradication^[58]. Nonetheless, due to the limited number of patients who could finally be included, the results by Ashorn *et al.*^[58] have to be interpreted with care. Large-scale multicenter trials performed in children are still needed to answer definitively the question whether a connection exists between *H. pylori* infection and RAP. Neither did the results of a very recent study give support for the use of *H. pylori* eradication in children with RAP^[59]. Based on a meta-analysis of 38 studies between 1966 and 2009, the study by Spee *et al.*^[59] has found no association between RAP (fulfilling Apley's criteria) and *H. pylori* infection in children. However, the authors have demonstrated that children who are referred to a gastroenterologist with unspecified abdominal pain (i.e. including children who do not fulfill Apley's criteria) or pain in the epigastric region are at 2-3-fold higher risk for *H. pylori* infection than children without these symptoms. Thus, these authors have postulated that unspecified abdominal pain in a hospital-based setting and epigastric pain in general might be associated with (acute) *H. pylori* infection. The potential for *H. pylori* to cause clinical symptoms that arise from gastric infection, in the absence of mucosal ulceration, requires additional studies using a strict study group definition. Functional dyspepsia and non-ulcer dyspepsia (i.e. epigastric pain in the absence of mucosal ulceration at esophago-gastro-duodenoscopy) must be evaluated as separate entities.

GASTROESOPHAGEAL REFLUX DISEASE

The interaction between *H. pylori* infection and GERD has been widely debated in the literature over the past decade, and the hypothesis that eradication of *H. pylori* leads to increased GERD has been the subject of many publications with contradictory conclusions in children as well as in adults^[38,60-76]. There are limited data in children because the prevalence of *H. pylori* infection is low and no randomized controlled trials have been conducted; therefore, inferences about the effects of *H. pylori* eradication and GERD need to be drawn from studies on adult patients^[77].

H. pylori has been found to be inversely correlated with the prevalence of GERD, and certain studies have shown aggravation of esophagitis after eradication^[60-66]. Suggested mechanisms include presence of atrophic or significant body gastritis that leads to a post-eradication increase in acid output; decreased buffering as a result of elimination of *H. pylori*, which produces ammonia *via* bacterial urease; masking of reflux by acid neutralizing medications given for *H. pylori*-related disease; and increased appetite with weight-gain-mediated reflux. These observations are controversial, because several studies have not found an association between eradication of *H. pylori* and reflux disease^[38, 66,70,74,78-80].

Most studies aimed at evaluating the effect of *H. pylori* eradication on reflux in adults have used selected populations such as those with duodenal ulcer or patients with GERD before eradication^[63,65,78,80]. The spectrum of risk factors found in adults, such as atrophic gastritis, duodenal ulcer, or significant esophagitis, might influence the outcome of the study. These factors are less common in children, therefore, these results might not be relevant to the decision to eradicate *H. pylori* when found in children^[38].

Dent has proposed that the effect of *H. pylori* eradication on GERD is most likely determined by the population studied^[67]. Acid secretion in predominant antral gastritis with preserved body mucosa is hyper-responsive, thus enabling increased duodenal or esophageal injury. In these patients, eradication should improve or not affect GERD. This hypothesis is consistent with the results of other studies that have shown improvement in GERD symptoms in patients with duodenal ulcer^[80,81]. However, in patients with atrophic gastritis or severe body gastritis, *H. pylori* eradication might result in increased acid secretion. Children and adolescents are more likely to behave like the first group, with predominant antral gastritis^[38].

The risks and benefits of *H. pylori* eradication are less well-defined for patients with gastritis alone, and vary according to the severity and pattern of gastritis^[67]. Although this is the patient group most likely to develop reflux esophagitis^[63], the risks from this are outweighed by those of continued *H. pylori* infection. Reflux esophagitis following *H. pylori* eradication is believed to carry little risk and, in particular, not to lead to intestinal metaplasia. By contrast, the risks of continued *H. pylori* infection are relatively high in patients who have had an episode of chronic duodenal, gastric or gastroduodenal ulceration^[67]. What is certain, is that *H. pylori* is a major risk factor for non-cardia gastric adenocarcinoma^[82], and children with this infection have at least a fivefold increased risk of developing stomach neoplasia in later life. This risk is likely to be reversed with *H. pylori* eradication^[77]. In a study of high-risk adults, no reduction in gastric cancer risk at the end of 7.5 years of follow-up was observed in *H. pylori* carriers who had previously undergone eradication therapy^[83]. However, in a subgroup analysis of patients who had no precancerous lesions at baseline, cancer risk was significantly reduced^[83]. Additional studies have suggested that prevention of gastric cancer might be possible in infected individuals without precancerous lesions^[84,85]. Therefore, children could well be the group to target in an effort to prevent the future development of gastric cancer.

IRON DEFICIENCY ANEMIA

In addition to the already known causes of IDA, over the past two decades, an association between *H. pylori* and pediatric IDA has been established^[86-92]. However, the issues of whether *H. pylori* infection is linked causally to IDA in children and whether treatment or resolution of *H. pylori* infection would improve iron stores or resolve IDA in children are still matters of great debate. In 1991,

Table 2 Randomized trials of *Helicobacter pylori* eradication for iron deficiency anemia and iron deficiency in children

Author (yr)/country	No. of children with IDA/ <i>H. pylori</i>	Follow-up (No. of children)	Outcome	
			IDA	ID
Choe <i>et al</i> ^[89] (1999)/Korea	43/25	8 wk (18)	Hb increased with: eradication + iron, eradication + placebo <i>vs</i> iron + placebo (<i>P</i> = 0.0086)	No significant differences in serum iron or ferritin
Sarker <i>et al</i> ^[106] (2008)/Bangladesh	260/200	3 mo (260)	IDA persisted with: eradication + iron, 11%; eradication alone, 33%; iron alone, 0%; placebo, 45%	ID persisted with: eradication + iron, 19%; eradication alone, 65%; iron alone, 7%; placebo, 78%
Gessner <i>et al</i> ^[105] (2006)/Alaska	219/219	14 mo (201)	IDA persisted with: eradication + iron, 22%; iron alone, 14%	ID persisted with: eradication + iron, 65%; iron alone, 72%
Fagan <i>et al</i> ^[104] (2009)/Alaska	219/219	40 mo (176)	IDA persisted with: eradication + iron, 5%; iron alone, 19%	ID persisted with: eradication + iron, 52%; iron alone, 58%

Hb: Hemoglobin; ID: Iron deficiency; IDA: Iron deficiency anemia; *H. pylori*: *Helicobacter pylori*.

an association between *H. pylori* infection and IDA due to microscopic blood loss was described in a 15-year-old girl with *H. pylori*-positive chronic active hemorrhagic gastritis, who showed no signs of gastrointestinal symptoms^[88]. Two years later, Dufour *et al*^[93] reported a 7-year-old child who presented with *H. pylori*-associated chronic antral gastritis without evidence of hemorrhage or clinical symptoms other than sideropenic anemia, which was refractory to oral iron administration and subsided after *H. pylori* eradication. These case reports were followed by other studies that have identified an association between *H. pylori* infection and pediatric unexplained or refractory IDA, and have indicated improvement of iron stores and anemia after successful *H. pylori* eradication^[94-100]. Yet, some pediatric studies have implicated *H. pylori* as a cause of IDA that is refractory to oral iron treatment^[94,95,99,100]. Thus, the above studies have supported a clinically significant influence of *H. pylori* infection on body iron stores and have led to a recommendation for *H. pylori* eradication in infected individuals with unexplained IDA^[101-103]. However, small sample sizes, lack of control groups, and other methodological issues, including the use of validated measures of active *H. pylori* infection such as biopsy-related tests to confirm *H. pylori* infection, are among factors that have limited the interpretation and ability to generalize the importance of the results of these studies in children.

To the best of our knowledge, only four population-based randomized trials of the effect of *H. pylori* infection treatment on IDA have been performed in children^[89,104-106], as shown in Table 2. Three of them lacked true placebo groups^[89,104,105]. Choe *et al*^[89] have demonstrated a beneficial effect of *H. pylori* eradication therapy plus iron or placebo in increasing hemoglobin levels. However, no significant differences among study groups were found at 8 wk follow-up for serum iron level, total iron-binding capacity, and ferritin level. Sarker *et al*^[106] have shown, in a relatively large cohort of Bangladeshi children with IDA, a similar improvement of IDA as well as iron deficiency, with anti-*H. pylori* therapy plus iron compared with iron therapy alone. Therefore, the improvement of iron status in children who receive combined therapy could be attributed to the effect of iron rather than anti-*H. pylori* therapy.

The findings from the Bangladeshi children corroborated well those of the study from rural Alaska, which showed that treatment and resolution of *H. pylori* infection did not substantially decrease levels of iron deficiency or mild anemia at 14 mo after treatment initiation, despite the relatively low rate of reinfection once the initial infection resolved^[105]. When an additional follow-up evaluation at 40 mo after treatment initiation was performed, it was found that sustained resolution of *H. pylori* infection substantially reduced the prevalence of mild IDA but modestly improved iron status^[104].

How can *H. pylori* gastritis cause IDA? Several theoretical mechanisms have been proposed to explain the possible relationship between *H. pylori* infection and decreased iron stores. It appears that chronic gastrointestinal blood loss is not the likely culprit, because most published cases and case series have found no bleeding lesions at the time of endoscopy, and have reported negative testing for fecal occult blood^[107]. Another explanation for a relationship between *H. pylori* infection and IDA involves the possible effect of *H. pylori* gastritis on gastric acid secretion and iron absorption. Non-heme iron accounts for 80% of dietary iron in industrialized countries^[107]. Crucial to the effective absorption of non-heme iron is hydrochloric acid in acid secretions. Reduction of the ferric to ferrous form is dependent upon the pH of the gastric juice, and reduction to the ferrous form facilitates membrane transport^[108]. An important promoter of iron absorption is ascorbic acid, which appears to act in two ways: by promoting reduction to the ferrous form, and by forming an absorbable molecular complex with ferric iron, which is insoluble at pH > 5^[107,109]. Gastric acid hyposecretion results from atrophy of the gastric glands and fundic mucosa, which has been associated with chronic *H. pylori* infection^[107]. It has been shown that adult patients with IDA and *H. pylori* infection are more likely to have a pattern of gastritis that involves the gastric corpus, with related decreases in gastric acid secretion and increases in intragastric pH that might impair iron absorption^[110]. There are no comparable data in children.

Another hypothesized mechanism is that *H. pylori* might lead to IDA by sequestering and utilizing iron, thus

Table 3 Cross-sectional studies on the association between *Helicobacter pylori* infection and growth retardation

Author (yr)/country	Total No. of patients (<i>H. pylori</i> +)	Age (range, yr)	Diagnostic test	Conclusion
Perri <i>et al</i> ^[114] (1997)/Italy	216 (49)	3-14	Urea breath test	<i>H. pylori</i> infection was associated with growth delay, and poor socioeconomic status
Oderda <i>et al</i> ^[115] (1998)/Italy	134 with short stature (27) 134 controls (18)	5-13	Serology	No association with short stature
Quiñonez <i>et al</i> ^[116] (1999)/Guatemala	211 (107)	5-10	Serology	No association with height for age and nutritional status
Choe <i>et al</i> ^[90] (2000)/Korea	375 (63)	10-15	Serology	<i>H. pylori</i> infection accompanied by IDA, rather than <i>H. pylori</i> infection <i>per se</i> , was associated with delayed pubertal growth
Richter <i>et al</i> ^[117] (2001)/Germany	3315 (213)	5-7	Urea breath test	<i>H. pylori</i> infection was associated with growth delay
Ertem <i>et al</i> ^[118] (2002)/Turkey	327 (162)	3-12	Urea breath test	<i>H. pylori</i> infection was associated with short stature independently of poor living standards
Sood <i>et al</i> ^[119] (2005)/UK	257 (97)	-	Urea breath test	No association with height and weight z scores, after adjustment for socioeconomic status and ethnicity
Süoglu <i>et al</i> ^[120] (2007)/Turkey	70 (35)	4-16	Endoscopy	<i>H. pylori</i> infection and IDA had a significant effect on height z scores, after adjustment for economic status
Mohammad <i>et al</i> ^[121] (2008)/Egypt	286 (208)	6-15	Urea breath test	<i>H. pylori</i> infection affected both body weight and height
Soylu <i>et al</i> ^[122] (2008)/Turkey	108 with dyspepsia (57) 50 healthy controls	7-17	Endoscopy	No association with anthropometry. But, dyspeptic children had worse nutritional status compared to controls, regardless of <i>H. pylori</i> status
Cherian <i>et al</i> ^[123] (2009)/Australia	182 (149)	< 16	Stool antigen	No association with BMI or other anthropometric measures
Gulcan <i>et al</i> ^[124] (2010)/Turkey	181 with RAP (121) 309 asymptomatic (110)	6-15	Endoscopy, 181 Serology, 309	RAP associated with gastric mucosal injury had a negative effect on BMI independent of <i>H. pylori</i> infection RAP originating from <i>H. pylori</i> infection affected both BMI and linear growth

BMI: Body mass index; RAP: Recurrent abdominal pain; IDA: Iron deficiency anemia; *H. pylori*: *Helicobacter pylori*.

competing with the human host^[107]. Ferrokinetic studies have suggested the diversion of iron to some extramedullary focus, hypothesized but not proven to be *H. pylori*-associated gastric infection^[95]. Like many bacteria, *H. pylori* requires iron as a growth factor, and it possesses a 19-kDa iron-binding protein that resembles ferritin, which has been considered to play a role in storage of excess iron sequestered by the bacterium^[111]. Another possible mechanism for IDA in *H. pylori*-infected subjects involves sequestration of iron in lactoferrin in the gastric mucosa, and uptake of iron by *H. pylori*. Lactoferrin is an iron-binding glycoprotein that is found in body fluids, and its secretion in the gastric mucosa seems to be influenced by some signal from *H. pylori*^[112]. It appears that *H. pylori* then absorbs the iron from lactoferrin *via* a specific lactoferrin-binding protein that is expressed by *H. pylori*^[107]. Lactoferrin levels in the gastric mucosa have been shown to be significantly higher in *H. pylori*-positive patients with IDA compared to those who are non-anemic *H. pylori*-negative, non-anemic *H. pylori*-positive, and *H. pylori*-negative with IDA^[112].

We conclude that future work in this area is needed. Randomized, double-blind, and placebo-controlled trials of sufficient size and power should evaluate the long-term effect of *H. pylori* eradication in children with IDA, who are living in developing as well as in developed countries. Additionally, these studies should evaluate the effect of *H. pylori* treatment among different pediatric populations, such as those with and without concurrent gastrointestinal symptoms, and those with a wide spectrum of IDA severity.

Based on our present knowledge, children with a first episode of IDA and no complications should be initially treated with iron supplementation alone, irrespective of *H. pylori* status^[2]. Eradication of *H. pylori* could be considered in cases that are refractory to iron supplementation and in the case of frequent relapses, assuming that other causes, such as celiac disease and inflammatory bowel disease, have been excluded^[2,102]. Of particular interest is the work by Memeo *et al*^[113] who have shown the frequent occurrence of duodenal intraepithelial lymphocyte expansion in individuals with *H. pylori* gastritis, and the considerable overlap of the intraepithelial lymphocyte counts as well as the distribution patterns with those described for celiac disease and other small bowel diseases.

GROWTH RETARDATION

The available evidence regarding *H. pylori* infection and its effect on growth in children is controversial. There have been many cross-sectional studies that point to either the presence or absence of such an association^[90,114-124], as shown in Table 3.

The Italian cross-sectional study by Perri *et al*^[114] suggests that *H. pylori* infection (as diagnosed by urea breath test) is associated with growth delay in older children, poor socioeconomic conditions, and household overcrowding. The findings by Perri *et al*^[114] are consistent with the hypothesis that *H. pylori* infection is one of the environmental factors capable of affecting growth. The cross-section-

al study by Richter *et al*^[117] of a large number of 5-7-year-old preschool and school children suggests that *H. pylori* infection (as diagnosed by urea breath test) is associated in German children with growth delay, growth retardation, or both, despite similar socioeconomic status between *H. pylori*-positive and -negative children. Likewise, Ertem *et al*^[118] also have suggested that *H. pylori* is associated with short stature through mechanisms that are independent of poor living conditions.

Other investigators have suggested that growth suppression reported in children with *H. pylori* infection could be due to socioeconomic, genetic and environmental factors. In their retrospective chart review of the growth parameters of children with dyspepsia referred to the Regional Paediatric Gastroenterology unit in Manchester, United Kingdom, Sood *et al*^[119] found that children with dyspepsia and *H. pylori* infection (as diagnosed by urea breath test) were shorter and lighter than patients with similar symptoms but no infection. Sood *et al*^[119] concluded that the differences in anthropometry might have been due to socioeconomic and ethnic factors rather than *H. pylori* infection. Yet, in a cross-sectional study of Turkish dyspeptic children who were evaluated by endoscopic gastric biopsy for *H. pylori* infection, as well as a control group of age and sex cross-matched children, Soyulu and Ozturk found that dyspeptic children with and without *H. pylori* infection had worse nutritional status compared to healthy controls^[122]. The authors concluded that *H. pylori* infection as a major cause of dyspepsia might be considered to cause malnutrition secondary to decreased caloric intake associated with dyspepsia^[122].

In a case-control study of children aged 5-13 years whose height was below the third centile, matched with children of the same age and sex whose height was above the 25th centile, Oderda *et al*^[115] found that *H. pylori* (diagnosed by serologic methods) was not a risk factor for short stature, and that reduced growth was related to genetic determinants such as parental height and to mixed genetic and environmental factors such as birth weight. Low socioeconomic status was also relevant^[115]. In a cross-sectional study of children aged 5-10 years who were attending an all-girl public school in inner Guatemala City, Quiñonez *et al*^[116] investigated the effect of *H. pylori* infection (diagnosed by serologic methods) on the anthropometric nutritional parameters (weight-for-height and height-for-age). After controlling for sociodemographic variables, the authors did not find significant differences in the nutritional parameters between infected and uninfected children. In another cross-sectional study of Turkish children aged 4-16 years who underwent upper gastrointestinal endoscopy for RAP and dyspeptic complaints, Süoglu *et al*^[120] found that the effect of *H. pylori* infection on mean SD scores of height for age was statistically insignificant after correction for breast feeding, IDA and socioeconomic level. In contrast, even after controlling for socioeconomic level, *H. pylori* infection remained the single and most important variable that had an effect on mean weight SD score. Among *H. pylori*-positive as well

as -negative children^[120], IDA had no significant effect on anthropometric measurements *per se*. However, when *H. pylori* and IDA were present, mean weight was found to be significantly lower than that of the *H. pylori*-negative patients without IDA^[120].

There are also longitudinal studies that support the hypothesis that *H. pylori* infection might influence growth rate in children. Thomas *et al*^[125] conducted two consecutive prospective, longitudinal cohort studies in Gambia, and found that, in both cohorts, children with early *H. pylori* colonization had lower values for both length- and weight-for-age Z scores than their peers in late infancy. No socioeconomic or demographic confounding variables were identified to explain this, and the weight deficit was no longer detectable when the children were aged 5-8 years. The authors concluded that *H. pylori* colonization at critical vulnerable ages might lead to malnutrition and growth retardation among infants in countries such as Gambia^[125]. In the prospective, longitudinal study by Bravo *et al*^[126], lower-middle class children from Colombia, in general good health, aged 1-5 years, who tested negative by urea breath test at baseline, were monitored over the following 2.5 years for anthropometric measurements every 2 mo, and for *H. pylori* by urea breath test every 4 mo. The authors found significant slowing of growth velocity in children infected with *H. pylori*, independent of socioeconomic variables or overcrowding^[126]. Likewise, Mera *et al*^[127] prospectively investigated in Colombian children, in general good health, aged 1-5 years, whether a newly acquired *H. pylori* infection affected height and weight of children within 16 mo, by performing breath tests and anthropometry every 2-4 mo. The authors observed that the impact of a new infection on height growth velocity was more pronounced right after the infection was diagnosed and slowly ebbed, and continued to be significant for up to 6 mo after infection, and became borderline significant at 8 mo after infection. No catch-up growth was evident in infected children, with crowding retarding linear growth. Compared with uninfected children, newly infected children also experienced a significant, but small, decrease in weight at the first follow-up visit, which was not statistically significant at 4 mo after infection. There was no catch-up in weight. The authors concluded that *H. pylori* caused a non-transient negative effect on height and weight in affected children, regardless of age at the time of infection^[127].

Taken together, the results of these studies pointing to the presence or absence of an association between *H. pylori* and growth are subject to some potential limitations. First, most studies were cross-sectional or retrospective and therefore were unable to evaluate the possible effect of new infections on growth velocity. Second, the definition of socioeconomic status is complex and no set of parameters was fully descriptive in most studies. Third, some studies used serological methods to determine *H. pylori* infection. However, serology does not indicate whether there is active or past infection. Even in those patients who are treated and cured of their *H. pylori* infection, evidence of IgG antibodies may exist for several months

and possibly for years. Serological assays also have varying levels of sensitivity and specificity when used in different populations, particularly in children^[128]. Fourth, in community-based studies, for example, in those that involve a blood specimen, participation rate is rarely more than 50%^[116,129]. This might also be the case for studies that involve gastrointestinal endoscopy. As such, we have no information on the non-participating children in some of the above studies; thus, we cannot estimate if any bias was introduced in the results or the generalizability of their findings to other populations.

We conclude that future work in this area is needed to elucidate the importance of these factors. One would expect growth velocity to improve following *H. pylori* eradication, if the infection were the primary cause of growth suppression.

IDIOPATHIC THROMBOCYTOPENIC PURPURA

ITP is an autoimmune disease that is characterized by a low circulating platelet count caused by the destruction of antibody-sensitized platelets in the reticuloendothelial system^[130]. The mechanisms that trigger the production of platelet autoantibodies remain poorly understood. Persistent thrombocytopenia for > 6 mo defines the chronic form of this disorder (cITP)^[130]. Lately, eradication of *H. pylori* from the gastric mucosa has been associated with an improvement of cITP.

Several studies in adults have reported improved platelet counts in *H. pylori*-positive patients following standard triple *H. pylori* eradication therapy^[131-140]. A meta-analysis of 13 cohort reports in adult cITP, with combined data from 193 patients, has indicated an overall response rate of 52% of patients after *H. pylori* eradication therapy^[141]. A recent systematic review of 25 published studies, with combined data from 696 adult patients with cITP, has demonstrated an overall response in platelet count after *H. pylori* eradication in 50.3% of patients (95% CI: 41.6%-59.0%)^[142]. Cohorts from Japan and Italy^[132,134,138,140] have reported higher response rates than from other countries^[143,144]. Several theories, including direct antigen mimicry between *H. pylori* *cagA* and platelet glycoprotein antigens, *H. pylori* binding to von Willebrand factor, and the immunomodulatory effect of antibiotics (e.g. macrolides) used in *H. pylori* eradication, have been proposed to explain the platelet response to anti-*H. pylori* therapy^[139,141]. It has also been postulated that platelet autoantibodies might be produced by autoreactive clonal B cells that are induced by chronic immunological stimulus by *H. pylori*^[141,145]. The relative toxicity profiles of triple therapy compared to standard ITP therapy certainly make eradication an attractive and generally safe option in adults. However, large controlled clinical trials of adult patients from various ethnic backgrounds are necessary to determine the response rate and mechanism of platelet response to *H. pylori* eradication therapy^[141].

In children, the natural history of cITP is clearly different from that observed in adults. Spontaneous recovery

occurs in one third of childhood cITP cases from several months to many years after their diagnosis, whereas only 5% of adults recover^[130,146]. Thus, the effects of *H. pylori* eradication in childhood cITP could be different from those in adults. The issue of whether *H. pylori* eradication has a beneficial effect on the course of cITP in children has been the subject of few, apparently contradictory studies with small sample sizes^[147-153]. Yet, the results of pediatric studies are difficult to compare because the prevalence of *H. pylori* infection and diagnostic methods vary among them^[154]. Of note, in children with cITP, no studies have assessed, at the initial as well as follow-up visits, *H. pylori* status by upper gastrointestinal endoscopy.

In a study from Taiwan, Jaing *et al.*^[147] evaluated 22 cITP children, nine of whom were *H. pylori*-infected and were treated with a 1-wk course of triple therapy [including clarithromycin, amoxicillin, and proton pump inhibitors (PPIs)]. Of these nine patients, five (55.6%) were in complete or partial remission over a median of 16 mo follow-up, while four showed no improvement in platelet counts during 8-19 mo follow-up. In a study from the Netherlands, Neeffjes *et al.*^[149] evaluated 47 children with cITP, three of whom were *H. pylori*-infected and were treated with a 2-wk course of the triple therapy mentioned above. Over a 6-mo follow-up, all three children achieved complete or partial remission. In a study from Iran, Hamidieh *et al.*^[150] evaluated 31 cITP children, four of whom were *H. pylori*-infected and were treated with a 2-wk course of the same triple therapy. None of the four patients achieved complete or partial remission after *H. pylori* eradication. In a study from Japan, Hayashi *et al.*^[148] evaluated 10 children with cITP, one of whom was *H. pylori*-infected and was treated with a 1-wk course of the same triple therapy. This child achieved complete remission throughout > 1 year of follow-up. In a study from Italy, Bisogno *et al.*^[151] evaluated 25 children with cITP, nine of whom were *H. pylori*-infected and had *H. pylori* eradication following 1-2 courses of 2 wk of the same triple therapy. Over 6-mo follow-up, of these nine patients, three had an increase in platelet count after eradication therapy, and one had complete remission and two had partial, transient remission followed by relapse a few months later. Over the same follow-up period, no significant increase in platelet count was seen in the other six eradicated patients. In the same study, Bisogno *et al.*^[151] also reported the platelet response in the 16 *H. pylori*-negative children with cITP. At 6-mo follow-up, two of these 16 patients achieved partial remission without any specific treatment. Yet, four of the *H. pylori*-negative children with cITP achieved spontaneous partial remission 1 year after diagnosis of *H. pylori* infection was excluded^[151]. At latest follow-up, the remaining 10 *H. pylori*-negative children presented with a count above $50 \times 10^9/L$ without any treatment. In another study from Italy, Loffredo *et al.*^[152] evaluated 39 children (median age, 136 mo) with cITP, eight of whom were *H. pylori*-infected and had *H. pylori* eradication following 1-3 courses of 2 wk of the same triple therapy. Over 1-year follow-up, none of the eight patients achieved complete or partial remission after *H. pylori* eradication^[152].

Recently, Treepongkaruna *et al*^[153] reported a multi-center randomized controlled trial of *H. pylori* eradication in 55 children with cITP. Of the 16 (29.1%) patients with cITP and *H. pylori* infection, seven were randomly treated with PPI-based triple therapy, while the remaining nine did not receive any specific treatment. If the first-line therapy failed to eradicate *H. pylori*, then second-line eradication therapy was used. Although eradication of *H. pylori* infection was successful in all patients in the treated group, the platelet recovery rate was not significantly different between the *H. pylori* treatment group and control group during the 6-mo period.

From the foregoing, whether antibiotic treatment of *H. pylori* infection should be considered in children with cITP is an unresolved question^[154]. In conclusion, in view of the published evidence in children with cITP and the sporadic benefit of *H. pylori* eradication on the platelet response, the relationship between *H. pylori* and cITP in children warrants further investigation with large randomized controlled trials of sufficient size and power and across different ethnic populations^[154].

ASTHMA AND ALLERGIC DISORDERS

In industrialized countries, the incidence of asthma, especially childhood asthma, has risen in recent years^[155]. Conversely, in developed countries, the rate of acquisition of *H. pylori* has decreased substantially over recent decades^[3,9]. The lack of early exposure to *H. pylori* has been suggested to be an important determinant of asthma risk in childhood^[156]. In a recent retrospective, cross-sectional study, using data from 3327 participants, aged 3-19 years, *H. pylori* seropositivity was found to be inversely associated with onset of asthma before 5 years of age and current asthma in children aged 3-13 years^[157]. *H. pylori* seropositivity also was inversely related to recent wheezing, allergic rhinitis, and dermatitis, eczema, or rash.

Allergic diseases and asthma are caused by exaggerated T-helper 2 (Th2)-biased immune response in genetically susceptible individuals^[158]. A number of recent studies have indicated that regulatory T cells (Tregs) play an important role in controlling such Th2-biased responses. Impaired expansion of natural and/or adaptive Tregs is hypothesized to lead to the development of allergy and asthma^[158]. Increased numbers of Tregs have been reported in the *H. pylori*-infected human gastric mucosa^[159,160]. Thus, the absence of early exposure to *H. pylori* might cause the loss of a metabolically active lymphoid compartment in the stomach, including Tregs, which ultimately could affect the activity of T cells present in other mucosal and cutaneous sites^[156,160]. Although this is an undoubtedly interesting theory, future prospective, longitudinal studies are needed to test the strength of the association between *H. pylori* status and asthma risk in children from developed and developing countries^[161].

CONCLUSION

Many areas of active scientific inquiry have been reported in

the recent literature about the disease spectrum of *H. pylori*. Several studies have demonstrated that *H. pylori* infection is not associated with specific symptomatology in children. Therefore, identification of children with *H. pylori*-associated gastritis on the basis of clinical presentation alone is not possible. Based on the best available evidence, testing for (and treating) *H. pylori* infection should be performed in children with endoscopically proven duodenal ulcer. Evidence from studies in adults supports the recommendation that testing for *H. pylori* should also be performed in children with a documented gastric ulcer. Endoscopy and biopsy are also recommended for children with persistent symptoms.

Pursuing *H. pylori* in asymptomatic children should be indicated for patients at increased risk of gastric cancer, for example, first-degree relatives of patients with gastric cancer, and individualized in populations at increased risk for gastric cancer, taking into consideration comorbid illness. Studies suggest that prevention of gastric cancer is possible in infected individuals with no precancerous lesions. Therefore, children might well be the group to target in an effort to prevent future development of gastric cancer.

Although dyspepsia and *H. pylori* infection are common in the general population, current data in the literature regarding a causal association between *H. pylori* gastritis and dyspepsia are conflicting. It is uncertain whether eradication of the infection leads to an improvement of symptoms. Randomized, placebo-controlled, double-blind trials with minimal loss to follow-up, strict group definition, and standardized and validated outcome measures are needed.

There is no compelling evidence to support routine testing in children with cITP, poor growth, and GERD. In children with refractory IDA, where other causes have been ruled out, testing for (and treating) *H. pylori* infection can be considered. Prospective, longitudinal studies are needed to test the strength of the newly reported association between *H. pylori* status and asthma risk in children. In the absence of these studies, there is little call to leave *H. pylori* infection untreated in patients with asthma and allergy. We believe that *H. pylori* eradication is strongly beneficial for curing peptic ulcer disease and gastric lymphoma and for prevention of gastric cancer, as well as other diseases that are putatively linked to infection, and it must be done in *H. pylori*-infected patients, whether or not they have asthma.

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Prognostic relevance of β -catenin expression in T2-3N0M0 esophageal squamous cell carcinoma

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Abstract

AIM: To study the expression of β -catenin in esophageal squamous cell carcinoma (ESCC) at stage T2-3N0M0 and its relation with the prognosis of ESCC patients.

METHODS: Expression of β -catenin in 227 ESCC specimens was detected by immunohistochemistry (IHC). A reproducible semi-quantitative method which takes both staining percentage and intensity into account was applied in IHC scoring, and receiver operating characteristic curve analysis was used to select the cut-off score for high or low IHC reactivity. Then, correlation of β -catenin expression with clinicopathological features and prognosis of ESCC patients was determined.

RESULTS: No significant correlation was observed between β -catenin expression and clinicopathological parameters in terms of gender, age, tumor size, tumor grade, tumor location, depth of invasion and pathologi-

cal stage. The Kaplan-Meier survival curve showed that the up-regulated expression of β -catenin indicated a poorer post-operative survival rate of ESCC patients at stage T2-3N0M0 ($P = 0.004$), especially of those with T3 lesions ($P = 0.014$) or with stage II B diseases ($P = 0.007$). Multivariate analysis also confirmed that β -catenin was an independent prognostic factor for the overall survival rate of ESCC patients at stage T2-3N0M0 (relative risk = 1.642, 95% CI: 1.159-2.327, $P = 0.005$).

CONCLUSION: Elevated β -catenin expression level may be an adverse indicator for the prognosis of ESCC patients at stage T2-3N0M0, especially for those with T3 lesions or stage II B diseases.

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Key words: Esophageal squamous cell carcinoma; β -catenin; Prognosis; Receiver operating characteristic curve; Immunohistochemistry

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INTRODUCTION

Esophageal carcinoma, an aggressive tumor with a poor prognosis, is one of the most common malignant tumors in Asia, especially in certain areas of China, and South

America^[1]. Esophageal squamous cell carcinoma (ESCC) accounts for over 90% of all esophageal cancers worldwide^[2]. Despite advances in imaging technologies enabling earlier diagnosis of ESCC, surgery and response rates of radiotherapy and chemotherapy, the clinical outcome of ESCC patients remains unsatisfactory. Even in the developed world, more than 85% of ESCC patients die within 2 years after its diagnosis^[3]. In China, the esophageal cancer mortality rate ranks fourth of cancer-related deaths^[4]. Thus, improvement in the efficacy of ESCC treatment is a major public health goal. New modalities based on a better understanding of the ESCC biology are indispensable. Since the classical staging criteria fail to differentiate the prognostic characteristics of ESCC patients adequately, molecular tumor analysis may provide a necessary means for defining the prognosis of ESCC patients. In order to further improve the survival rate of ESCC patients, it is essential to identify the relevant biomarkers with adverse prognostic significance, and to modify the therapeutic strategies for individual patients according to their molecular tumor status.

β -catenin is an 88kDa versatile protein that has at least two different cellular functions^[5-7]. First, β -catenin is an important structural component of both normal epithelium and malignant cells. Together with a structurally homologous γ -catenin, β -catenin participates in cell-cell and cell-matrix adhesion by binding to the intracellular domain of *E-cadherin*, a homotypic cell-to-cell interaction molecule ubiquitously expressed in epithelial cells^[6,8,9]. In addition, these catenins play an important role in cell polarity by binding to the actin filament network of cytoskeleton through *a-catenin* as a linker^[6,8]. Unlike other known catenins, β -catenin is also a key mediator in the Wnt/Wingless/Wnt signal transduction pathway^[7,8,10]. In cytoplasm of normal cells, the amount and location of β -catenin are controlled exquisitely through its association with the adenomatous polyposis coli (*APC*) tumor-suppressor gene product, a scaffolding protein *Axin*, and a glycogen synthetase kinase (*GSK-3 β*) enabling phosphorylation and degradation of free β -catenin^[6-10]. Once located in nuclei, β -catenin can act as a transcription factor by serving as a coactivator of the lymphoid enhancer factor/TCF family of DNA-binding proteins^[10]. Activation of Wnt signaling involves the inhibition of catenin degradation by proteasomes, resulting in its cytoplasmic and nuclear accumulation and transcriptional activation of the target gene^[5-7,10]. It is believed that β -catenin integrity impairment-related intracellular network may be closely associated with the dedifferentiation, hyperproliferation, invasion and metastatic potential of malignancy^[10,11]. This biomarker has thereby been extensively studied in a variety of neoplasms, such as hepatocellular carcinoma^[12], colorectal carcinoma^[13], gastric cancer^[14,15], pancreatic cancer^[16], ovarian cancer^[17], lung cancer^[18-20], breast cancer^[21], nasopharyngeal carcinoma^[22], prostate cancer^[23] and even lymphoma^[24], with regard to its potential role as a prognostic factor in cell polarity. The present findings in ESCC are controversial in the literature^[25-28].

The role of β -catenin in development of ESCC and its prognostic significance remain to be defined. In the present study, the expression level of β -catenin was measured in specimens from a relatively homogeneous cohort of ESCC patients with no lymph node involved, which was correlated with the clinical outcome of ESCC patients.

MATERIALS AND METHODS

Patients and tissue samples

The study was approved by the Ethics Committee of Sun Yat-Sen University Cancer Center. A total of 227 consecutive patients with node-negative ESCC at stage I B-II B who underwent curative surgery from January 1993 to August 2004 were enrolled in this study. β -catenin expression level was measured in resected specimens with immunohistochemistry (IHC). Patients were followed up prospectively and their survival data were recorded through October 2009. The inclusion criteria were patients with histopathologically-proven ESCC, those with esophageal cancer at T2-3N0M0 based on the seventh edition of the American Joint Committee on Cancer staging system^[29], those with at least 15 lymph nodes to be removed for pathological evaluation, those at the age of at least 18 years, those with no evidence of metastatic disease as determined by history, physical examination, and blood chemistry analysis or routine computed tomography, those with no history of adjuvant therapy. Patients with a history of previously treated cancer other than basal or squamous cell carcinoma of the skin, preoperative chemotherapy and/or radiotherapy, or with unknown causes of death in follow-up were excluded from the study.

Immunohistochemistry

β -catenin (CAT-5H10, Fuzhou Maxim Inc., Fuzhou, Fujian province, China) was diluted at 1:100. ESCC tissue was cut into 4 μ m-thick paraffin sections, which were stained with immunoperoxidase. The sections were deparaffinized in xylene, hydrated prior to antigen retrieval by microwaving in sodium citrate buffer (pH 6.0), and incubated with a peroxidase block followed by primary antibody. After washed with PBS, the sections were incubated first with secondary antibody followed by 3,3'-diaminobenzidine, and then counterstained with hematoxylin (Hematoxylin 7211; Richard-Allen Scientific, Kalamazoo, Michigan, USA). The peroxidase block, secondary antibody and 3,3'-diaminobenzidine were all obtained from the Dako-Cytomation EnVision System (Glostrup, Denmark).

Immunohistochemical scoring

β -catenin was scored with IHC using a semi-quantitative system as previously described^[30,31]. Each section was assigned a score and the score of tumor cell staining was multiplied by the score of staining intensity. Tumor cell staining was scored using a semi-quantitative six-category grading system: 0 = no tumor cell staining, 1 = 1%-10% of tumor cells staining, 2 = 11%-25% of tumor cells staining, 3 =

26%-50% of tumor cells staining, 4 = 51%-75% of tumor cells staining, 5 = over 75% of tumor cells staining. Stain intensity was scored using a semi-quantitative four-category grading system: 0 = no staining, 1 = weak staining, 2 = moderate staining, 3 = strong staining. Two experienced pathologists blinded to the clinical follow-up data independently scored the 400 ESCC samples including the cases used in this study. The complete score agreement of the two pathologists was 87% of all cases, indicating that the scoring method is reasonably reproducible. A third blinded pathologist intervened and evaluated the patients with different IHC scores. If the third pathologist agreed with one of the previous scores, it was used for analysis. The three pathologists were asked to reach an agreement on the cases from which three different scores were obtained.

Selection of cut-off scores

Cut-off scores for β -catenin expression were selected based on receiver operating characteristic (ROC) curve analysis. ROC curve was plotted for the outcome of ESCC patients under study by calculating the sensitivity and specificity on its points. The score closest to the points (0.0, 1.0) on the curve with a maximum sensitivity and specificity was selected as the cut-off score leading to the greatest number of tumors classified with or without clinical outcome. The area under the ROC curve was calculated to estimate the discriminatory power of β -catenin over the entire range of scores for overall survival (OS) rate of ESCC patients. The ROC curve was generated and analyzed using the MedCalc statistical software package 11.0.1 (MedCalc Software bvba, Belgium).

Statistical analysis

Association between categorical variables was analyzed by χ^2 test. Survival curves were calculated with the Kaplan-Meier method and compared by the log-rank test. Time of death was calculated from the date of surgery to the date of death. The time variable was censored on the date of last follow-up of event-free subjects. Multivariate analysis of prognostic factors was performed using the Cox's regression model. $P < 0.05$ was considered statistically significant. All statistical analyses were performed using the SPSS 13.0 for Windows software system (SPSS Inc., Chicago, IL).

RESULTS

Characteristics of patients and expression of β -catenin

The demographic and clinicopathological parameters of ESCC patients included in this study are listed in Table 1. Various intensities of positive β -catenin reaction were detected in cytoplasm and membrane of cancer cells (Figure 1). According to the ROC curves for OS rate, a threshold value of 1.3333 was the optimal point for maximum sensitivity and specificity, and selected as the cut-off score (Figure 2). The 227 ESCC specimens were then catego-

Table 1 Demographic and clinicopathological parameters of esophageal squamous cell carcinoma patients included in this study n (%)

Demographic and clinicopathological parameters	Patients with ESCC
Sex	
Male	165 (72.7)
Female	62 (27.3)
Age (yr)	
Median	58
Range	33-77
Tumor size (cm)	4.92 \pm 2.046
Tumor grade	
Grade 1	57 (25.1)
Grade 2	114 (50.2)
Grade 3	56 (24.7)
Tumor location	
Upper	25 (11.0)
Middle	152 (67.0)
Lower	50 (22.0)
Depth of invasion	
T2	88 (38.8)
T3	139 (61.2)
AJCC staging system (7th ed)	
I B	12 (5.3)
II A	83 (36.6)
II B	132 (58.1)

ESCC: Esophageal squamous cell carcinoma; AJCC: American Joint Committee on Cancer.

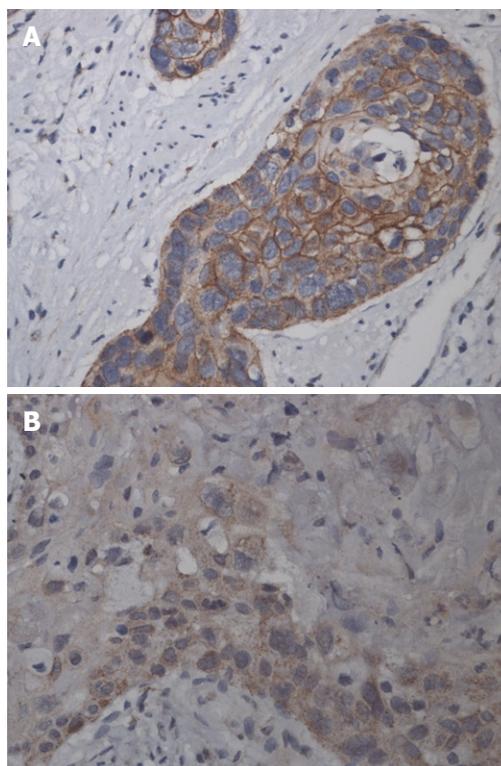


Figure 1 Expression of β -catenin in esophageal squamous cell carcinoma tissue samples (magnification \times 400). A: Immunohistochemical staining of β -catenin in cytoplasm and membrane of cancer cells (immunohistochemistry score: 15); B: Immunohistochemical staining of β -catenin in cytoplasm of cancer cells (immunohistochemistry score: 3).

Table 2 β -catenin expression in esophageal squamous cell carcinoma patients *n* (%)

Parameters of ESCC patients	<i>n</i>	Expression of β -catenin		<i>P</i> -value
		Low	High	
Sex				
Male	165	57 (34.5)	108 (65.5)	0.354
Female	62	26 (41.9)	36 (58.1)	
Age (yr)				
≤ 60	138	49 (35.5)	89 (64.5)	0.778
> 60	89	34 (38.2)	55 (61.8)	
Tumor size (cm)				
≤ 5.0	155	54 (34.8)	101 (65.2)	0.461
> 5.0	72	29 (40.3)	43 (59.7)	
Tumor grade				
Grade 1	57	17 (29.8)	40 (70.2)	0.473
Grade 2	114	44 (38.6)	70 (61.4)	
Grade 3	56	22 (39.3)	34 (60.7)	
Tumor location				
Upper	25	11 (44.0)	14 (56.0)	0.545
Middle	152	52 (34.2)	100 (65.8)	
Lower	50	20 (40.0)	30 (60.0)	
Depth of invasion				
T2	88	34 (38.6)	54 (61.4)	0.672
T3	139	49 (35.3)	90 (64.7)	
AJCC staging system (7th ed)				
I B	12	3 (25.0)	9 (75.0)	0.694
II A	83	31 (37.3)	52 (62.7)	
II B	132	49 (37.1)	83 (62.9)	

ESCC: Esophageal squamous cell carcinoma; AJCC: American Joint Committee on Cancer.

alized into high and low β -catenin expression groups. The expression level of β -catenin was up-regulated in 144 cases (63.4%) and down-regulated in 83 cases (36.6%).

Correlation between β -catenin expression and clinicopathological features

The correlation between β -catenin expression in and clinicopathological features of ESCC patients are shown in Table 2. No significant correlation was identified between β -catenin expression and any clinicopathological parameters, including gender, age, tumor size, tumor grade, tumor location, depth of invasion and pathological stage based on the seventh edition of AJCC staging system^[29].

β -catenin expression and survival rate

At the time of data analysis (October 2009), 72 patients (31.7%), with a median follow-up time of 32 mo (range 5-138 mo), remained alive and 155 patients (68.3%) died. The overall 1-, 3- and 5-year survival rates for the patients were 58%, 39%, and 33%, respectively.

The Kaplan-Meier survival curves (Figure 3) showed that the post-operative survival rate of patients with a low β -catenin expression level was significantly higher than that of those with a high β -catenin expression level (*P* = 0.004). Further stratified analysis split by depth of invasion (Figure 4) showed that the expression of β -catenin had a statistically significant influence on the survival rate of patients with T3 diseases (*P* = 0.014) rather than on the survival rate of

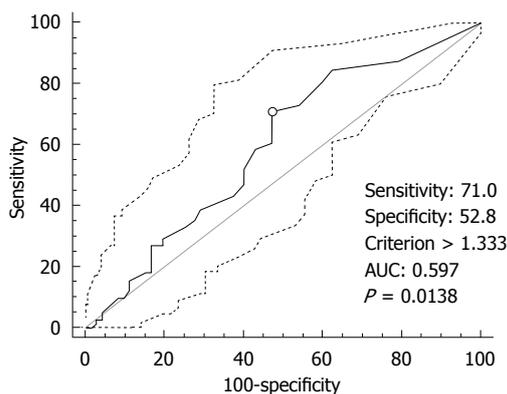


Figure 2 Receiver operating characteristic curve analysis of β -catenin and selection of cut-off score.

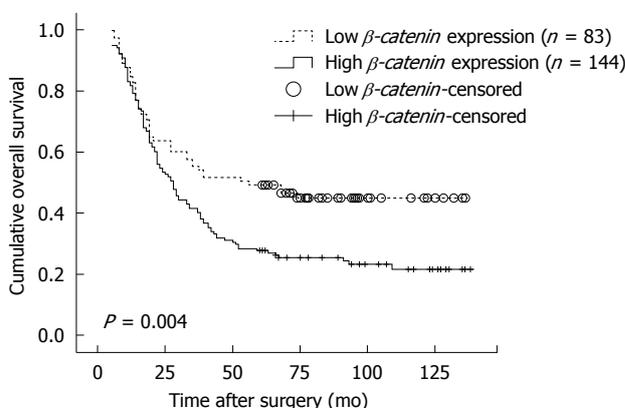


Figure 3 Kaplan-Meier survival curves for patients with esophageal squamous cell carcinoma at stage T2-3N0M0 according to β -catenin expression.

those with T2 lesions (*P* = 0.145). Furthermore, the stratified analysis split by pathological stage based on the new staging system (Figure 5) revealed that β -catenin expression had a significant influence on the prognosis of patients with ESCC at stage II B (*P* = 0.007) but not on the prognosis of those with II A diseases (*P* = 0.253). Patients with ESCC at stage I B were not included in this analysis due to a small sample size.

Factors involved in OS rate of ESCC patients were identified using the Cox proportional hazards model (Table 3). Univariate analysis showed that tumor grade, depth of invasion and β -catenin expression were found to be the significant prognostic indicators for the OS rate of ESCC patients, and thereby selected as the parameters to be included in the same Cox regression model. Further multivariate analysis also confirmed that β -catenin expression (relative risk = 1.642, 95% CI: 1.159-2.327, *P* = 0.005), tumor grade (relative risk = 1.549, 95% CI: 1.095-2.190, *P* = 0.013) and depth of invasion (relative risk = 1.493, 95% CI: 1.066-2.089, *P* = 0.020) were the independent prognostic factors for the OS rate of ESCC patients.

DISCUSSION

To date, several IHC studies have been performed in order

Table 3 Univariate and multivariate analysis of overall survival rate of esophageal squamous cell carcinoma patients with Cox proportional hazards model

Variable	Univariate analysis			Multivariate analysis		
	Hazard ratio	95% CI	P-value	Hazard ratio	95% CI	P-value
Age (yr)						
≤ 60 vs > 60	1.023	0.740-1.414	0.889			
Gender						
Male vs female	0.692	0.474-1.009	0.056			
Tumor size (cm)						
≤ 5 vs > 5	0.987	0.704-1.386	0.942			
Grade						
G1 vs G2 and 3	1.498	1.060-2.116	0.022 ^a	1.549	1.095-2.190	0.013 ^a
Tumor location						
Upper and middle vs lower	0.954	0.657-1.385	0.804			
Depth of invasion						
T2 vs T3	1.461	1.045-2.043	0.026 ^a	1.493	1.066-2.089	0.020 ^a
AJCC staging system (7th ed)						
I B and II A vs II B	1.192	0.865-1.643	0.284			
β -catenin						
Low vs high	1.644	1.161-2.329	0.005 ^b	1.642	1.159-2.327	0.005 ^b

^a $P < 0.05$, ^b $P < 0.01$ vs univariate analysis. AJCC: American Joint Committee on Cancer; CI: Confidence interval.

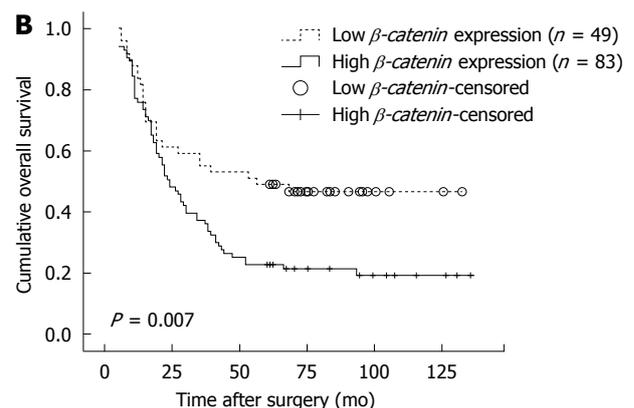
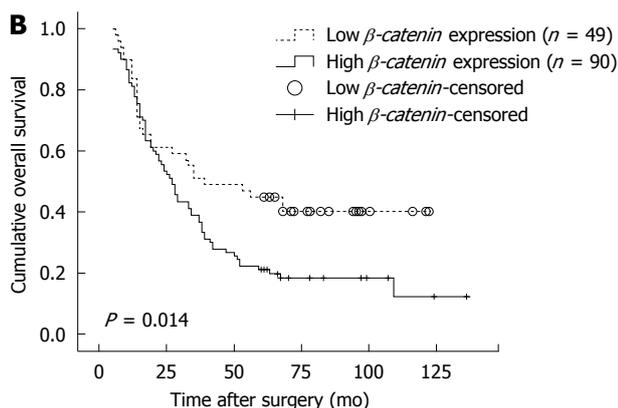
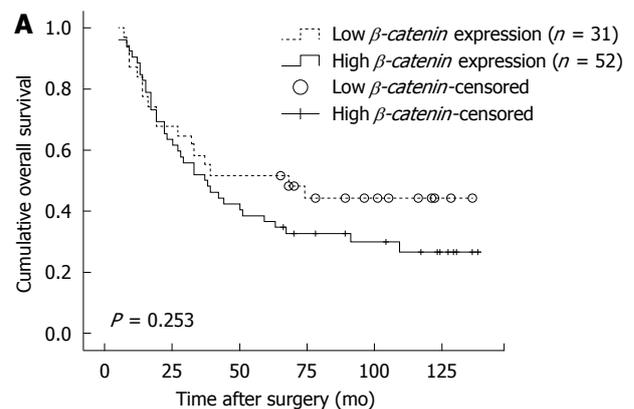
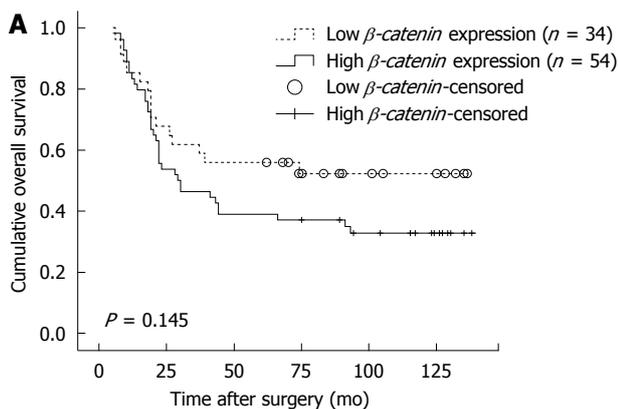


Figure 4 Kaplan-Meier survival curves for patients with esophageal squamous cell carcinoma according to β -catenin expression. A: Correlation between β -catenin expression and post-operative survival rate of patients with T2 lesions; B: Correlation between β -catenin expression and post-operative survival rate of patients with T3 lesions.

Figure 5 Kaplan-Meier survival curves for patients with esophageal squamous cell carcinoma stratified for pathological stage according to β -catenin expression. A: Correlation between β -catenin expression and post-operative survival rate of patients with II A diseases; B: Correlation between β -catenin expression and post-operative survival rate of patients with II B diseases.

to elucidate the role of β -catenin in ESCC, but the current findings in terms of its expression pattern and potential involvement in formation and progression of ESCC are contradictory in the literature^[25-28]. One problem faced by

researchers is the determination of tumor immunohistochemical positivity for β -catenin which is clinically and biologically relevant. Previous studies have applied different scoring systems in predetermination of cut-off scores

which might be set arbitrarily^[30-33]. A lack of consistent, widely applicable methodology may have been primarily responsible for the contradictory results of these studies evaluating β -catenin and its prognostic value in ESCC patients. Therefore, our study used a reproducible scoring method which takes both staining percentage and intensity into account, and the cut-off score was selected based on ROC curve analysis, so that the trade-off between sensitivity and specificity was the smallest, leading to the greatest overall number of correctly classified tumors with and without clinical outcome.

In the present study, univariate and multivariate analyses showed that high expression level of β -catenin in completely resected samples from patients with ESCC at stage T2-3N0M0 was significantly correlated with the worse post-operative survival rate of ESCC patients, which is consistent with the reported findings^[27]. Krishnadath *et al*^[34] reported that low expression level of β -catenin is significantly correlated with the poor prognosis of esophageal adenocarcinoma patients, especially at early-stage. It has been shown that the higher the expression level of β -catenin is, the better the outcome of esophageal adenocarcinoma patients is, and the β -catenin expression level is higher in more invasive tumors than in superficial tumors^[35]. However, Zhao *et al*^[26] and Lin *et al*^[28] demonstrated that β -catenin expression does not imply more aggressive malignant behaviors of ESCC or predict the poor prognosis of ESCC patients. Krishnadath *et al*^[34] and Osterheld *et al*^[35] showed a different histological type of tumor (adenocarcinoma) when they analyzed these contradictory results. In addition, esophageal carcinoma at stages I-IV was involved in the studies^[26,28,34,35], suggesting that different therapeutic strategies including adjuvant or neoadjuvant chemotherapy and radiotherapy for more advanced disease may introduce confounding factors affecting the application of molecular analysis in assessing the prognosis of ESCC patients.

β -catenin protein not only serves as a pivotal component of *E-cadherin/catenin* complex which participates in cell-cell and cell-matrix adhesion^[6,8,9], but also as a key mediator in the Wntless/Wnt signal transduction pathway^[5,7], indicating that disruption of *E-cadherin/catenin* complex or physical and functional loss of β -catenin protein can lead to loosening of cell-cell contact and promote tumor invasion and metastasis. On the other hand, β -catenin can be oncogenically activated either by direct gene mutation^[36] and inactivation of the *APC* tumor suppressor^[37], or by activation of the Wntless/Wnt signal transduction pathway^[38], thus resulting in post-translational stabilization of β -catenin protein. Excess cytoplasmic accumulation of β -catenin protein can then increase the influx of this molecule into nuclei, leading to over-expression of tumor-promoting genes, such as *cyclin-D1* and *c-myc*^[5,6], and promote cell mitosis and growth^[39,40]. Therefore, either up-regulated or down-regulated expression of β -catenin contributes to invasive and metastatic potentials of esophageal cancer. Obviously, the question is which physiopathological process takes the advantage in different circumstances, such

as different histological types or different pathological stages. Further analysis of the role of β -catenin gene and its products in formation and progression of esophageal carcinomas may provide a better understanding of this pathogenic process.

In this study, further stratified analysis split by pathological stage and depth of invasion showed that β -catenin exhibited its effect on the prognosis of patients with ESCC at stage II B or with T3 lesions, indicating that this biomarker is more valuable in predicting the outcome of ESCC patients at advanced stages, which is consistent with the findings in other studies^[12,22]. Further study is needed to verify this trend. In this study, no significant correlation was found between β -catenin expression and prognostic parameters, including tumor grade, tumor location, depth of invasion and pathological stage. Multivariate survival analysis of all potential prognostic variables also confirmed that β -catenin was an absolutely independent prognostic factor, which is in accordance with the reported findings^[25,28]. However, other studies showed that β -catenin is significantly correlated with the accepted prognostic parameters of ESCC^[26,27,41]. Further study with a large sample size is needed to obtain a clearer picture.

In conclusion, elevated β -catenin expression level is an adverse prognostic factor for ESCC patients at stage T2-3N0M0, especially for those with T3 lesions or with stage II B diseases. However, further study with a larger cohort of patients is required to verify this observation, especially in view of the contradictory results.

COMMENTS

Background

Esophageal squamous cell carcinoma (ESCC), an aggressive tumor with a poor prognosis, is one of the most common malignant tumors in Asia, especially in certain areas of China. Despite advances in early diagnosis and therapies, the clinical outcome of ESCC patients remains unsatisfactory. Since the classical staging criteria fail to differentiate prognostic characteristics of ESCC patients adequately, many efforts have been made to identify relevant biomarkers with adverse prognostic significance, and to modify therapeutic strategies for individual patients. β -catenin, as a prognostic factor for ESCC, has been extensively studied in a variety of neoplasms. However, the exact role of β -catenin and its prognostic significance in ESCC remain to be defined.

Research frontiers

β -catenin protein not only serves as a pivotal component of *E-cadherin/catenin* complex which participates in cell-cell and cell-matrix adhesion, but also as a key mediator in the Wntless/Wnt signal transduction pathway. The hotspot in molecular tumor analysis of β -catenin is whether β -catenin involves and how it involves in the formation and progression of esophageal carcinoma.

Innovations and breakthroughs

Previous immunohistochemistry studies showed contradictory results in β -catenin expression pattern and its prognostic value for ESCC, due to lack of consistent, widely applicable methods. Therefore, the present study used a reproducible scoring method which takes both staining percentage and intensity into account, and the cut-off score was selected based on receiver operating characteristic (ROC) curve analysis so that the trade-off between sensitivity and specificity was the smallest, leading to the greatest overall number of correctly classified tumors with and without clinical outcome. This is the first study to evaluate β -catenin expression in ESCC patients with this novel method, showing that elevated β -catenin expression is an adverse prognostic factor for ESCC patients at stage T2-3N0M0, especially for those with T3 lesions or stage II B diseases.

Applications

The novel methods used in this study can be applied in treatment of ESCC patients at stage T2-3N0M0.

Terminology

ROC curve analysis: In signal detection theory, a ROC curve is a graphical plot of the sensitivity, or true positivity vs (1-specificity), or false positivity for a binary classifier system as its discrimination threshold is varied. The ROC curve can also be represented equivalently by plotting the fraction of true positivity (TPR = true positive rate) vs the fraction of false positivity (FPR = false positive rate). ROC curve analysis provides tools to select possibly optimal models and to discard suboptimal ones independently from (and prior to specifying) the cost context or the class distribution. ROC curve analysis is related in a direct and natural way to cost/benefit analysis of diagnostic decision making. β -catenin: β -catenin protein was originally identified as a component of adherence junction, a multi-protein complex supporting tight cell-cell contacts in the presence of extracellular calcium. However, β -catenin also plays a key role in the Wnt signaling transduction pathway.

Peer review

The authors studied the expression of β -catenin in ESCC at stage T2-3N0M0 and its prognostic significance by analyzing the expression of β -catenin in 227 ESCC specimens with IHC and ROC curve analysis to select the cut-off score for high or low IHC reactivity. Then, they correlated the β -catenin expression with clinicopathological features of ESCC patients and its relation with the prognosis of ESCC patients. No significant correlation was observed between β -catenin expression in and clinicopathological parameters of ESCC patients, but multivariate analysis confirmed that β -catenin was an independent prognostic factor for the overall survival rate of ESCC patients at stage T2-3N0M0. The manuscript reads nicely and is easy to follow. Tables are legible and easy to understand. I believe that the method used in this study is plausible and the conclusion is well supported by the data. This manuscript adds to the current knowledge on this topic and it is a pleasure to read it.

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Classification of histological severity of *Helicobacter pylori*-associated gastritis by confocal laser endomicroscopy

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Abstract

AIM: To classify the histological severity of *Helicobacter pylori* (*H. pylori*) infection-associated gastritis by confocal laser endomicroscopy (CLE).

METHODS: Patients with upper gastrointestinal symptoms or individuals who were screened for gastric cancer were enrolled in this study. Histological severity of *H. pylori* infection-associated gastritis was graded according to the established CLE criteria. Diagnostic value of CLE for histological gastritis was investigated and compared with that of white light endoscopy (WLE). Targeted biopsies from the sites observed by CLE were performed.

RESULTS: A total of 118 consecutive patients with *H. pylori* infection-associated gastritis were enrolled in this study. Receiver operating characteristic curve analysis showed

that the sensitivity and specificity of CLE were 82.9% and 90.9% for the diagnosis of *H. pylori* infection, 94.6% and 97.4% for predicting gastric normal mucosa, 98.5% and 94.6% for predicting histological active inflammation, 92.9% and 95.2% for predicting glandular atrophy, 98.6% and 100% for diagnosing intestinal metaplasia, respectively. Post-CLE image analysis showed that goblet cells and absorptive cells were the two most common parameters on the CLE-diagnosed intestinal metaplasia (IM) images ($P < 0.001$). More histological lesions of the stomach could be found by CLE than by WLE ($P < 0.001$).

CONCLUSION: CLE can accurately show the histological severity of *H. pylori* infection-associated gastritis. Mapping IM by CLE has a rather good diagnostic accuracy.

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Key words: Confocal laser endomicroscopy; *Helicobacter pylori*; Gastritis; Classification; Histology

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INTRODUCTION

Helicobacter pylori (*H. pylori*) is a well accepted major etiological factor for gastric diseases, such as chronic gastritis, peptic ulcer and gastric carcinoma^[1-3]. Therefore, endos-

copists must determine the presence of *H. pylori* infection in the stomach during or after endoscopy. The updated Sydney system for classification of gastritis has established the association between *H. pylori* infection and histological evidence of gastritis^[4]. Gastric atrophy especially accompanying intestinal metaplasia (IM), which is the severest stage of gastritis and has a high risk for gastric cancer, is closely associated with *H. pylori* infection^[5]. Although the Sydney system has been widely used, multiple biopsies are rarely performed for gastritis evaluation but only for suspected lesions of cancer in clinical practice, thus leading to omission of some precancerous lesions which are difficult to find by white light endoscopy (WLE)^[6]. Therefore, *in vivo* detection of *H. pylori* infection and its related complications by endoscopy is a simple, noninvasive and inexpensive procedure. *H. pylori*-induced gastritis must be evaluated and graded especially in Eastern countries because of a high prevalence of *H. pylori* infection and a high incidence of gastric cancer^[7]. Furthermore, it can facilitate the clinical assessment and timely treatment of gastritis. The association between *H. pylori* infection and endoscopic findings has been extensively studied using modern endoscopic techniques such as magnification endoscopy and narrow-band imaging^[8-10].

Confocal laser endomicroscopy (CLE) can detect gastrointestinal diseases, such as Barrett esophagus, gastric carcinoma and colonic neoplasia^[11,12]. CLE can observe real-time histological-like cellular and subcellular conditions of gastric mucosal layer at the magnification \times 500-1000. It was reported that acriflavine-aided CLE can observe *H. pylori in vivo*^[13]. In addition, gastric pit patterns of various gastropathies have been accurately classified and IM has been studied by CLE^[14,15]. However, no systematic data are available on the CLE characteristics of chronic gastritis and the classification of chronic gastritis has not been investigated by CLE.

In this study, the CLE features of gastritis mainly caused by *H. pylori* infection were compared to evaluate the accuracy of CLE in diagnosing *H. pylori* infection and the severity of gastritis.

MATERIALS AND METHODS

Patients

Consecutive patients with upper gastrointestinal symptoms or individuals who were screened for gastric carcinoma, admitted to our hospital from June to November 2009, were enrolled in this study. The following patients were excluded from the study, including those who received proton pump inhibitors, antibiotics, or bismuth subsalicylate in the previous 6 wk, those with a history of using nonsteroidal anti-inflammatory drugs and medication for *H. pylori* infection, those undergone stomach surgery, those with systematic diseases or known gastric carcinoma, pregnant or breast-feeding females, those who did not give their informed consent or had an allergy to fluorescein. All participants gave their written informed consent before endoscopy. The study was approved by the Ethics Committee of Qilu Hospital.

CLE system

A confocal laser endomicroscope (Pentax ISC-1000, Pentax, Tokyo, Japan) was used in this study. It is novel digestive endoscope with a confocal laser microscope integrated into the distal tip, can realize a histological-like examination during routine endoscopy and accurately diagnose gastrointestinal diseases at the magnification \times 1000. CLE was performed to scan the gastric mucosa from the top layer to 250 μ m beneath the surface. The CLE and white-light endoscopy (WLE) images were captured and stored.

CLE procedure

CLE was performed by an endoscopist experienced with the system. All patients received oral chymotrypsin (20000 U) to eliminate the slime layer of the stomach for better visualization. One mL of 2% fluorescein (a contrast agent) was intravenously injected before endoscopy. After a first WLE of the stomach, 10 mL of 10% fluorescein was intravenously injected, and CLE images could be seen after a few seconds. Five standardized sites (2 from the lesser and greater curvatures of the antrum about 2-3 cm near the pylorus, 2 from the middle portion of the lesser and greater curvatures of the corpus about 8 cm from the cardia, and 1 from the angulus), as recommended by the updated Sydney system, were examined separately on CLE images. Shallow-deep CLE images were captured at each site and stored as digital files for further analysis. At the standardized locations, real-time image assessment and targeted biopsies were performed by CLE for histopathology. For *H. pylori* testing, 2 specimens were taken from the greater curvature of the antrum and corpus, respectively. If necessary, other scanning and biopsies were performed for lesions such as those with color changes or erosions, polyps, ulcers, or abnormal folds.

CLE classification of *H. pylori* infection-associated gastritis severity

In our study, the severity of gastritis was divided into 6 levels by CLE: normal mucosa, *H. pylori*-associated active inflammation (3 levels), glandular atrophy and IM.

CLE criteria for normal gastric mucosa and *H. pylori*-associated active inflammation:

The published CLE classification of gastric pit patterns was used for one part of our classification of *H. pylori*-associated active inflammation^[14]. In addition, a new marker, fluorescein leakage, was introduced to define the active inflammation in stomach on CLE images (Figure 1). Each of the 5 standardized sites was assigned to a confocal gastritis score (CGS) and a corresponding histologic gastritis score (HGS). The CGS for normal mucosa, and mild, moderate and marked active inflammation was 0, 1, 2 and 3, respectively. The severity of histological activity and chronic inflammation was also defined as normal, mild, moderate and marked with a score of 0-3, respectively. Finally, the mean CGS and HGS (mCGS and mHGS) were calculated for specimens from each stomach.

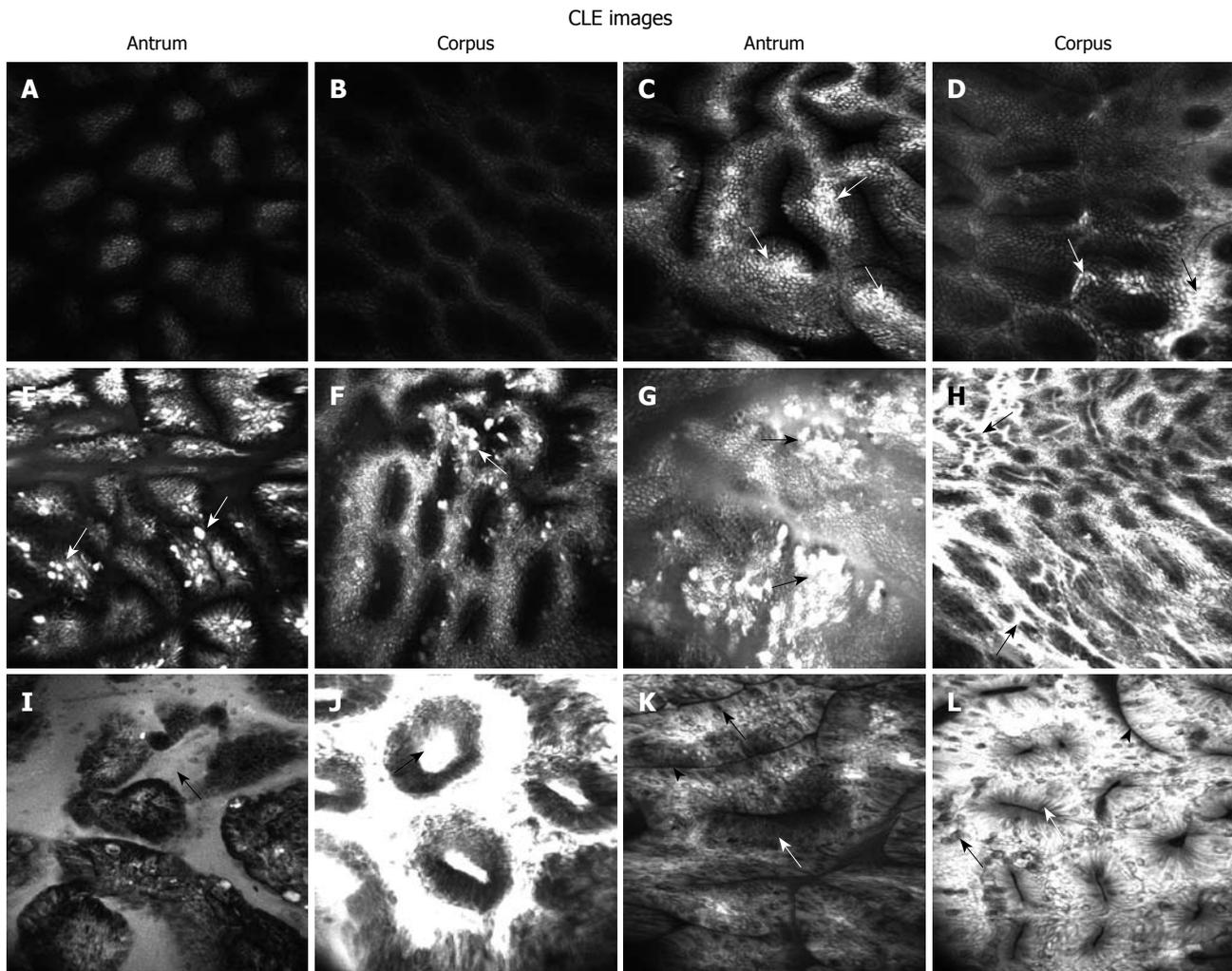


Figure 1 Confocal laser endomicroscopy classification of *Helicobacter pylori*-associated gastritis severity in gastric antrum and corpus. A, B: Normal mucosa with normal antral and corporal pits, and free of fluorescein leakage; C, D: Active inflammation (mild) with slightly distorted pits and intact epithelium, scattered focal fluorescein leakage (arrows); E, F: Active inflammation (moderate) with more distorted pits and partly destroyed epithelium (arrows), and more fluorescein leakage; G, H: Active inflammation (marked) with markedly distorted pits and dilated opening, destroyed epithelium (arrows), and widespread fluorescein leakage; I, J: Glandular atrophy with decreased gastric pits and markedly dilated opening (arrows); K, L: Intestinal metaplasia with villous-like gastric pits and goblet cells (black arrows), absorptive cells (white arrows) and brush border (arrowheads) appearing. CLE: Confocal laser endomicroscopy.

CLE criteria for glandular atrophy and IM: Glandular atrophy and IM are the severest stage of chronic gastritis. The CLE classification of glandular atrophy and IM was defined as decreased gastric pits with a dilated opening and as villous-like gastric pits with goblet cells, absorptive cells and brush border, respectively (Figure 1). To assess the CLE images, the mean number of gastric pits on each grade image was calculated and compared, except for that on IM images. The clinical values for IM features on CLE images were assessed by calculating their mean ratio present in each IM site on CLE images.

Final diagnosis of *H. pylori* infection

Rapid urease testing and Giemsa staining confirmed *H. pylori* infection. If only one test was positive for *H. pylori* infection, ^{13}C -urea breath test was performed for further confirmation. The *H. pylori* infection was classified into Hp (-), Hp (+), Hp (++) and Hp (+++).

Histopathology

All specimens were fixed in 10% formalin. An experienced histopathologist analyzed the histological features of each sample with hematoxylin and eosin staining and made the diagnosis according to the updated Sydney classification. The histological parameters assessed in this study included histological activity, chronic inflammation, glandular atrophy and intestinal metaplasia, which were identified blinding to the results of CLE or WLE.

Statistical analysis

Data were collected from CLE images and histological examination. analysis of variance and box-plot analysis of mCGS were used in pairwise comparison of mCGS among the 4 *H. pylori* test groups [Hp (-), Hp (+), Hp (++) and Hp (+++)]. $P < 0.05$ was considered statistically significant. The efficacy of CGS for predicting *H. pylori* infection was evaluated by area under the receiver oper-

Table 1 Characteristics of patients enrolled in this study

Patients	118
Gender	
Female	44
Male	74
Age (yr), median (range)	49.8 (19-67)
<i>H. pylori</i> infection (mCGS, mean ± SD)	
Positive	41
+	15 (1.11 ± 0.53)
++	15 (1.68 ± 0.51)
+++	11 (2.42 ± 0.45)
Negative	77 (0.61 ± 0.39)
Indication for CLE	
Upper GI symptoms	87
Screened for gastric cancer	31
Endoscopic diagnosis	
Normal stomach	6
Gastritis	92
Peptic ulcer	5
Polyps	13
Early gastric cancer	2

H. pylori: *Helicobacter pylori*; mCGS: Mean confocal gastritis score; CLE: Confocal laser endomicroscopy; GI: Gastrointestinal.

ating characteristic (ROC) curve analysis. On the other hand, the sensitivity, specificity, positive and negative predictive values (PPV, NPV) of the CLE criteria for diagnosing normal gastric mucosa, *H. pylori*-associated active inflammation, glandular atrophy and IM were calculated, respectively. Correlation between mCGS and mHGS was analyzed with the coefficient of determination. SPSS v16.0 (SPSS Inc., Chicago, IL) was used for all statistical analyses.

RESULTS

Collection of data

One hundred and eighteen patients including 74 males, at a mean age of 49.8 years (range 19-67 years) were enrolled in this study. A total of 12243 CLE images (mean 104 images per patient) and 653 optical biopsy images (mean 5.5 biopsy images per patient) were obtained. The median endoscopy time was 23.2 min (range 15-33 min) (Table 1). The quality of over 90% of CLE images was good, while that of the remaining 10% was not satisfactory because it was difficult to fix the distal tip on the gastric angle and the artifacts were motile in gastrointestinal tract. No endoscopic complications or adverse reactions to fluorescein were observed.

CLE diagnosis of *H. pylori* infection

Association between mCGS and *H. pylori* infection:

Of the 118 patients enrolled in this study, 41 were positive for *H. pylori*. Detailed data on *H. pylori* level are shown in Table 1. The mCGS was significantly differed among Hp (-), Hp (+), Hp (++) and Hp (+++) groups ($P < 0.001$). The median mCGS was significantly higher in Hp (+) and Hp (+++) groups than in Hp (-) and Hp (++) groups ($P < 0.001$), and higher in Hp (++) group than in Hp (+) and Hp (-) groups ($P < 0.001$) (Figure 2).

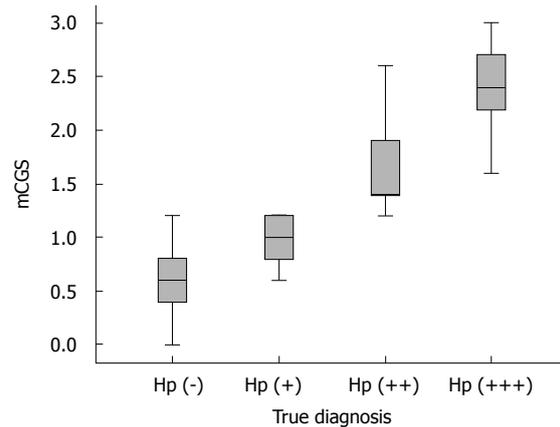


Figure 2 Box plot analysis of mean confocal gastritis score in 4 *Helicobacter pylori* test groups. mCGS: Mean confocal gastritis score.

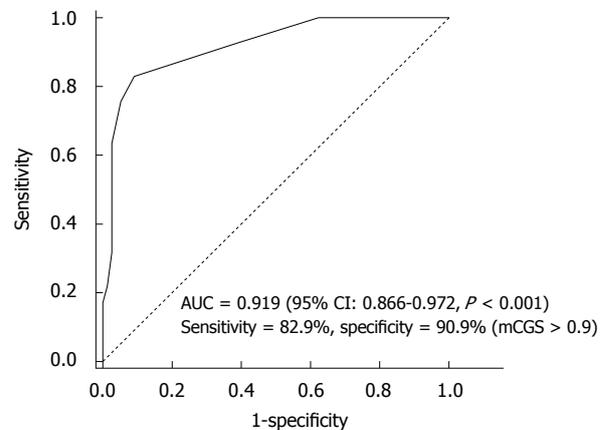


Figure 3 Receiver operating characteristic curve analysis showing the sensitivity and specificity of confocal laser endomicroscopy and mean confocal gastritis score for diagnosing *Helicobacter pylori* infection. AUC: Area under curve; mCGS: Mean confocal gastritis score.

Sensitivity and specificity of CLE for *H. pylori* detection:

The ROC curve for mCGS was plotted to determine a cut-off value of sensitivity relative to specificity for diagnosing *H. pylori* infection. The area under the ROC curve was 0.919 (95% CI: 0.866-0.972), showing an excellent accuracy (Figure 3). The sensitivity and specificity of CEL were 82.9% and 90.9%, respectively, for mCGS > 0.9. With this cut-off value, CLE could correctly diagnose *H. pylori* infection.

CLE classification of histological gastritis severity

Normal gastric mucosa: A good correlation was found between normal mucosa detected by CLE and histology. The sensitivity, specificity, PPV and NPV of CLE were 94.6% (95% CI: 91.9%-97.4%), 97.4% (95% CI: 95.8%-99.1%), 96.5% (95% CI: 94.2%-98.7%), and 96.1% (95% CI: 94.1%-98.1%), respectively, for predicting gastric normal mucosa lesions (Table 2).

Chronic active inflammation: The CLE criteria correlated well with the active inflammation detected by histology. The sensitivity, specificity, PPV and NPV of CLE

Table 2 Sensitivity, specificity, positive predictive values and negative predictive values of confocal laser endomicroscopy for the diagnosis of normal mucosa, *Helicobacter pylori*-associated active inflammation, glandular atrophy and intestinal metaplasia (per specimen) [% (95% CI)]

CLE classification	Sensitivity	Specificity	PPV	NPV
Normal mucosa	94.6 (91.9-97.4)	97.4 (95.8-99.1)	96.5 (94.2-98.7)	96.1 (94.1-98.1)
Active inflammation	98.5 (97.2-99.8)	94.6 (91.9-97.4)	95.9 (93.7-97.9)	98.0 (96.3-99.7)
Glandular atrophy	92.9 (87.0-98.9)	95.2 (93.3-97.0)	72.5 (63.4-81.7)	98.9 (98.1-99.9)
Intestinal metaplasia	98.6 (95.7-100.0)	100 (100.0-100.0)	100 (100.0-100.0)	99.8 (99.4-100.0)

CLE: Confocal laser endomicroscopy; PPV: Positive predictive value; NPV: Negative predictive value.

Table 3 Confocal laser endomicroscopy and white-light endoscopy in predicting histological changes

Biopsy sites	CLE normal sites ¹	CLE abnormal sites ¹			
		Inflammation	Atrophy	IM	Early cancer
WLE normal sites	216	173	41	45	0
WLE abnormal sites ²	31	83	25	23	2

¹The normal and abnormal sites on confocal laser endomicroscopy (CLE) images were confirmed by histology; ²Abnormal sites include erythema, erosion, nodules and petechiae, *etc.*, with no noticeable lesions such as ulcers or polyps on white light endoscopy (WLE) images. IM: Intestinal metaplasia.

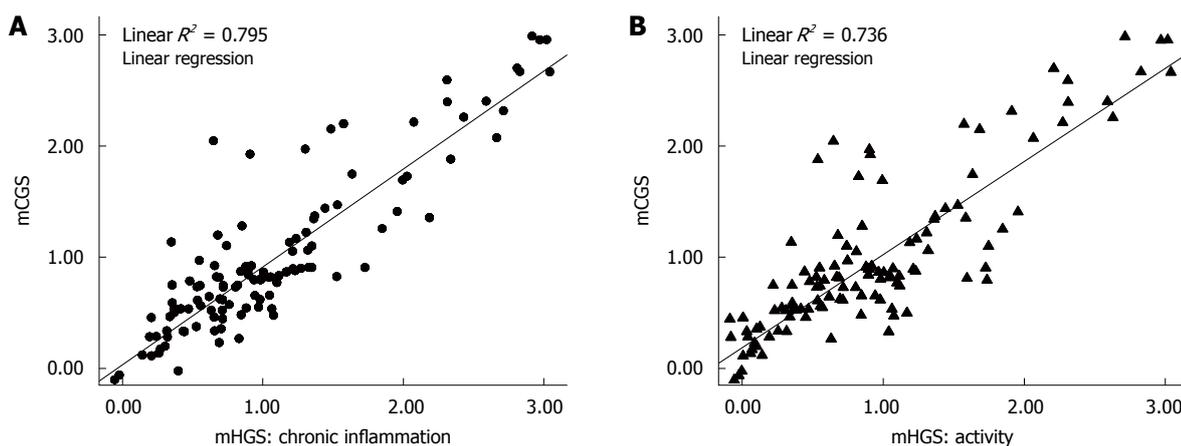


Figure 4 Correlation between mean confocal gastritis score and mean histologic gastritis score for histological chronic inflammation ($R^2 = 0.795$, A) and activity ($R^2 = 0.736$, B). mCGS: Mean confocal gastritis score; mHGS: Mean histologic gastritis score.

were 98.5% (95% CI: 97.2%-99.8%), 94.6% (95% CI: 91.9%-97.4%), 95.9% (95% CI: 93.7%-97.9%), and 98.0% (95% CI: 96.3%-99.7%), respectively, for predicting active inflammation detected by histology (Table 2). In particular, the histological activity and chronic inflammation were significantly differed among the 3 levels of active inflammation on CLE images, based on the evidence that histological activity and chronic inflammation were positively and linearly correlated with the mCGS ($R^2 = 0.795$, $R^2 = 0.736$, $P < 0.001$) (Figure 4).

Glandular atrophy and IM: The sensitivity, specificity, PPV and NPV of CLE were 92.9% (95% CI: 87.0%-98.9%), 95.2% (95% CI: 3.3%-97.0%), 72.5% (95% CI: 63.4%-81.7%) and 98.9% (95% CI: 98.1%-99.9%), respectively, for glandular atrophy (Table 2). Furthermore, a post-CLE analysis of CLE images showed that the mean number of gastric pits in glandular atrophy was significantly

less than that in IM on CLE images ($P < 0.001$) (Figure 5).

The sensitivity, specificity, PPV and NPV of CLE for IM were 98.6% (95% CI: 95.7%-100.0%), 100% (95% CI: 100.0%-100.0%), 100% (95% CI: 100.0%-100.0%), and 99.8% (95% CI: 99.4%-100.0%), respectively, for predicting IM (Table 2). Of the IM features on CLE images, goblet cells and absorptive cells were more common and easier to note than the other features ($P < 0.001$) (Figure 6).

CLE and WLE for predicting histological conditions:

In our study, 54.5% (259/475) normal sites were found to be abnormal on WLE by CLE (173 inflamed sites, 41 atrophic sites and 45 IM sites). In contrast, of the 164 abnormal sites on WLE images, 18.9% (31/164) were found to be normal on CLE images. All the findings on CLE images were confirmed by histology, indicating that CLE can show more histological lesions than WLE ($P < 0.001$) (Table 3).

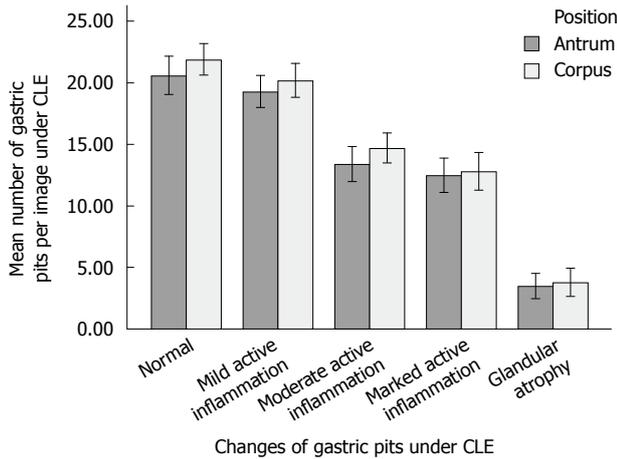


Figure 5 Gastric pits on confocal laser endomicroscopy images. CLE: Confocal laser endomicroscopy.

DISCUSSION

Conventional endoscopy is not frequently correlated with histological alterations, WLE is not accurate for predicting histological gastritis with nonspecific erythema, prominent area gastrica, nodularity, or erosions, *etc.*^[16], and gastroscopy without biopsy is incomplete in routine clinical practice. In recent years, novel endoscopies, such as magnification endoscopy and narrow band imaging, have been evaluated for gastric pathologic conditions with a good accuracy^[17]. High resolution, magnification and advanced electronic dye techniques, can identify the mucosal and vascular details of *H. pylori* infection and its related complications, with a high diagnostic sensitivity and specificity^[18].

More details of gastric pits can be clearly observed on CLE images at the magnification $\times 1000$. Zhang *et al.*^[14] reported that CLE can reveal inflamed pits with marked morphological alterations. The sensitivity and specificity of type B⁺D⁺ pits are 81.9% and 99.3%, respectively, for predicting moderate to severe active inflammation. In our study, *H. pylori* infection was positively correlated with progressively increasing changes in gastric pits due to direct injury caused by *H. pylori* and inflammatory infiltration. CLE could accurately distinguish normal mucosa from *H. pylori*-infected mucosa in the stomach. ROC curve analysis showed a high sensitivity (82.9%) and specificity (90.9%) of mCGS for diagnosing *H. pylori* infection. The mCGS cut-off value was 0.9, indicating an accurate and balanced result. Fluorescein leakage can classify active inflammation in ulcerative colitis^[19] and fluorescein leakage into crypt lumen is positively correlated with histological active inflammation, because of increased colonic permeability. Fluorescein leakage is often present in the stomach, which contributes to the diagnosis of *H. pylori*-associated gastritis. When normal gastric mucosa is observed on CLE images, the fluorescence is confined to beneath the subepithelium and evenly distributed, epithelial cells are clearly visible and well-demarcated, showing a uniform gray cytoplasm and black border (Figure 1A and B). However, in *H. pylori*-infected mucosa, fluorescein easily leaks

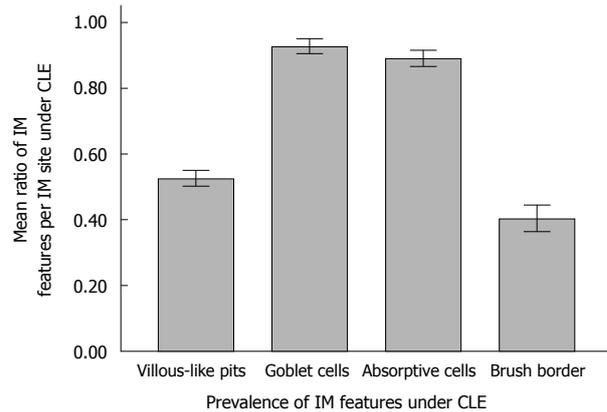


Figure 6 Prevalence of intestinal metaplasia features on confocal laser endomicroscopy images. IM: Intestinal metaplasia; CLE: Confocal laser endomicroscopy.

onto the surface through the damaged epithelium or normal epithelium with a high permeability. That is why this region is brighter than the surrounding normal epithelium. Sometimes, with a mass of the seepage, the entire field of vision can be white (Figure 1C-H). However, because fluorescein leakage is only an indirect response to mucosal damage and histological inflammation, the specificity of fluorescein is lower. In our study, fluorescein in combination with other CLE features was used to diagnose *H. pylori* infection following the active inflammation criteria defined by CLE^[4]. The CLE scoring system used in our study could offer an objective evaluation of the entire stomach. High mCGS of the stomach indicated severe *H. pylori* infection, whereas low mCGS indicated mild or no *H. pylori* infection. Because the CGS agrees with the grading of confocal images, a high score represents severely injured gastric mucosa. It was reported that *H. pylori* organisms are usually observed singly or in groups along the surface epithelium but rarely in deeper mucosa^[20]. Adherence of *H. pylori* to epithelial cells is the first step in *H. pylori* infection. When urease is secreted by *H. pylori*, and inflammatory and immune processes are activated by Vac A and Cag A toxin, the epithelium is depleted of mucin with irregular and missing cells (“drop-out cells”). In our study, similar alterations in moderate and severe active inflammation were found on CLE images, and clusters of destroyed epithelial cells (drop-out cells) on the two grade images were closely correlated with *H. pylori* infection, suggesting that CLE can display the drop-out cells because such microscopic lesions may progress to micro-erosions and precursors of gastric ulcer. However, when mCGS is less than 0.9, it can result in 7 false-positive and 7 false-negative diagnoses. False-positive cases are mainly diagnosed as mild active inflammation based on the CLE images of antrum, because normal mucosa on CLE images is sometimes misdiagnosed as mild inflammation when some fibrin or debris appears on the mucosal surface. The 7 false-negative cases are diagnosed as mild inflammation with a low *H. pylori* level and the corresponding mucosal changes are thus not obvious to be identified.

The second endpoint was to demonstrate the histologi-

cal severity of gastritis by CLE, which showed that the 6 CLE grades were well correlated with the corresponding parameters of histological gastritis. Active inflammation was classified into 3 levels by CLE. On the other hand, obvious drop-out cells were observed at the moderate and marked levels with a high risk for gastric ulcer formation and management of these groups of patients. The severity of chronic inflammation was much higher at moderate and marked levels on CLE images ($R^2 = 0.736$ and 0.795), probably because interstitial infiltration of inflammatory cells can easily squeeze the glands and damage the epithelium with an increasing severity of inflammation and *H. pylori* infection, leading to aggravated pit distortion and fluorescein leakage.

Gastric glands would be destroyed, and glandular atrophy and/or intestinal metaplasia would occur when they are infected with *H. pylori* and infiltrated with inflammatory cells. Glandular atrophy is manifested as thinner mucosa without gastric rugae but with visibly vascular pattern on WLE images^[21]. However, gastric atrophy is poorly correlated with histological atrophy on WLE images^[22]. It was reported that CLE shows a good sensitivity and specificity for gastric atrophy^[14]. In our study, the diagnostic sensitivity and specificity of CLE were 92.9% and 95.2% for glandular atrophy. A further analysis of CLE-diagnosed glandular atrophy was performed with a more objective method. The mean number of gastric pits was calculated on different CLE images, and the mean number of pits in glandular atrophy was significantly less than that in gastritis on CLE images ($P < 0.001$). However, IM on CLE images was not analyzed because the gastric pits were replaced by intestinal mucosa, which became another form of atrophy or metaplasia. Although the sensitivity and specificity of CLE were high for glandular atrophy, the PPV was relatively low (72.5%) probably due to the low prevalence of atrophy in histology (71 sites/590 sites, 12.0%), indicating that there is a certain false positive rate when CLE is used to diagnose glandular atrophy, and identification of mild glandular atrophy is a big challenge for CLE.

Although the Sydney system has suggested a definition of endoscopic intestinal metaplasia for “grey-white patches with a slight opalescent tinge and/or a villous appearance on close inspection”, studies demonstrated that these features are quite difficult to be identified by conventional endoscopy^[21,23]. The detection of IM needs multiple biopsy specimens. Tahara *et al.*^[18] reported that magnifying narrow-band imaging endoscopy can show IM with a sensitivity of 73.3% and a specificity of 95.6%. In this study, IM was further analyzed following the CLE criteria^[15]. The sensitivity and specificity of CLE were 98.6% and 100%, respectively, for IM in our study, and were higher than those reported by Tahara *et al.*^[18]. In addition, goblet cells and absorptive cells were more frequently and easily observed than other features or parameters in IM on CLE images in our study ($P < 0.001$). Because diagnosis of IM is often disregarded by naked eyes or by chromoendoscopy in clinical practice, more powerful endoscopic techniques, such as CLE and magnifying endoscopy, should be used to map IM^[24].

Microscopic examination is essential for endoscopists to make a final diagnosis of gastritis, because the term of gastritis has been used indiscriminately and whether histological inflammation is present or not. However, CLE plays a pathological role in improving the diagnostic rate of WLE. In this study, CLE could discover 54.5% of lesions missed by WLE and correct 18.9% of normal mucosal sites misdiagnosed as abnormal sites by WLE, because the micro-gastric inflammation may appear completely normal on WLE images, suggesting that the presence or absence of gastritis should not be determined only based on gross WLE images. However, CLE can detect these micro-changes.

The main limitations of our study are as follows. First, we did not establish a control group, or a follow-up group to validate our hypothesis from multiple aspects, leading some bias in determination of *H. pylori* infection and histological gastritis. Second, we did not evaluate inter- and intra-observer variability. The repeatability of our CLE criteria should be assessed in a future single study. Third, due to the scanning depth and resolution limitations of CLE, there is still some gap when compared with *in vitro* histology. Therefore, the CLE equipment needs to be constantly upgraded.

In conclusion, *H. pylori* infection is related to its related CLE image features. Histologically active inflammation can be classified by CLE. Two most accurate markers, goblet cells and absorptive cells for IM, are established. Although CLE itself still has some limitations as a novel technique, it is a promising new procedure for accurate histological assessment *in vivo*.

COMMENTS

Background

The accurate diagnosis of chronic gastritis still relies on histopathology. Confocal laser endomicroscopy (CLE) can show gastric pit patterns and epithelial cells *in vivo*, thus, contributing to an accurate diagnosis of chronic gastritis *in vivo*.

Research frontiers

CLE has been extensively investigated in cancerous or precancerous mucosa of Barrett's esophagus and its related neoplasia, early esophageal cancer, gastric intestinal metaplasia, neoplasia and early cancer, colonic neoplasia and cancer, and ulcerative colitis, *etc.*

Innovations and breakthroughs

Endoscopic diagnosis of chronic gastritis and *Helicobacter pylori* (*H. pylori*) infection is still challenge to clinical endoscopists. This study first used CLE to classify *H. pylori* infection-associated chronic gastritis, which could accurately diagnose chronic gastritis *in vivo* without multiple biopsy specimens.

Applications

By using the classification criteria for chronic gastritis established in this study, clinical endoscopists could use CLE to evaluate the conditions of the entire stomach, and calculate the abnormal mucosal sites in the entire stomach.

Terminology

CLE is novel digestive endoscope. It is a conventional white-light endoscope with a confocal laser microscope integrated into the distal tip. CLE can realize a histological-like examination during routine endoscopy and accurately diagnose gastrointestinal diseases at the magnification $\times 1000$.

Peer review

The authors established the classification criteria for chronic gastritis, and compared CLE and white light endoscopy in diagnosis of gastritis and intestinal metaplasia, thus proving a novel method for the diagnosis of gastritis and intestinal metaplasia by CLE, which has a higher sensitivity and specificity than conventional endoscopy.

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Smad7 dependent expression signature highlights BMP2 and HK2 signaling in HSC transdifferentiation

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Abstract

AIM: To analyse the influence of Smad7, antagonist of transforming growth factor (TGF)- β canonical signaling pathways on hepatic stellate cell (HSC) transdifferentiation in detail.

METHODS: We systematically analysed genes regulated by TGF- β /Smad7 in activated HSCs by microarray analy-

sis and validated the results using real time polymerase chain reaction and Western blotting analysis.

RESULTS: We identified 100 known and unknown targets underlying the regulation of Smad7 expression and delineated 8 gene ontology groups. Hk2, involved in glycolysis, was one of the most downregulated proteins, while BMP2, activator of the Smad1/5/8 pathway, was extremely upregulated by Smad7. However, BMP2 dependent Smad1 activation could be inhibited *in vitro* by Smad7 overexpression in HSCs.

CONCLUSION: We conclude (1) the existence of a tight crosstalk of TGF- β and BMP2 pathways in HSCs and (2) a Smad7 dependently decreased sugar metabolism ameliorates HSC activation probably by energy withdrawal.

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Key words: Transforming growth factor- β ; Smad7; Hepatic stellate cell; Gene regulation; Glucose metabolism; BMP2

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INTRODUCTION

Histopathological changes of chronic liver diseases usually

start with inflammatory hepatitis, followed by fibrosis and the final stage of cirrhosis, possibly leading to liver cancer. Hepatic fibrosis is characterized by increased and altered deposition of newly generated or deficiently degraded extracellular matrix (ECM) in response to injury^[1]. Hepatic stellate cells (HSCs) are the major fibrotic precursor cells that transdifferentiate in inflammatory liver tissue to fibrogenic myofibroblasts (MFs), by undergoing morphological changes, increased expression of α -SMA and synthesis of large amounts of ECM components^[2].

Transdifferentiation of HSCs is driven by a variety of cytokines with transforming growth factor (TGF)- β playing a master role. It stimulates quiescent HSCs by paracrine and transdifferentiated MFs by autocrine mechanisms activating intracellular Smad cascades. A great variety of cytokines, chemokines and mitogens (TNF- α , IFN- γ , EGF, PDGF, CTGF, ID1, YB1) display complex crosstalk with TGF- β ^[3-6].

Smad7 is a powerful antagonist of TGF- β in HSCs blunting downstream signaling by inhibiting receptor (R)-Smad phosphorylation^[7]. In quiescent HSCs, expression of Smad7 itself is induced by the R-Smad cascade, thereby providing a negative feedback loop to terminate TGF- β signals^[8]. We demonstrated before phenotypically and functionally that overexpressed Smad7 inhibits HSC transdifferentiation and attenuates the extent of fibrosis^[7] suggesting that Smad7 is a promising antifibrotic tool for treatment approaches.

Therefore, in this study we analyzed the influence of Smad7 on the HSC gene expression pattern in great detail using microarray analysis. Its overexpression affects a great variety of cellular pathways involved in development, angiogenesis, differentiation, transcription, immune response, apoptosis, proliferation, signal transduction, ion and electron transport, sugar and lipid metabolism, morphogenesis, protein synthesis and modification, DNA synthesis and repair, cell adhesion, stress response, blood circulation, cell cycle and growth, cell motility, muscle contraction and organization of the cytoskeleton. The strongest regulated proteins are Pla2g2a, Cyp4b1, both upregulated and, Hk2 and VEGFa, which were downregulated significantly. Interestingly, BMP2, a member of the TGF- β family and alternative activator of the Smad1/5/8 pathway, was strongly induced by Smad7 overexpression in HSCs.

MATERIALS AND METHODS

Affymetrix gene chip array

Primary HSCs of male Sprague-Dawley were isolated as previously described^[9,10]. To identify Smad7 dependent gene responses, HSCs were infected with adenoviruses encoding for Smad7 (AdSmad7; kindly provided by C. Heldin (Ludwig Institute for Cancer Research, Uppsala, Sweden)) or LacZ (AdLacZ) as control 2 d after seeding^[7].

RNA sample collection and generation of biotinylated complementary RNA probes was carried out according to the Affymetrix GeneChip[®] Expression Analysis Technical

Manual (Affymetrix, Santa Clara, CA, USA). In brief, total RNA was prepared at day 4 from 5×10^6 cultured primary HSCs that were infected with AdLacZ or AdSmad7 at day 2. Twenty five micrograms total RNA was reversely transcribed into double-stranded cDNA using HPLC-purified T7-(dt) 24 primers (MWG, Ebersberg, Germany) and the Superscript choice cDNA synthesis system (Invitrogen Corp., Carlsbad, CA). Purified cDNA was used to synthesize biotinylated complementary RNA using the BioArray High Yield RNA Transcription Labeling Kit (Enzo Diagnostics, Enzo Life Science Inc., Farmingdale, NY, USA). Each sample was hybridized to an Affymetrix rat Genome RG-U34A microarray (8799 probe sets) for 16h at 45°C. Expression values of each probe set were determined and AdSmad7 infected samples were compared to AdLacZ infected controls using the Affymetrix Microarray Suite 5.0 software.

Intensities across multiple arrays were normalized to a target intensity of 2500 using global normalization scaling. Two separate experiments with HSCs from different animals were performed under identical conditions. Genes whose expression levels were changed more than 2-fold with $P < 0.001$ in both experiments were considered to be significantly regulated by Smad7. These genes were investigated according to their molecular function and biological process by searching the gene ontology (GO) term database. Genes differentially expressed in AdSmad7 treated compared to controls were classified by "pathway" analysis [KEGG (<http://www.genome.jp/kegg/pathway.html>), PathwayArchitect, Stratagene].

Reverse-transcription and quantitative real-time polymerase chain reaction

Total RNA was collected from 3 (3 d-) or 7 d old (7 d-)HSCs, which were either infected with AdSmad7 or AdLacZ 2 d earlier or were uninfected^[11]. cDNA from cell culture samples was synthesized as described^[11]. Quantitative real-time polymerase chain reaction (RT-qPCR) was performed as in^[11] with modified conditions: 95°C for 60 s, then 40 cycles (50 cycles for low copy genes) of 95°C for 10 s, 60°C for 10 s and 72°C for 15 s. Annealing temperature was set at 58°C for U92564 and 62°C for rat VEGF1. Primers are listed in Table 1. The quantity of target mRNA was determined using a TGF- β RI standard curve^[11]. A cDNA fragment was amplified and column-purified using the QIAquick PCR purification kit (Qiagen) and the following primers: TGF β RI (GI: 416397) 180 bp; F (5'-CGTCTGCATTGCACTTATGC-3'), R (5'-AGCAGTGGTAACCTGATCC-3'). A standard curve was generated from serial 10 time logarithmic dilutions of the cRNA by reverse transcription.

Western blotting analysis

Isolated primary HSCs of female Wistar rats were cultured as in^[7]. Following overnight starvation (0.5% FCS) HSCs were stimulated with 5 ng/mL human recombinant TGF- β (Peprotech, Hamburg, Germany) or 20 ng/mL BMP2 (R&D, Minneapolis, MN), respectively.

Table 1 Primer used for quantitative real-time polymerase chain reaction validation of array results

Gene	Probe set ID	Forward	Reverse
CYP4B1	M29853	5'CCGAAGGCTGCAGATGTGT3'	5'TTTGGCCCATCCAGAACTAGTAG3'
mSmad7		5'GGTGCTCAAGAACTCAAGG3'	5'CAGCCTGCAGTCCAGGCG3'
BMP2	L02678_at	5'TGCCCCCTAGTGTCTTAGAC3'	5'GGGAAGCAGCAACACTAGAAGAC3'
SGIII	U02983	5'CAAGCAGGACCGAGAATCAG3'	5'CGTTGGACAAGGTCAAGGTG3'
Zfp423	U92564	5'GCAGTGCTACACCTGACTCG3'	5'GTCATCCCGCATCTTCTTCTG3'
Pla2g2a	x51529	5'GCTCAATTCAGTCCAGGG3'	5'CCACCCACACCAATGG3'
EST189231	AA799734	5'CGGCTCACTGAGCTTGAAGTAG3'	5'ACACGACGGAGGAGCTTCTG3'
Olr1	AB005900	5'CAGAGAGAAGTGAAGGAACAG3'	5'GGACCTGAAGAGTTTGCAGC3'
ID1	L23148_g_at	5'TGGACGAAACAGCAGGTGAAC3'	5'TCTCCACCTTGCTCACTTTCG3'
HK2	D26393exon_s_at	5'CTCAGAGCGCCTCAAGACAAG3'	5'GATGGCACGAACCTGTAGCA3'
Slc16a3	U87627	5'CTCATCGGACCCCATCAG3'	5'CGCCAGGATGAACACATACTTG3'
ratVEGF.1		5'TGCCAAGTGGTCCCAGGC3'	5'ATTGGACGGCAATAGCTGCG3'

For Smad7 overexpression studies, HSCs were infected on day 3 or day 6 with 50 IFU/cell (infectious units) Smad7 encoding adenovirus for 24 hr in medium containing 5% FBS. Four days old HSCs are considered to be in the transactivation process, while 7 d old HSCs are considered to be fully activated. After infection cells were serum-starved overnight and stimulated with 5 ng/mL TGF- β 1 or 20 ng/mL BMP2. Generally, more than 90% of HSCs were infected.

For Western blotting analysis 20 μ g protein was separated (4%-12% Bis-Tris Gel, NuPAGE, Invitrogen) and transferred to nitrocellulose membranes (Pierce, Rockford, IL). Nonspecific binding was blocked with 5% milk/TBST for Smad7 and GAPDH (Santa Cruz, CA, USA) or 5% BSA/TBST for pSmad1/3 antibodies (Epitomics/Biomol). Horseradish peroxidase-linked goat anti-rabbit antibody (Santa Cruz, CA, USA) served as secondary antibody. Membranes were developed with Supersignal Ultra (Pierce, Hamburg, Germany).

RESULTS

Smad7 dependent gene expression pattern

At day 2 of culture, primary rat HSCs were infected with AdSmad7 or AdLacZ (control). Two days later, when HSCs are in the process of transdifferentiation, the expression of genes displayed on 8799 probe sets was compared between cells overexpressing Smad7 and controls. Confirming Western blotting analysis of HSC lysates^[12], microarray data revealed tremendous overexpression of Smad7 in AdSmad7 infected HSCs (40.79 times).

One hundred and twenty-nine probe sets were found differentially expressed due to Smad7, including 10 unknown proteins, 1 predicted protein and 89 known proteins (Table 2 provides a full list). According to their biological role, these genes were classified into eight main GO groups (Figure 1A). 37% of the regulated genes are involved in development. 22% can be assigned to signal transduction processes, which was expected since Smad7 represses TGF- β signaling and thus has impact on manifold different cross-talking signaling pathways. 15% refer to multicellular organismal processes (i.e. processes involved in intercellular interaction of any kind), 35% to response to stimulus, 21% to localization, 38% to meta-

bolic processes, 25% to cell differentiation and 5% to cell adhesion. Note that the total percentage is greater than 100% as some regulated genes can be assigned to different ontology groups. A similar classification of all differentially expressed genes was carried out according to their molecular function (Figure 1B). Figures 2 and 3 graphically summarize regulation of all genes according to their ontology groups.

In general, many known mediators of TGF- β signaling were differentially expressed in AdSmad7 infected HSCs, confirming a direct link of Smad7 effects to TGF- β signalling (Table 2). ECM proteins like Col1a1 and Fn1 which are induced during HSC activation and fibrogenesis were negatively regulated upon Smad7 overexpression. Further profibrogenic cytokines like CXCL10 and HGF were upregulated. In addition, Cyp proteins like Cyp1b1, Cyp2E1 and Cyp4B1, Id proteins 1, 2, and 3, as well as PDGFR A were identified as Smad7 dependent in activated HSCs. Unexpectedly, several genes involved in glucose metabolism, so far annotated as predominantly associated with hepatocytes were influenced by Smad7 overexpression in HSCs.

As expected, Smad7 led to an opposite regulation of a number of recently systematically identified genes induced during HSC activation^[14]. Table 3 contains a complete list of proteins identified to be regulated in both studies. In total, 37 genes of our study overlapped with the array results reported by^[14]. Twenty-two of those (60%), e.g. HK2, were induced during activation^[14] and decreased by Smad7 (this study) and therefore probably represent profibrogenic TGF- β target genes. There were also a few genes strongly upregulated by Smad7, which were downregulated during *in vivo* HSC activation, e.g. BMP2. Some of the proteins found to be differently regulated by activation *vs* Smad7 overexpression are already known to be TGF- β target genes and related to fibrogenesis, i.e. BMP2, Cnn1, Col1a1, Ddah1, Fn1, Lox, Pdgfra, Slc2a1, Slc16a3, and VEGF. Others might represent yet unidentified target genes of profibrogenic TGF- β signaling and/or new markers of HSC activation. Their specific influence on HSC transdifferentiation *in vivo* needs to be carefully investigated in future as they display potential antifibrotic target genes. In some cases De Minicis *et al.*^[14] reported opposite effects in regards to regulation of gene expression

Table 2 One hundred genes selected as being differentially expressed after Smad7 overexpression in hepatic stellate cells (note that some specific transcripts are detected by more than one probe set)

Official symbol	Average log ₂ fold	SD log ₂ fold	Affymetrix probe set ID	Official full name
Downregulated (<i>n</i> = 72)				
Acta2	-0.85	0.21	X06801cdds_i_at	Smooth muscle α -actin
Ak3l1	-1.20	0.42	rc_AA891949_at	Adenylate kinase 3-like 1
Akap12	-1.00	0.57	U75404UTR#1_s_at	A kinase (PRKA) anchor protein (gravin) 12
Akr1b1	-0.70	0.42	M60322_g_at	Aldo-keto reductase family 1, member B1 (aldose reductase)
Atp6v1b2	-1.10	0.14	Y12635_at	ATPase, H transporting, lysosomal V1 subunit B2
Btg1	-0.65	0.49	L26268_g_at	B-cell translocation gene 1, anti-proliferative
Clec4f	-2.40	3.39	M55532_at	C-type lectin domain family 4, member f
Cml5	-1.30	0.42	rc_AA894273_at	Camello-like 5
Cnn1	-1.30	0.57	D14437_s_at	Calponin 1
Col1a1	-1.51	0.53	M27207mRNA_s_at/rc_AI231472_s_at/ U75405UTR#1_f_at/Z78279_at/Z78279_g_at	Procollagen, type 1, α 1
Cryab	-1.13	0.32	M55534mRNA_s_at/X60351cdds_s_at	Crystallin, α B
Cyp11b1	-1.10	0.28	rc_AI176856_at/U09540_at/U09540_g_at	Cytochrome P450, family 1, subfamily b, polypeptide 1
Ddah1	-0.95	0.21	D86041_at	Dimethylarginine dimethylaminohydrolase 1
Dpysl2	-0.95	0.64	rc_AA875444_at	Dihydropyrimidinase-like 2
Egr2	-1.25	0.64	U78102_at	Early growth response 2
Eif4ebp1	-1.05	0.07	U05014_at	Eukaryotic translation initiation factor 4E binding protein 1
Emp1	-0.65	0.78	Z54212_at	Epithelial membrane protein 1
Eno2	-0.80	0.71	X07729exon#5_s_at	Enolase 2, γ
Erc1	-0.75	0.49	rc_AA892791_at	Excision repair cross-complementing rodent repair deficiency, complementation group 1
EST (unknown)	-2.65	0.64	rc_AI102814_at	EST
EST (unknown)	-2.60	0.28	rc_AI230256_at	EST
EST (unknown)	-2.00	0.14	rc_AA874889_g_at	EST
EST (unknown)	-1.40	0.85	rc_AA866419_at	EST
EST (unknown)	-1.35	0.64	X62950mRNA_f_at	EST
EST (unknown)	-1.10	0.99	rc_AA859740_at	EST
EST (unknown)	-0.85	0.35	rc_AA800708_at	EST
EST (unknown)	-0.40	1.41	X62951mRNA_s_at	EST
F3	-1.85	0.92	U07619_at	Coagulation factor III
Fabp5	-0.80	0.57	S69874_s_at	Fatty acid binding protein 5, epidermal
Fkbp1a	-0.65	0.49	rc_AI228738_s_at	FK506 binding protein 1a
Fn1	-1.15	0.36	L00190cdds#1_s_at/U82612cdds_g_at/ X05834_at	Fibronectin 1
Fntb	-1.28	0.49	rc_AI136396_at/rc_AI230914_at	Farnesyltransferase, CAAX box, β
Gabbr1	-1.25	0.92	rc_AI639395_at	γ -aminobutyric acid (GABA) B receptor 1
Gpx3	-1.10	0.14	D00680_at	Glutathione peroxidase 3
Hig1	-0.95	0.49	rc_AA891422_at	Hypoxia induced gene 1
Hk2	-3.20	0.00	D26393exon_s_at	Hexokinase 2
Id1	-2.55	0.35	L23148_g_at	Inhibitor of DNA binding 1
Id2	-2.45	0.21	rc_AI137583_at	Inhibitor of DNA binding 2
Id3	-1.85	0.13	AF000942_at/rc_AI009405_s_at	Inhibitor of DNA binding 3
Idi1	-0.70	0.57	AF003835_at	Isopentenyl-diphosphate delta isomerase
LOC686781	-1.25	0.21	rc_AA799657_at	Similar to NF κ B interacting protein 1
Lox	-1.10	0.17	rc_AA875582_at/rc_AI234060_s_at/ S77494_s_at	Lysyl oxidase
Lpl	-1.20	0.71	L03294_at/L03294_g_at/rc_AI237731_s_at	Lipoprotein lipase
Lrrc59	-0.65	0.64	D13623_at	Leucine rich repeat containing 59
Lum	-0.80	0.42	X84039_at	Lumican
Ncam1	-1.35	0.78	X06564_at	Neural cell adhesion molecule 1
Olr1	-2.43	0.99	AB005900_at/AB018104cdds_s_at/ rc_AI071531_s_at	Oxidized low density lipoprotein (lectin-like) receptor 1
P4ha1	-0.85	0.21	X78949_at	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), α 1 polypeptide
Pcsk6	-1.10	0.71	rc_AI230712_at	Proprotein convertase subtilisin/kexin type 6
Pfkfb	-1.25	0.54	L25387_at/L25387_g_at	Phosphofructokinase, platelet
Plaur	-1.20	0.71	X71898_at	Plasminogen activator, urokinase receptor
Plod2	-1.00	0.28	rc_AA892897_at	Procollagen lysine, 2-oxoglutarate 5-dioxygenase 2
Pmepa1	-1.55	0.07	rc_AI639058_s_at	Prostate transmembrane protein, androgen induced 1
Ptk2	-0.85	0.35	S83358_s_at	PTK2 protein tyrosine kinase 2
Rasl11a	-2.25	0.49	rc_AI169372_at	RAS-like family 11 member A
Rasl11b	-1.03	0.24	rc_AA800853_at/rc_AA800853_g_at	RAS-like family 11 member B
Rcn2	-0.90	0.57	U15734_at	Reticulocalbin 2

RGD1306841	-1.10	0.14	rc_AI639203_at	Similar to RIKEN cDNA 2410006F12
RGD1310444_predicted	-1.25	0.21	rc_AA866432_at	LOC363015 (predicted)
Rgs4	-1.45	0.64	U27767_at	Regulator of G-protein signaling 4
Sc4mol	-1.10	0.45	E12625cds_at/rc_AI172293_at	Sterol-C4-methyl oxidase-like
Schip1	-1.00	0.42	rc_AA800036_at	Schwannomin interacting protein 1
Serpine1	-1.90	0.00	M24067_at	Serine (or cysteine) peptidase inhibitor, clade E, member 1
Slc12a2	-0.80	0.99	AF051561_s_at	Solute carrier family 12, member 2
Slc16a3	-2.05	0.35	U87627_at	Solute carrier family 16 (monocarboxylic acid transporters), member 3
Slc2a1	-1.15	0.35	S68135_s_at	Solute carrier family 2 (facilitated glucose transporter), member 1
Spink8	-2.55	1.48	rc_AA799734_at	Serine peptidase inhibitor, kazal type 8
Tfrc	-0.90	0.42	M58040_at	Transferrin receptor
Tnc	-0.90	0.28	U09401_s_at	Tenascin C
Tnnt2	-1.70	0.42	M80829_at	Troponin T2, cardiac
Vegfa	-2.25	1.28	L20913_s_at/M32167_g_at/rc_AA850734_at	Vascular endothelial growth factor A
Wfdc1	-1.70	0.14	AF037272_at	WAP four-disulfide core domain 1
Up-regulated (n = 28)				
Adora2a	0.85	0.35	S47609_s_at	Adenosine A2a receptor
Agtr1a	0.95	0.21	M74054_s_at/X62295cds_s_at	Angiotensin II receptor, type 1 (AT1A)
Bmp2	2.83	1.31	L02678_at/rc_AA997410_s_at	Bone morphogenetic protein 2
Col3a1	0.90	0.42	M21354_s_at/X70369_s_at/	Procollagen, type III, α 1
Cxcl10	1.05	0.21	U17035_s_at	Chemokine (C-X-C motif) ligand 10
Cyp2e1	1.00	0.14	M20131cds_s_at	Cytochrome P450, family 2, subfamily e, polypeptide 1
Cyp4b1	3.25	0.49	M29853_at	Cytochrome P450, family 4, subfamily b, polypeptide 1
Ednrb	0.70	0.42	rc_AA818970_s_at	Endothelin receptor type B
Ephx1	1.15	0.21	M26125_at	Epoxide hydrolase 1, microsomal
EST (unknown)	0.80	0.28	rc_AA874873_g_at	EST
EST (unknown)	0.90	0.28	rc_AI177256_at	EST
Glul	0.90	0.23	M91652complete_seq_at/rc_AA852004_s_at	Glutamate-ammonia ligase (glutamine synthase)
Hgf	1.03	0.05	E03190cds_s_at/X54400_r_at	Hepatocyte growth factor
Hsd11b1	0.95	0.49	rc_AI105448_at	Hydroxysteroid 11- β dehydrogenase 1
Igfbp3	1.15	0.30	M31837_at	Insulin-like growth factor binding protein 3
Kif4	1.05	0.07	rc_AA859926_at	Kinesin family member 4
Lhx2	0.95	0.21	L06804_at	LIM homeobox protein 2
Notch1	0.80	0.42	X57405_g_at	Notch gene homolog 1 (Drosophila)
Nr2f1	0.95	0.21	U10995_g_at	Nuclear receptor subfamily 2, group F, member 1
Pdcd4	1.00	0.14	rc_AI172247_at	Programmed cell death 4
Pdgfra	1.10	0.28	rc_AI232379_at	Platelet derived growth factor receptor, α polypeptide
Pla2g2a	3.60	0.00	X51529_at	Phospholipase A2, group II A (platelets, synovial fluid)
Ptn	2.10	0.57	rc_AI102795_at	Pleiotrophin
Scg3	2.70	0.85	U02983	Secretogranin III
Serping1	0.85	0.21	rc_AA800318_at	Serine (or cysteine) peptidase inhibitor, clade G, member 1
Smad7	5.35	1.20	AF042499_at	MAD homolog 7 (Drosophila)
Sod3	1.05	0.07	Z24721_at	superoxide dismutase 3, extracellular
Zfp423	1.85	1.47	U92564_at/U92564_g_at	Zinc finger protein 423

The average change in expression after Smad7 overexpression is given as log₂ fold. SD: Square root of the variance; NF κ B: Nuclear factor κ B.

in “culture activated” cells compared to “*in vivo* activated” cells. This leaves a final evaluation of Smad7 influence on the regulation of these genes in HSC activation processes open.

Confirmation of array data using quantitative real-time PCR

To validate our microarray results, we selected 12 genes from array data identified as highly regulated in dependency to Smad7 for RT-qPCR analysis. Transdifferentiating (3 d in culture) and fully activated (7 d in culture) HSCs were investigated. TGF- β RI mRNA expression is not modulated during transdifferentiation^[15,16] and was used as the expression reference. A synopsis of Smad7 associated modulation of gene expression, given in Figure 4 as log₂ fold of LacZ, generally supports the array results. We con-

firmed upregulation of Cyp4B1, BMP2, SGIII, Zfp423, Pla2g2a and downregulation of EST189231, Olr1 and Id1 (Table 4) independent of time during the transdifferentiation process.

Interestingly, when comparing 3 d- with 7 d-HSCs, opposite effects of Smad7 were found for HK2 (0.38-fold in 3 d-, 3.85-fold in 7 d-HSCs), Slc16a3 (0.59-fold in 3 d-, 2.25-fold in 7 d-HSCs) and VEGF.1 (0.51-fold in 3 d-, 1.07-fold in 7 d-HSCs), underlining temporal differences and modulation of the TGF- β signal during HSC activation^[15].

Smad7 inhibits BMP2 dependent Smad1 expression

BMP2 was strongly upregulated in Smad7 expressing HSCs (Table 2, Figure 4A and B). Here, we further demonstrate that nevertheless Smad7 blunted BMP2 and

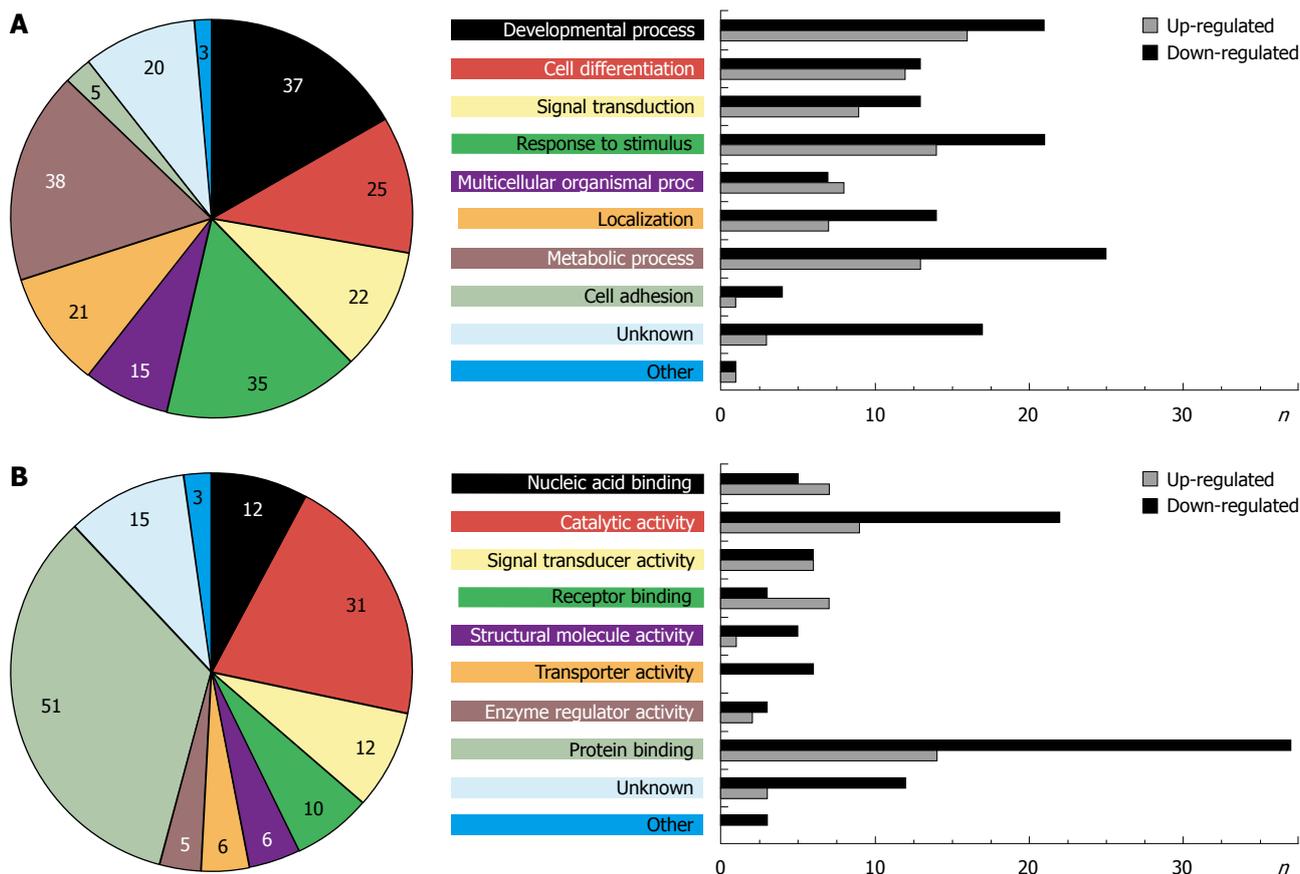


Figure 1 Genes whose expression levels were changed ($n = 100$) after overexpression of Smad7 in hepatic stellate cells are matched to 8 gene ontology annotations using GoMiner^[13]. Left part: Percentage of genes matching to the given gene ontology. Note the total percentage is greater than 100% as the same regulated genes can be assigned to different annotations; Right part: Bar diagram shows number of upregulated (grey bars) and downregulated (black bars) genes matching to the given gene ontology (unknown = percentage/number of genes without annotation, other = percentage/number of genes which are not assignable to the given annotations). A: GO group: biological process; B: GO group: molecular function.

TGF- β dependent signalling *via* Smad1 upon AdSmad7 infection in transdifferentiating (4 d in culture) rat HSCs (Figure 5) and infected CFSC (data not shown). Fully activated (7 d in culture) HSCs, which are insensitive to TGF- β , remain responsive to BMP2 mediated Smad1 phosphorylation, show the same tendency when stimulated with BMP2.

DISCUSSION

Using the Affymetrix Microarray approach, we systematically analyzed the effects of Smad7 overexpression during HSC transdifferentiation. About 100 genes were identified to be regulated upon Smad7 overexpression. For obvious reasons, only some of the regulated genes can be discussed below in detail. Nevertheless, all gene expression changes found constitute potential starting points for future research projects to unravel the process of liver fibrogenesis.

Tumor suppressor genes were upregulated by Smad7 overexpression in HSCs

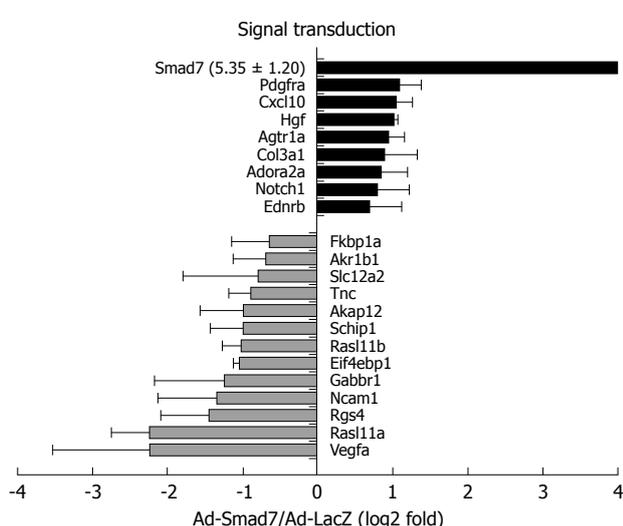
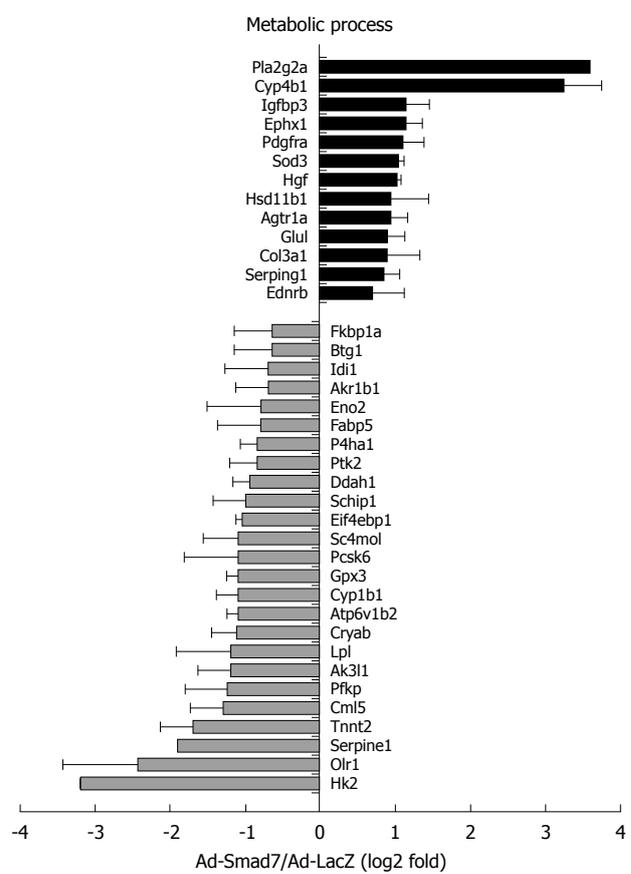
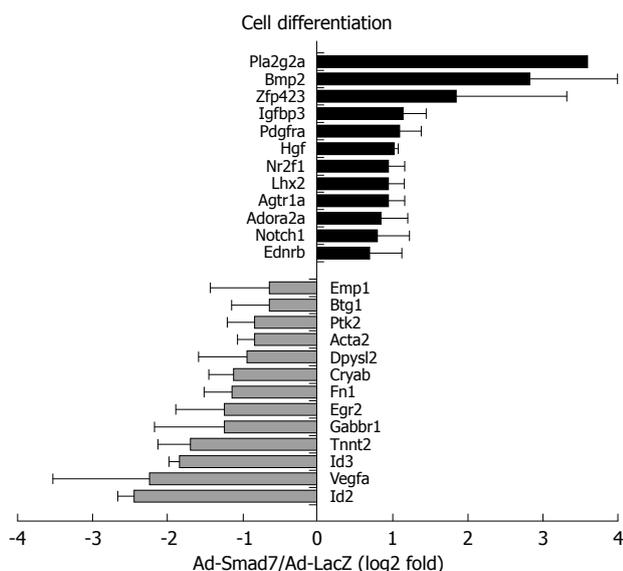
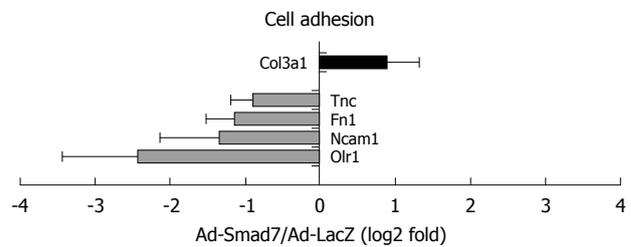
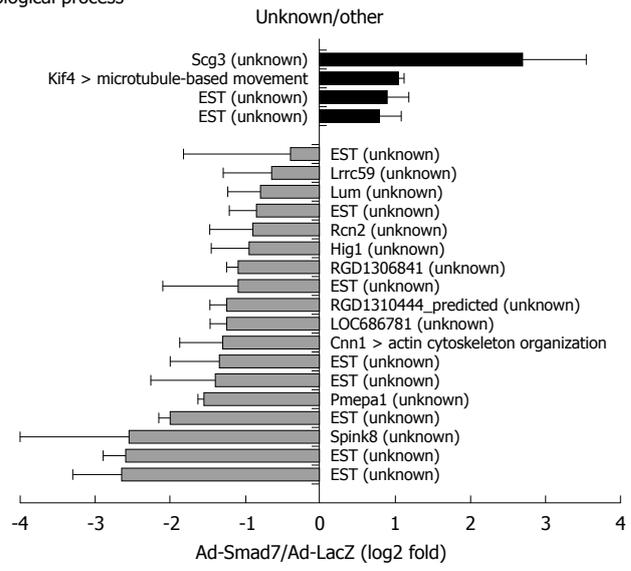
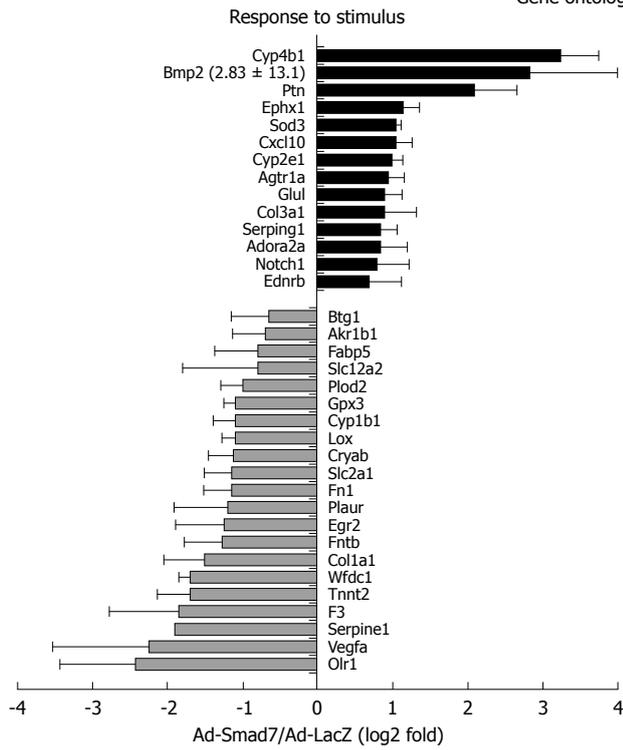
Pla2g2a and Cyp4B1 were strongly upregulated after Smad7 overexpression in HSCs. Pla2g2a participates in lipid metabolism/catabolism and was previously described

as a tumor repressor in different cancer models, i.e. intestinal tumorigenesis, neuroblastoma, melanoma and colon cancer cell lines^[17,18]. VEGF and Glut1, both known to be upregulated in tumor cells^[19,20] were Smad7 dependently downregulated in HSCs. These results suggest an influence of Smad7 on tumor development and progression which is a long debated issue considering its regulative impact on ambiguous TGF- β signaling in tumorigenesis.

Cytochrome P450s are haem-thiolate proteins involved in oxidative degradation of particularly environmental toxins and mutagens and play a role in electron transport reactions. Additionally, they are key players in alcohol induced oxidative stress in liver, causing hepatocyte necrosis, apoptosis and liver fibrosis^[21]. During steatosis, lipid peroxidation by Cyp2E1 is associated with inflammation and HSC activation including increased TGF- β production, possibly through up-regulation of KLF6^[22]. Members of the Cyp P450 family are also upregulated during HSC activation^[14].

Interestingly, overexpression of Smad7 increased the expression of some members of the Cytochrome P450 system through HSC activation, i.e. Cyp4B1 which is important in the metabolism of drugs, cholesterol, steroids and lipids, and Cyp2E1, while others are downregulated

Gene ontology: biological process



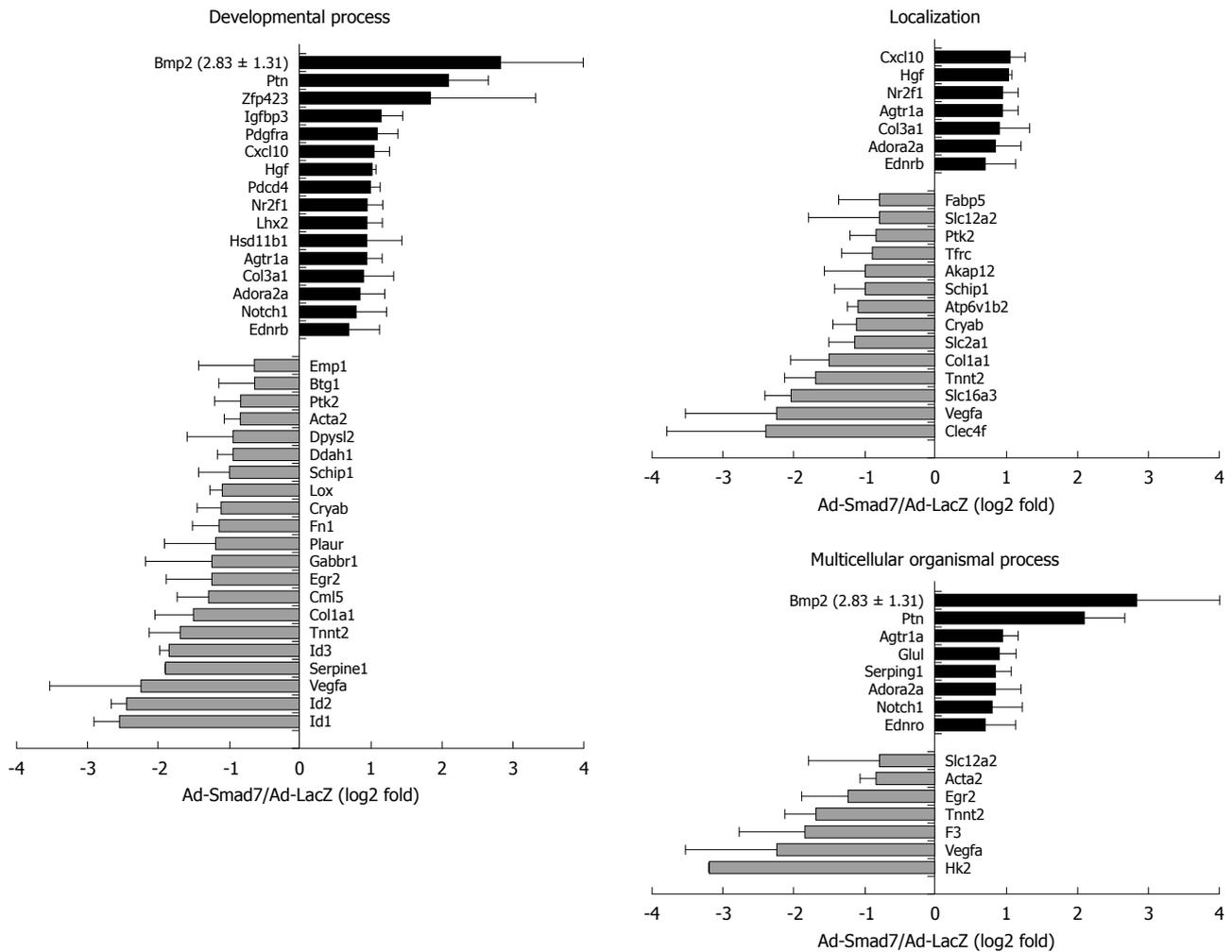
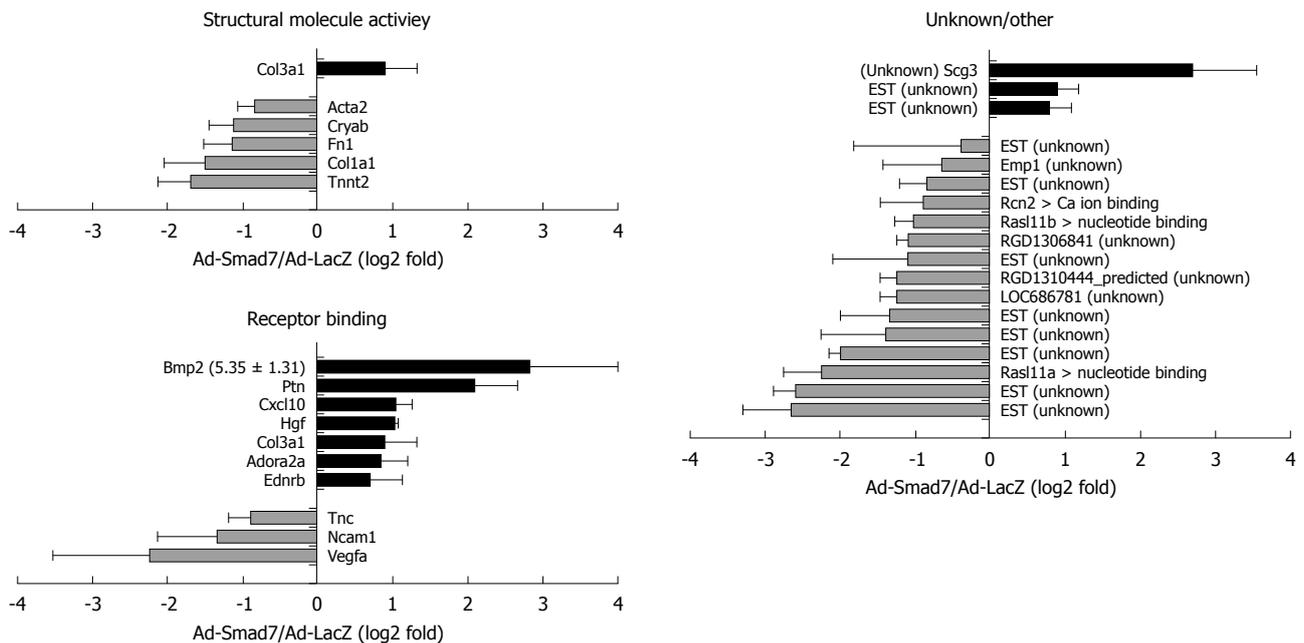


Figure 2 Genes with changed expression levels after overexpression of Smad7 are matched to 8 gene ontology terms of the biological process and to unknown/other. Unknown: Genes without annotation; Other: Genes with another annotation not assignable to the given annotations, details in brackets. Change of expression is given as log2 value of the fold factor with the SD. Black bars: Upregulated; Gray bars: Downregulated.

Gene ontology: molecular function



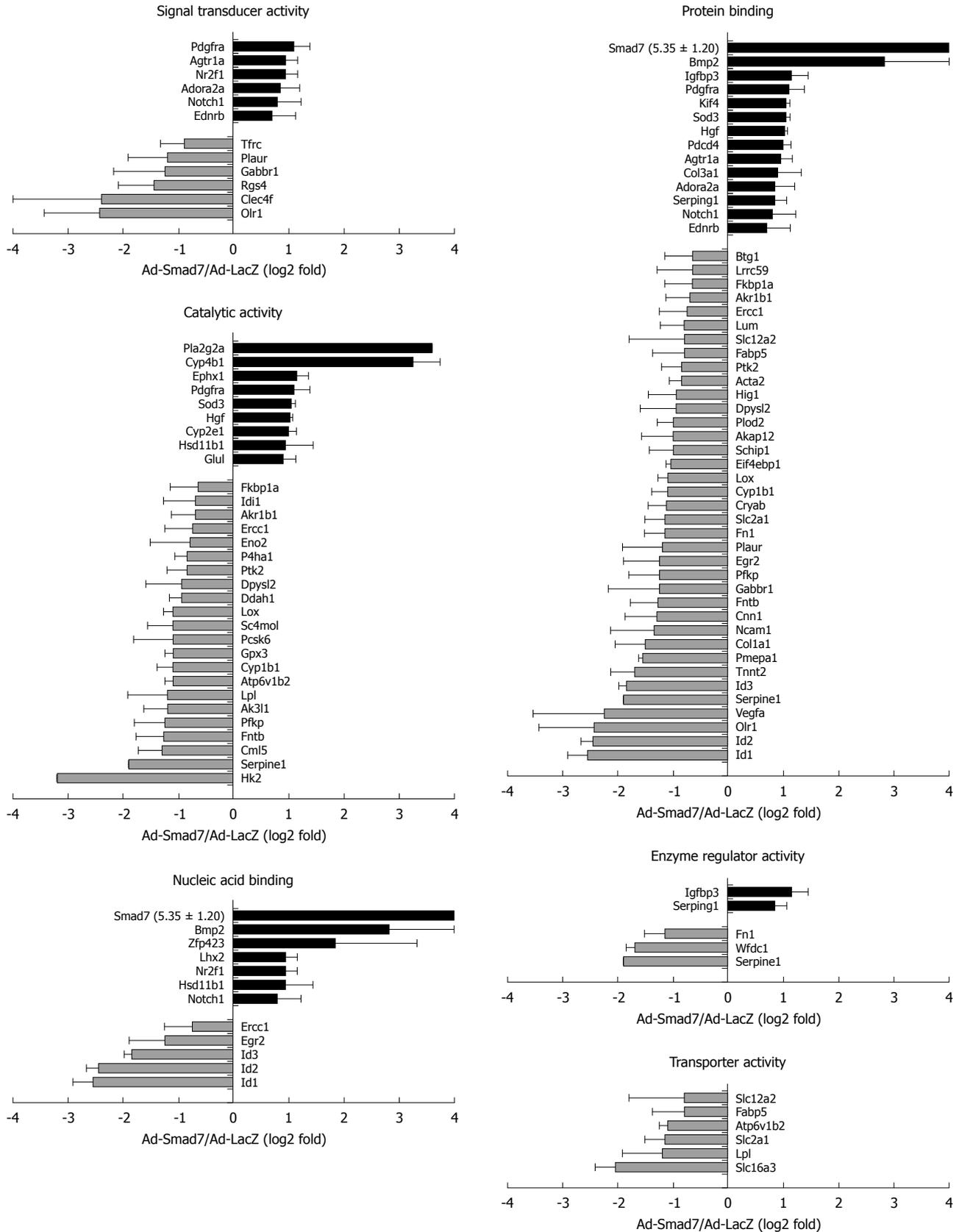


Figure 3 Genes whose expression levels were changed after overexpression of Smad7 are matched to 8 gene ontology terms of the molecular function and to unknown/other. Unknown: Genes without annotation; Other: Genes with another annotation not assignable to the given annotations, details in brackets. Change of expression is given as log2 value of the fold factor with the SD. The term nucleic acid binding includes the annotations nucleic acid binding, transcription factor activity, RNA binding, and transcription regulator activity. Black bars: Upregulated; Gray bars: Downregulated.

Table 3 Comparison of gene regulation in activated hepatic stellate cells *in vivo* (De Minicis *et al.*¹³¹)

Gene symbol	Smad7 overexpressing HSCs	<i>In vivo</i> activated untransformed HSCs
Acta2	↓	↑
BMP2 ¹	↑	↓
Cnn1	↓	↑
Col1a1	↓	↑
Col3a1	↑	↑
Cryab	↑	↓
Cyp1b1	↓	↑
Ddah1	↓	↑
Ednrb	↑	↑ ²
Eno2	↓	↓
Ephx1	↓	↑ ²
Fn1	↓	↑
Gabbr1	↓	↓
Hgf	↑	↑ ²
Hk2 ¹	↓	↑
Hsd11b1	↓	↑ ²
Id1	↓	↓
Igfbp3	↑	↑ ²
Kif4	↑	↑
Lox	↓	↑
Lpl	↓	↑ ²
Lum	↓	↑
Ncam1	↓	↑
P4ha1	↓	↑
Pdgfra	↑	↓
Pfkf	↓	↑
Plod2	↓	↑
Rasl11b	↓	↑
Serping1	↑	↑
Slc16a3	↓	↑
Slc2a1	↓	↑
Sod3	↑	↑
Tmepai_predicted	↑	↓ ²
Tnc	↓	↓ ²
Tnnt2	↓	↑
VEGFa ¹	↓	↑ (VEGFa) ¹
Wfdc1	↓	↑ ²

Gene expression profiles during hepatic stellate cell activation in culture and *in vivo* (*Gastroenterology* 2007; 132: 1937-1946¹³¹) and Smad7 overexpressing hepatic stellate cells (HSCs) (our study). ¹Genes regulated the strongest in our study are marked; ²The regulation of *in vivo* activated HSCs which is different compared to culture activated HSCs in De Minicis study. In total 37 genes overlap in both studies, 22 of those (60%) are oppositely regulated indicating participation of transforming growth factor-β/Smad7 on the regulation of those genes *in vivo*.

upon Smad7 overexpression, e.g. Cyp1B1. These ambiguous effects probably reflect the complex control of oxidative metabolism in the cell.

Glucose metabolism and angiogenesis/vascularisation is downregulated by Smad7

Hk2 is a hexokinase, one of the best known enzymes of glycolysis, and is involved in cell cycle progression. According to the results of the microarray analysis it represents the most downregulated gene in AdSmad7 infected HSCs. One feature of activated HSCs is the ability to proliferate. TGF-β antagonizes proliferation in quiescent HSCs, whereas it has a growth promoting effect in transdifferentiated MFBs. Thus, Hk2 might be induced by TGF-β in HSCs during activation, subsequently stimulating HSC

Table 4 Comparison of gene regulation according to quantitative real-time polymerase chain reaction analysis and array analysis

Gene	Probe set ID	Array	RT-PCR analysis
Cyp4B1	M29853_at	Up	Up
Smad7	AF042499_at	Up	Up
BMP2	L02678_at/ rc_AA997410_s_at	Up	Up
SGIII	U02983_at	Up	Up
Zfp423	U92564_at/ U92564_g_at	Up	Up
Pla2g2a	x51529_at	Up	Up
EST189231	AA799734_at	Down	Down
Olr1	AB005900_at/ AB018104cds_s_at/ rc_AI071531_s_at	Down	Down
ID1	L23148_g_at	Down	Down
HK2	D26393exon_s_at	Down	3 d down/7 d up
Slc16a3	U87627_at	Down	3 d down/7 d up
VEGFa/ratVEGF.1 in RT-PCR	L20913_s_at/ M32167_g_at	Down	3 d down/7 d up

Different results in array and quantitative real-time polymerase chain reaction (RT-PCR) analysis are marked bold.

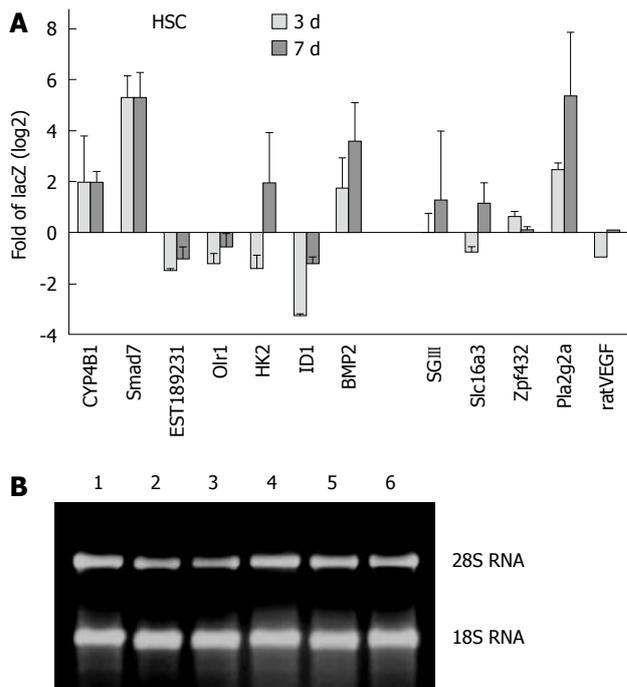


Figure 4 Validation of microarray results using quantitative real-time polymerase chain reaction. **A:** SYBR Green I-based real-time quantification to compare the mRNA expression patterns of 12 selected genes in hepatic stellate cell which were infected either with AdLacZ or AdSmad7. Transforming growth factor-β RI, not affected by Smad7 overexpression, served as a house-keeping gene. Results are given as relative expression of log2 fold of LacZ. 3 d (light grey column) and 7 d (dark grey column): 3 d and 7 d after adenoviral infection. Values are the mean of three measurements each performed in duplicates ± SD from independent experiments; **B:** Total RNA purity and integrity was verified by formaldehyde agarose gel electrophoresis. Lane 1: LacZ, 7 d; Lane 2: LacZ, 3 d; Lane 3: Smad7, 7 d; Lane 4: Smad7, 3 d; Lane 5: Untreated control, 7 d; Lane 6: Untreated control, 3 d.

proliferation and thus providing at least part of the growth stimulatory effect of TGF-β. Although physiological ef-

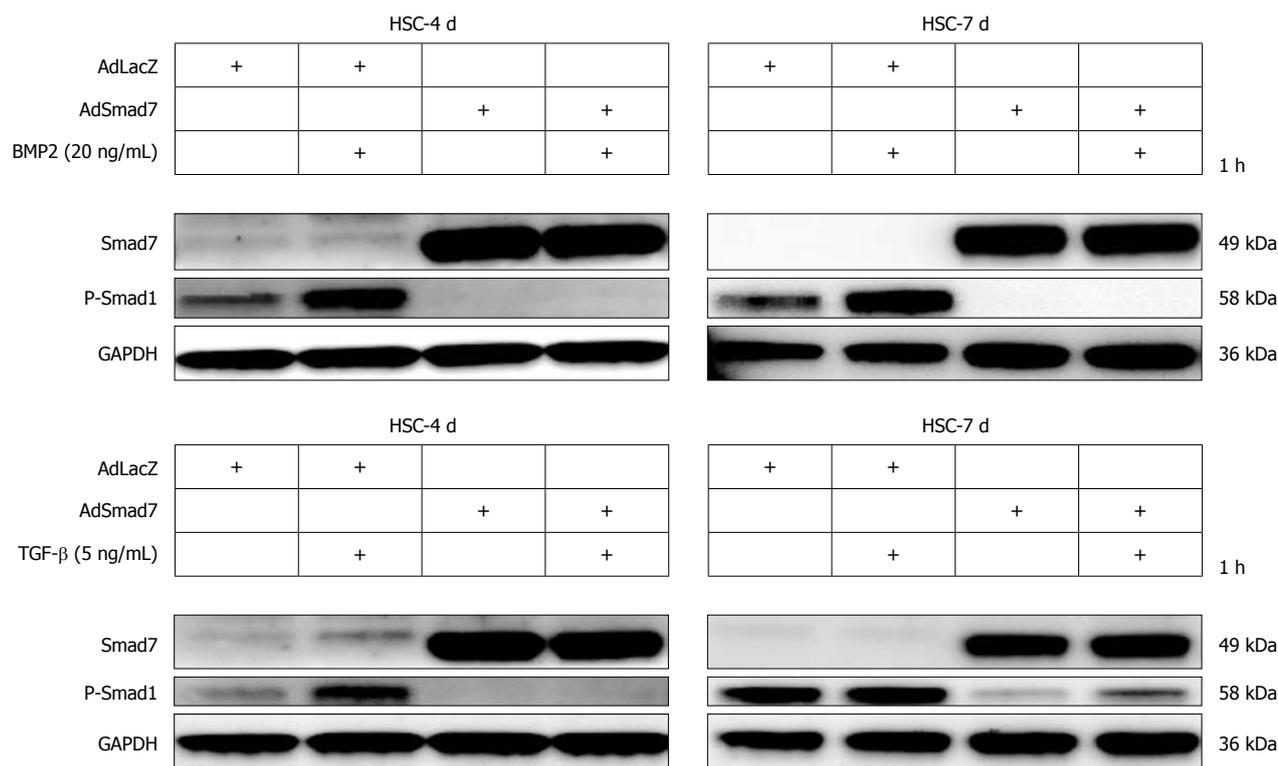


Figure 5 Smad7 overexpression inhibits BMP2 and transforming growth factor- β dependent Smad1 phosphorylation. Transdifferentiating (4 d old) and fully activated (7 d old) hepatic stellate cells (HSCs) infected or non-infected with either AdLacZ (control) or AdSmad7 were stimulated for 1 h with 20 ng/mL BMP2 or 5 ng/mL transforming growth factor (TGF)- β as indicated. Smad7 overexpression and Smad1 phosphorylation were analysed using Western blottings. GAPDH served as a reference. While transdifferentiating HSCs are sensitive to both BMP2 and TGF- β stimulation, fully activated HSCs are only responsive to BMP2.

fects of glucose metabolism in the liver are traditionally associated to hepatocytes and provide a direct link to fibrogenesis *via* hyperglycemia and insulin resistance^[23-25], one could speculate that activated HSCs need more energy and thus, glycolysis is upregulated TGF- β dependently in this cell type. In line, HSCs become sensitive to glucose signaling during activation, high glucose concentrations stimulate ROS production through PKC-dependent activation of NADPH oxidase and induce MAP kinase phosphorylation subsequent to proliferation and type I collagen production in this cell type^[26] suggesting a crucial role of HSC-sugar metabolism in fibrogenesis.

Upregulation of Hk2 during activation of HSCs further suggests that glycolysis induction and increased levels of involved proteins may occur by other means than elevated blood glucose levels^[14], our study). This in turn indicates a direct connection between fibrosis and enhanced glycolysis independent of inducing external stimuli of either process.

Beside Hk2 regulation, other genes encoding enzymes of glycolysis (Eno2, PFKP) or related to glucose metabolism were downregulated Smad7 dependently, e.g. VEGFa, PAI-1 (Serpin1), F3, Slc2a1 (Glut1), FN1, EIF4ebp1 and PTK2 (Figure 6). A list of all references proving the relation of these genes to glucose metabolism will be provided to interested readers on request.

Glut1 is a glucose transporter protein which becomes upregulated in activated HSCs or upon HSC activation^[14]. Since Smad7 decreases Glut1 expression levels and other

proteins involved in glycolysis, TGF- β seems to enhance glucose metabolism and energy supply during HSC activation thus enabling the cells to proliferate and transdifferentiate towards activated myofibroblasts.

In contrast, decreased numbers of Glut1 molecules are reported in hepatocytes subjected to chronic alcohol consumption^[27] resulting in a reduced availability of glucose for glycolysis in hepatocytes. The resulting energy deficiency has been shown to impair this cell type's ability to perform critical functions and to contribute therefore to cell death and alcoholic liver disease.

In line with our results, relations between glucose metabolism and fibroproliferative processes were identified in other organs. For example in human kidney^[28,29] exposure of proximal tubule cells and cortical fibroblasts to high extracellular glucose concentrations results directly in altered cell growth and collagen synthesis.

IGFBP3 and Cyp2E1, known to participate in glucose metabolism were upregulated in AdSmad7 infected HSCs, indicating that they might be under negative control through TGF- β . However, upregulation of IGFBP3 in our study could be simply due to "culture" but not "*in vivo* activation" of HSCs (for term definition compare^[14]) instead of being mechanistically important. Interestingly, Smad7 even seems to enhance the upregulation of IGFBP3, which already occurs upon HSC activation. If there is any pathologic relevance of this finding, it suggests a mechanism of regulation independent of canonical TGF- β /Smad7 signaling in HSC activation.

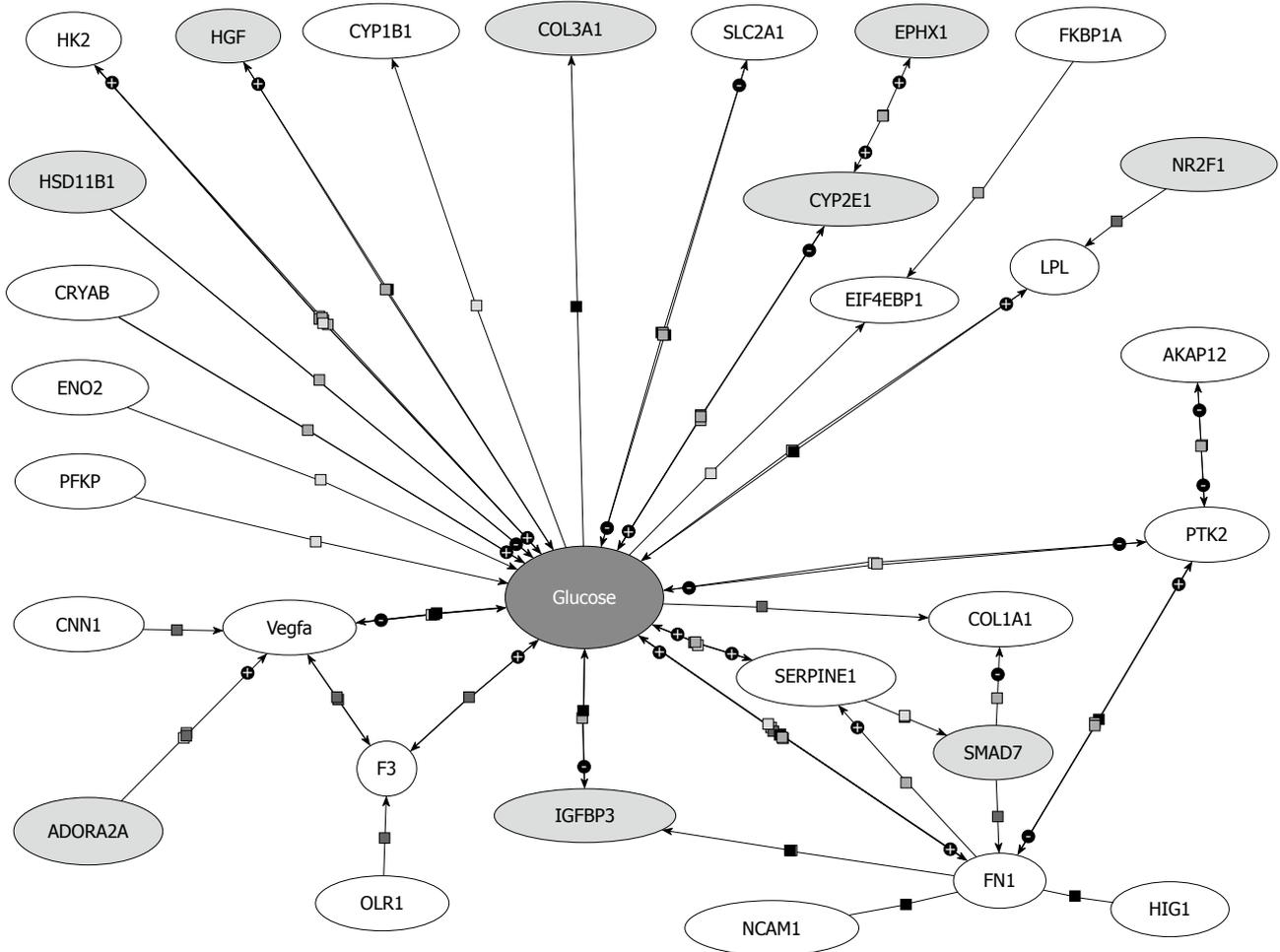


Figure 6 Biological interaction between glucose and genes up- (light grey) or down-regulated (white) in primary hepatic stellate cells after overexpression of Smad7. Genes linked to glucose by binding or regulatory interactions are depicted as interconnecting lines between glucose and the gene symbols. Pathway analysis was done with Pathway Architect software (Stratagene).

VEGFs are growth factors involved in angiogenesis, vasculogenesis and endothelial cell growth, promotion of cell migration, apoptosis inhibition and induction of blood vessel permeabilization. De Minicis *et al*^[14] showed VEGF_c to be upregulated^[14], while in the present report VEGF_a was downregulated after Smad7 overexpression in activated HSCs, indicating its induction as a response to profibrogenic TGF- β signaling. Previous investigation of hypoxia in a stellate cell line demonstrates upregulation of VEGF expression^[30]. Hypoxia leads to cell dysfunction or death and occurs during liver damage and inflammation. HIF1, considered to be the major regulator of about 100 genes including VEGF and PAI-1, is also upregulated in that study. In contrast HIF1 did not display an altered expression in our study indicating that HIF1 expression in HSCs is TGF- β independent and that another TGF- β dependent route exists to induce PAI-1 (serpine1) and VEGF_a expression.

Smad7 decreases cell adhesion regulators in HSCs

Expression of several proteins linked to cell adhesion, i.e. Olr1, Ncam1, Fn1 and Tnc was decreased after Smad7 overexpression in HSCs. Accordingly, Ncam1 and Fn1

were upregulated in activated HSCs^[14]. Although for Olr1 no information about the regulation in activated HSCs is available so far, we assume from our results that Smad7 antagonizes cell adhesion features of activated HSCs. This suggests that profibrogenic TGF- β signaling improves cell adhesion for transdifferentiating HSCs. Nevertheless it should be noted that downregulation of Tnc in activated HSCs is supported by Smad7.

Smad7 induces BMP2 expression in HSCs

Generally, TGF- β signals *via* Smad2 and Smad3 but also induces the second canonical pathway *via* ALK1/Smad1/5/8. BMP2, another member of the TGF- β family, solely signals *via* Smads1/5/8 utilizing ALK3 and ALK6^[12]. Here we show that (1) BMP2 was strongly upregulated in Smad7 expressing HSCs (Table 2, Figure 4A and B); and (2) Smad7 potently inhibited BMP2 dependent and TGF- β dependent Smad1 phosphorylation. Even in fully activated HSCs which are not responsive to TGF- β concerning Smad1 phosphorylation, BMP2 dependent Smad1 phosphorylation was abolished (Figure 5).

These results indicate a tight crosstalk between TGF- β and BMP signaling pathways in HSCs. It seems that HSCs

try to keep up a functional Smad1 signaling upon blocking TGF- β pathways with Smad7. Accordingly, BMP2 is capable of inducing Smad1 signaling in fully activated 7 d-HSCs which are no longer responsive to TGF- β stimulation. Thus BMP2 expression might be induced to overcome a lack of TGF- β /Smad1 signaling upon Smad7 expression or HSC activation using a corresponding auto-crine loop. Although our *in vitro* experiments demonstrate that Smad7 is able to inhibit BMP2/Smad1 signaling effectively, Smad7 dependent induction of BMP2 expression in HSCs *in vivo* might be strong enough to sustain an active Smad1/5/8 signaling pathway. Further experiments could delineate whether BMP2 expression is directly induced by the recently described DNA binding activity of Smad7^[31], if a running TGF- β signaling pathway has a negative regulatory role toward the BMP2 promoter or if other mechanisms are responsible for BMP2 induction in Smad7 overexpressing HSCs.

In summary we conclude that genes regulated contrarily during HSC activation^[14] vs ectopic Smad7 expression (this study) most probably represent critical profibrogenic components. As Smad7 is able to blunt HSC transdifferentiation *in vitro* and *in vivo*^[7] we assume glucose metabolism and the crosstalk between the TGF- β and the BMP2 pathways are critical components of HSC activation.

In general our study underlines the potential of top down systemic approaches to delineate effects of cell signaling regulation and opens the opportunity to find targets for drug development.

COMMENTS

Background

Activation of hepatic stellate cells (HSCs) as a consequence of liver damage includes proliferation and extracellular matrix (ECM) deposition and represents a major step in fibrogenesis. Transforming growth factor (TGF)- β is a master contributor and its signaling pathway is modulated during the HSC activation process, whereby its cytostatic action is lost and ECM producing effects become predominant. Smad7 is a powerful antagonist of TGF- β . Expression of Smad7 is transiently induced by the canonical TGF- β /R-Smad signaling cascade, thereby providing a negative feedback loop to regulate TGF- β signals. Smad7 is able to inhibit HSC transdifferentiation and attenuate the extent of fibrosis, suggesting Smad7 is a promising antifibrotic compound.

Research frontiers

The findings offer important new information about the process of HSC transdifferentiation and fibrogenesis as well as cell biology of signal transduction in the liver. Moreover, providing a list of genes previously not known as participants in HSC activation and fibrogenesis, members of the field may use these data as starting points to get new insight into mechanisms of HSC (patho)physiology. Thus, it will definitely be of interest to the scientific community, especially in the field of hepatology and gastroenterology.

Innovations and breakthroughs

In the present report, the authors systematically investigated transcriptional effects of Smad7 overexpression in cultured HSCs by microarray analysis. Using this powerful top down approach, the authors identified 100 target genes to be significantly regulated by Smad7 overexpression. These represent potential targets for delineating mechanisms of HSC activation and to set up therapeutic approaches. The results imply a crosstalk between TGF- β and BMP2 signaling pathways in HSCs and for the first time a significant involvement of glucose metabolism in the HSC transdifferentiation processes.

Applications

The results are of special interest for future attempts to understand the process

of stellate cell activation and to set up TGF- β and/or Smad7 directed treatment approaches in chronic liver diseases, especially as they reflect the most powerful negative regulatory process of TGF- β signaling.

Terminology

Bone morphogenetic protein (BMP): BMPs are multi-functional growth factors belonging to the TGF- β superfamily. BMPs were originally discovered by their ability to induce the formation of bone and cartilage, but are now considered to constitute a group of pivotal morphogenetic signals, orchestrating tissue architecture throughout the body. BMP signals are mediated by type I and II BMP receptors and their downstream molecules Smad1, 5 and 8. Microarray: A method for profiling gene and protein expression in cells and tissues. A microarray consists of different nucleic acid/protein probes that are chemically attached to a substrate, which can be a microchip, a glass slide or a microsphere-sized bead. Hybridization of test samples to these probes can be measured by different means.

Peer review

This is a potentially interesting study aimed at clarifying Smad7-regulated gene expression during the transdifferentiation of hepatic stellate cells, a major profibrogenic cell type in the liver. Overall, the study is well-performed and the manuscript is well-written.

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Transient elastography: A non-invasive tool for assessing liver fibrosis in HIV/HCV patients

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Abstract

AIM: To assess the prevalence of advanced liver fibrosis (ALF) in human immunodeficiency virus (HIV), hepatitis C virus (HCV) and HIV/HCV patients using transient elastography, and to identify factors associated with ALF.

METHODS: Between September 2008 and October 2009, 71 HIV mono-infected, 57 HIV/HCV co-infected and 53 HCV mono-infected patients on regular follow-up at our Center were enrolled in this study. Alcohol intake, the main parameters of liver function, presence of HCV-RNA, HIV-RNA, duration of highly active anti-retroviral

therapy (HAART) and CD4 cell count were recorded. ALF was defined as liver stiffness (LS) ≥ 9.5 kPa. To estimate liver fibrosis (LF) a further 2 reliable biochemical scores, aspartate aminotransferase platelet ratio index (APRI) and FIB-4, were also used.

RESULTS: LS values of co-infected patients were higher than in either HIV or HCV mono-infected patients ($\chi^2_{MH} = 4, P < 0.04$). In fact, LS ≥ 9.5 was significantly higher in co-infected than in HIV and HCV mono-infected patients ($\chi^2 = 5, P < 0.03$). Also APRI and the FIB-4 index showed more LF in co-infected than in HIV mono-infected patients ($P < 0.0001$), but not in HCV mono-infected patients. In HIV/HCV co-infected patients, the extent of LS was significantly associated with alcohol intake ($P < 0.04$) and lower CD4+ cell count ($P < 0.02$). In HCV patients, LS was correlated with alcohol intake ($P < 0.001$) and cholesterol levels ($P < 0.03$). Body mass index, diabetes, HCV- and HIV-viremia were not significantly correlated with LS. In addition, 20% of co-infected patients had virologically unsuccessful HAART; in 50% compliance was low, CD4+ levels were < 400 cells/mm³ and LS was > 9.5 kPa. There was no significant correlation between extent of LF and HAART exposure or duration of HAART exposure, in particular with specific dideoxynucleoside analogues.

CONCLUSION: ALF was more frequent in co-infected than mono-infected patients. This result correlated with lower CD4 levels. Protective immunological effects of HAART on LF progression outweigh its hepatotoxic effects.

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Key words: Liver fibrosis; Transient elastography; Aspartate aminotransferase platelet ratio index; FIB-4 test; Fibrosis evaluation; Human immunodeficiency virus infection; Hepatitis C virus infection

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INTRODUCTION

In the last few years, liver disease associated with hepatitis C virus (HCV) has emerged as a significant problem in human immunodeficiency virus (HIV)-infected patients, thanks to improved survival in the highly active antiretroviral therapy (HAART) era^[1]. It has been reported that HIV and HCV co-infection leads to a more rapid progression of liver disease to cirrhosis^[2,3]. Other factors such as severe immune suppression and alcohol consumption accelerate the progression of HCV-related fibrosis^[4,5]. Virologically successful HAART slows the progression of liver fibrosis (LF) and reduces hepatic necroinflammatory activity in HIV/HCV co-infected patients^[2,6]. In contrast, antiretroviral-related liver toxicity could contribute to liver damage in HIV- and HIV/HCV-infected patients^[7]. Mitochondrial toxicity of nucleoside analogues^[8], and glucose or lipid abnormalities, such as hyperglycemia and lipodystrophy, which are particularly common when using some protease inhibitors^[9], may produce or enhance LF progression in HIV mono- and HIV/HCV co-infected patients. Currently, in this respect, a growing number of cases of cryptogenetic liver disease in symptomatic and asymptomatic HIV-infected patients has been reported^[10,11].

Percutaneous liver biopsy is the gold standard for assessing LF. However, it may be associated with sampling variability^[12], is an invasive technique with rates of morbidity of 3% and mortality of 0.03%^[13,14], and as a consequence, is not suitable for repeated assessment, which is required when monitoring LF.

For these reasons, new non-invasive methods for the assessment of LF have been developed. Transient elastography (TE) (Fibro-Scan[®]; EchoSens, Paris, France) is a rapid, reliable and tolerable imaging technique for the assessment of LF by measuring liver stiffness (LS)^[15,16].

On the other hand, many biochemical markers have been implemented to estimate LF, with the aim of reducing the number of liver biopsies^[14].

The advent of TE and biochemical markers has been demonstrated to be very helpful in the non-invasive measurement of LF, particularly in asymptomatic HIV-infected patients in whom liver biopsy is not recommended^[11]. TE has already been validated for the measurement of LF in HIV and HCV seropositive patients^[17,18].

The aim of this study was to assess the prevalence of

LF and cirrhosis in a group of HIV mono-infected, HCV mono-infected and HIV/HCV co-infected patients using TE and biochemical markers. In addition, we evaluated which of the factors studied correlated with advanced LF (ALF) and cirrhosis.

MATERIALS AND METHODS

Study population

Between September 2008 and October 2009 all consecutive HIV mono-infected and HIV/HCV co-infected patients on regular follow-up at the AIDS Center of the University of Palermo, as well as HCV mono-infected patients seen consecutively at the Outpatient Clinic of the Department of Clinical Medicine and Emerging Pathologies of the University of Palermo were enrolled in this study.

Information on age, gender, risk factors for HCV and HIV infections, cumulative exposure to non-nucleoside and nucleoside reverse-transcriptase inhibitors, protease inhibitors and specific antiretroviral drugs within each class were all recorded in a database designed for this study.

For all HIV-infected patients the absolute number of CD4+ T-cells and plasma HIV-RNA levels was assessed. In HCV-infected patients, HCV-genotype and plasma HCV-RNA levels were also recorded. In addition, at baseline, complete blood cell counts, alanine aminotransferase (ALT), aspartate aminotransferase (AST), γ -glutamyl transferase (γ GT), total cholesterol, high-density lipoprotein cholesterol, low-density lipoprotein cholesterol, triglycerides and glycemia were measured.

Alcohol intake > 20 g/d either at the time of the study or in the past was recorded through patient interviews. Diabetes or impaired fasting glucose (IFG) were defined according to the Expert Committee on the Diagnosis and Classification of Diabetes Mellitus criteria^[19].

Patients with acute liver decompensation, hepatocellular carcinoma or chronic hepatitis B were excluded.

The study protocol conformed to the ethical guidelines of the 1975 Declaration of Helsinki. Patients were enrolled after written informed consent was obtained.

Assessment of LF

LF was assessed by a single certified operator (trained by the manufacturer) using TE (FibroScan[®]; EchoSens, Paris, France). TE provides an assessment of LS expressed in kPa units. In brief, an ultrasound transducer probe is mounted on the axis of a vibrator. Vibrations of mild amplitude and low frequency are transmitted by the transducer, inducing an elastic shear wave that propagates through the underlying tissues. The speed of propagation of this vibration across the liver is directly related to tissue stiffness.

The tip of the probe transducer was placed in the intercostal spaces at the right lobe of the liver. Only patients with 10 valid elastometric measures, interquartile ranges > 30% and \geq 60% success rate (the number of validated

measurements divided by the total number of measurements) were considered to be reliable. ALF (severe fibrosis and cirrhosis) was defined as a median LS of 9.5 kPa. As previously published, this cut-off value is strongly correlated with a Metavir score of F3, both in HCV mono-infected and HCV/HIV co-infected patients^[17,18].

LF was also assessed biologically using 2 different well-validated indices, the aspartate aminotransferase platelet ratio index (APRI) index and the FIB-4 index. The APRI was calculated as follows: AST/upper limit of normal \times 100/platelet count ($10^9/L$)^[20,21]. The FIB-4 index was calculated as follows: age \times AST (IU/L)/{[platelet count ($10^9/L$)] \times [ALT (IU/L)]^{1/2}}^[22]. The prevalence of ALF was estimated using as a reference a FIB-4 index $>$ 3.25 and an APRI index $>$ 1.5^[20,22].

Statistical analysis

When data distribution was Gaussian, values were expressed as mean \pm SD and their differences were calculated using the Student *t*-test; otherwise, data were expressed as the median and range and analyzed using the Mann-Whitney *U* test. Fisher's exact and χ^2 tests, the χ^2 test of Mantel Haenszel, Spearman's rank correlations (ρ) and Pearson's correlation (*r*) were used where appropriate. Multiple linear regression analysis was used to study the association between increased values of LS and variables statistically significant at univariate analysis. All analyses were performed using the SPSS software package (version 13.0; Chicago, IL, USA).

RESULTS

Study population

A total of 201 patients on regular follow-up at both our Centers were enrolled in the study.

In 11 patients (4 HIV mono-infected, 6 HCV mono-infected and one co-infected) a valid elastometric assessment could not be obtained because of truncular obesity, therefore 190 patients were finally included in this study. There were 137 HIV-infected patients, including 71 HIV mono-infected and 66 HIV/HCV co-infected, and 53 HCV mono-infected patients. Patient characteristics at the time of LS measurement are summarized in Table 1.

HIV patients were significantly younger than HCV mono-infected individuals ($P < 0.002$). Body mass index (BMI) was significantly higher in HCV mono-infected patients than in HIV and HIV/HCV co-infected patients ($P < 0.002$). The most frequent risk factor of HCV contamination was intravenous drug use in co-infected *vs* mono-infected HCV patients ($P < 0.0001$), while it was transfusion of blood products in HCV mono-infected *vs* co-infected patients ($P < 0.0001$). Most HIV mono-infected (80.2%) and HIV/HCV co-infected patients (90.9%) were under HAART. However, only 62% of HIV mono-infected and 68% of HIV/HCV co-infected patients had an HIV-RNA load of $<$ 47 copies/mL. In addition, 20% of co-infected patients had virologically unsuccessful HAART; in 50% compliance was low, and CD4+ levels were $<$ 400 cells/mm³. HIV/HCV co-infected patients

Table 1 Demographic characteristics of the study populations (mean \pm SD) *n* (%)

	HIV (<i>n</i> = 71)	HCV (<i>n</i> = 53)	HIV/HCV (<i>n</i> = 66)
Age (yr)	43.3 \pm 10.3 ^a	49.7 \pm 12.5	45.6 \pm 12.5
Male gender	50 (70)	36 (67.9)	49 (74.2)
BMI (kg/m ²)	23.6 \pm 3.4 ^a	26.0 \pm 3.6	22.8 \pm 3.0 ^b
Risk group			
Transfusion	-	17 (32.1)	4 (6.1) ^b
Homosexual men	21 (29.5)	-	1 (1.5)
Intravenous drug use	4 (5.6)	7 (13.2) ^c	41 (62.1)
Others	-	12 (22.6)	-
Unknown	9 (12.6)	16 (30.2)	8 (12.1)
HCV genotype 3:non3	-	7:46 ^d	20:46
HAART	57 (80.2)	-	60 (90.9)
Alcohol	6 (8.4)	4 (7.5)	5 (7.5)
Diabetes + IFG	2 (2.8)	4 (7.5) ^e	11 (16.6)

^a $P < 0.002$, ^b $P < 0.0001$ *vs* hepatitis C virus (HCV); ^c $P < 0.0001$, ^d $P < 0.03$, ^e $P < 0.001$ *vs* human immunodeficiency virus (HIV)/HCV. IFG: Impaired fasting glucose; BMI: Body mass index; HAART: Highly active anti-retroviral therapy.

were more often infected by HCV genotype 3 compared with HCV mono-infected patients ($P < 0.03$).

Table 2 shows the main hematological and virological parameters in the 3 study groups. Serum ALT levels were significantly higher in HCV mono-infected patients than in HIV/HCV co-infected and HIV mono-infected patients ($P < 0.02$). Serum AST, ALT and γ GT levels were significantly higher in HIV/HCV co-infected than in HIV mono-infected patients ($P < 0.0001$). Only γ GT levels were more elevated in HIV/HCV co-infected patients than in HCV mono-infected patients ($P < 0.01$). TG levels were significantly higher in HIV mono-infected and HIV/HCV co-infected patients than in HCV mono-infected patients ($P < 0.004$).

Extent of LF

In the overall population LS measured by TE ranged from 3.2 to 48.8 kPa. In 9 HIV/HCV co-infected patients, HCV-RNA was undetectable and for this reason these patients were excluded from the analysis, which was thus carried out only in the remaining 57 co-infected patients. However, their LS was lower than in the remaining co-infected group (data not shown).

Table 3 shows the distribution of LS values measured in all 3 study groups. Co-infected patients had higher LS values than mono-infected patients ($\chi^2_{MH} = 4$, $P < 0.04$). The HIV/HCV-co-infected population had LS \geq 9.5 kPa (50.9%) more often than HCV and HIV mono-infected patients (28.3%) ($\chi^2 = 5$, $P < 0.03$). In this respect 60% of co-infected patients under virologically unsuccessful HAART showed LS \geq F3. The individual values of LS increased from HIV to HCV and to HIV/HCV infected patients ($\rho = 0.5$, $P < 0.0001$) (Figure 1).

Overall, by multiple linear regression analysis, the variables significantly associated with ALF were AST values ($\beta = 0.47$, $P < 0.0001$) and HIV/HCV co-infection ($\beta = 0.25$, $P < 0.002$). To better understand which variables

Table 2 Main hematological and virological parameters in the three study groups (mean ± SD)

	HIV (n = 71)	HCV (n = 53)	HIV/HCV (n = 66)
AST/ALT	1 ± 0.4	0.72 ± 0.28 ^{aj}	0.9 ± 0.4
ALT (U/L), mean (range)	22 (7-113) ^{ih}	75 (16-551)	56.5 (9-280) ^{je}
AST (U/L), mean (range)	21 (11-56) ^{ih}	52.5 (18-209)	42.5 (14-281)
γGT (IU/L), mean (range)	33 (9-461) ^h	40.5 (10-479) ⁱ	76.5 (11-479)
Mean platelet count (10 ⁹ /L)	208 ± 59	184 ± 60	173 ± 61 ^b
T-Chol (mg/dL)	201 ± 46	175 ± 28 ^d	171 ± 48 ^c
HDL-Chol (mg/dL)	44 ± 16	47 ± 12	44 ± 15
LDL-Chol (mg/dL)	123 ± 32	108 ± 37.5	97 ± 40 ^e
TG (mg/dL), mean (range)	137 (36-615)	103 (32-354) ^{gi}	118 (49-614)
HCV-RNA (IU/mL) > 700.000	-	29 (54.7)	44 (66.6)
HIV-RNA (copies/mL), mean (range)	6050 (50-700000)	-	3300 (60-1100000)
HIV-RNA < 47 copies/mL (%)	44 (62)	-	45 (68.1)
CD4+ count (cells/μL), mean (range)	466.5 (17-1282)	-	446 (35-1445)
CD4+ < 200 cells/μL	38 ¹	-	38 ²

^aP < 0.0001, ^bP < 0.002, ^cP < 0.001, ^dP < 0.004, ^eP < 0.02 vs human immunodeficiency virus (HIV); ^fP < 0.0001, ^gP < 0.02 vs hepatitis C virus (HCV); ^hP < 0.0001, ⁱP < 0.01, ^jP < 0.05 vs HIV/HCV. ¹Data available in 66 patients; ²Data available in 56 patients. AST: Aspartate aminotransferase; ALT: Alanine aminotransferase; γGT: γ-glutamyl transferase; T-Chol: Total cholesterol; HDL: High density lipoprotein; LDL: Low density lipoprotein; TG: Triglyceride.

Table 3 Estimates of liver fibrosis using transient elastography in the study population n (%)

LS	Metavir	HIV (n = 71)	HCV (n = 53)	HIV/HCV (n = 57)	
< 7.1	F0-F1	56 (78.8)	23 (43.4)	19 (33.3)	
7.1-9.4	F2	11 (15.4)	15 (28.3)	9 (15.8)	
9.5-12.4	F3	1 (1.4)	4 (7.5)	9 (15.8)	
≥ 12.5	F4	3 (4.2)	11 (20.7)	20 (35.1)	χ ² _{MH} = 4, P < 0.04
≥ F3		4 (5.6)	15 (28.3)	29 (50.9)	χ ² = 5, P < 0.03

HIV: Human immunodeficiency virus; HCV: Hepatitis C virus; LS: Liver stiffness.

Table 4 Estimates of liver fibrosis using biochemical markers and transient elastography, mean (range)

	HIV (n = 71)	HCV (n = 53)	HIV/HCV (n = 57)
APRI	0.31 (0.1-1.6) ^{ab}	0.93 (0.28-6.07)	0.92 (0.17-19.7)
FIB-4	0.93 (0.39-4.28) ^a	1.62 (0.47-12.6)	1.63 (0.63-23.8)
LS	5.4 (3.2-26.6) ^{ab}	7.3 (3.4-40.9) ^c	9.8 (4.3-48.8)

^aP < 0.0001 vs hepatitis C virus (HCV); ^bP < 0.0001, ^cP < 0.05 vs human immunodeficiency virus (HIV)/HCV. LS: Liver stiffness; APRI: Aspartate aminotransferase platelet ratio index.

were associated with LS in patients with HIV mono- and co-infection, we also performed multiple linear regression analysis of these 2 groups and found that ALF correlated positively with AST serum levels (β = 0.34, P < 0.0001) and presence of HIV/HCV co-infection (β = 0.4, P < 0.0001) and negatively with lower CD4+ cell counts (β = -0.21, P < 0.003).

Median values of APRI and FIB-4 were significantly higher in HCV mono- and co-infected patients than in HIV mono-infected patients. There were no significant differences in APRI and FIB-4 medians in HCV mono- and HIV/HCV co-infected patients (Table 4). Median val-

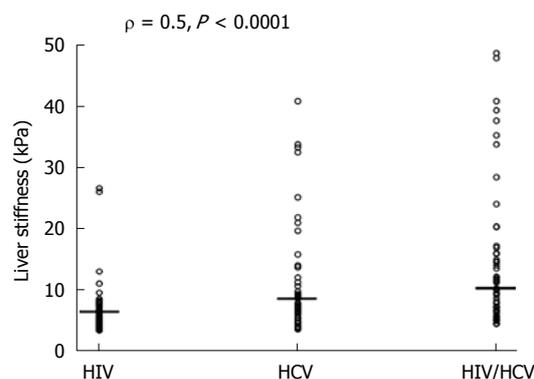


Figure 1 Median and distribution of liver stiffness in human immunodeficiency virus, hepatitis C virus, human immunodeficiency virus/hepatitis C virus patients. HIV: Human immunodeficiency virus; HCV: Hepatitis C virus.

ues of LS were significantly lower in HIV mono-infected than in HCV mono- and HIV/HCV co-infected patients (P < 0.0001). Median values of HIV/HCV co-infected patients were also significantly higher than in HCV mono-infected patients (P < 0.05).

Overall, correlations between LS and APRI values and LS and FIB-4 values were statistically significant (r = 0.60, P < 0.0001 and r = 0.64, P < 0.0001, respectively). However, when correlations were made according to the 3 cut-off values of LS, we found a significant correlation only for values of LS ≥ 9.5 (r = 0.50, P < 0.0001 vs APRI and r = 0.53, P < 0.0001 vs FIB-4) (Table 5).

Correlation between LS and risk factors studied

Table 6 shows the factors associated with LS in the 3 groups. No correlation between the studied parameters and LS was found in the HIV mono-infected group. In HCV mono-infected patients, LS positively correlated with alcohol intake > 20 g/d (P < 0.001) and AST serum level (P < 0.0001), while it negatively correlated with the

Table 5 Correlation between liver stiffness and aminotransferase platelet ratio index/FIB-4 values according to the liver stiffness cut-offs

	LS < 7.1 kPa (n = 98)		LS (7.1-9.4 kPa) (n = 35)		LS ≥ 9.5 kPa (n = 48)	
	r	P	r	P	r	P
APRI	0.01	NS	0.23	NS	0.50	< 0.0001
FIB-4	0.01	NS	0.25	NS	0.53	< 0.0001

APRI: Aminotransferase platelet ratio index; LS: Liver stiffness; NS: Not significant.

Table 6 Correlation (*r* or ρ) between liver stiffness and studied parameters

	LS		
	HIV	HCV	HIV/HCV
BMI	0.11	-0.1	0.02
HCV genotype 3/non 3	-	-0.1	-0.26
HCV-RNA	-	-	-0.26
HIV-RNA	0.21	-	0.18
Time HAART	-0.047	-	0.09
CD4 cells count	0.074	-	-0.32 ^d
Alcohol	-0.096	0.70 ^a	0.30 ^e
T-Chol	-0.09	-0.32 ^b	-0.18
TG	0.06	0.18	0.1
HDL-Chol	-0.1	0.05	-0.16
Diabetes + IFG	-0.01	0.19	0.14
Time HCV	-	0.24	-0.02
ALT	0.03	0.1	0.23
AST	0.18	0.56 ^c	0.40 ^a
Platelets	-0.02	-0.56 ^c	-0.61 ^c
APRI score	0.04	0.70 ^c	0.50 ^c
FIB-4 score	0.06	0.75 ^c	0.60 ^c

LS: Liver stiffness; HIV: Human immunodeficiency virus; HCV: Hepatitis C virus; BMI: Body mass index; HAART: Highly active anti-retroviral therapy; AST: Aspartate aminotransferase; ALT: Alanine aminotransferase; T-Chol: Total cholesterol; HDL: High density lipoprotein; TG: Triglyceride; IFG: Impaired fasting glucose; APRI: Aminotransferase platelet ratio index. ^a $P < 0.001$; ^b $P < 0.03$; ^c $P < 0.0001$; ^d $P < 0.02$; ^e $P < 0.04$.

number of platelets ($P < 0.0001$) and serum cholesterol levels ($P < 0.03$). APRI and FIB-4 values were significantly associated with LS both in HCV and HIV/HCV co-infected patients ($P < 0.0001$).

In HIV/HCV-co-infected patients the extent of LS was significantly correlated with alcohol intake ($P < 0.04$) AST level ($P < 0.0001$) and lower CD4+ cells count ($P < 0.02$) and was negatively correlated with platelets ($P < 0.0001$).

BMI, presence of diabetes or IFG, HCV- and HIV-viremia were not significantly correlated with LS in any of the 3 study groups. In addition, there was no significant correlation between the extent of LF under HAART exposure and duration of HAART exposure. There was no significant correlation either between extent of LF and cumulative exposure to each class of antiretroviral drugs (non-nucleoside/nucleoside reverse-transcriptase inhibitors, protease inhibitors) and of specific dideoxynucleoside analogues (didanosine, stavudine, zidovudine).

DISCUSSION

Our results, in agreement with other studies, confirmed that LF is more severe in HIV/HCV co-infected patients than in HCV or HIV mono-infected patients^[5,23,24]. In addition, ALF was significantly associated with a lower CD4+cell count in co-infected patients. There is convincing evidence that co-infection with HIV worsens the prognosis of HCV-related liver disease. It has been reported that in patients co-infected with HIV and HCV the risk of progressing to cirrhosis and liver failure is higher than in those infected with only HCV^[25,26], especially in individuals with CD4 < 200 cells/ μ L and alcohol consumption^[2].

In our study, 20% of HIV/HCV co-infected patients were under virologically unsuccessful HAART and in 50% CD4+ levels were below 400 cells/ mm^3 suggesting, in agreement with former findings, that the less successful the response to HAART, the less marked is its clinical benefit. In fact, immune recovery under HAART has been associated with longer overall survival, slower progression of HCV-related liver damage in HIV co-infected patients and with lengthier survival times before death attributable to liver disease^[27]. In the same way, Pineda *et al*^[27] demonstrated that liver decompensation emerged earlier in patients who maintained an undetectable HIV viral load for a shorter period during follow-up. Nevertheless, the association between ALF and lower CD4 cell count suggests that the response to HAART, measured using CD4 cell gain and HIV viral load decline, determines the evolution of liver disease and that virologically and immunologically successful HAART may slow progression of LF in HIV/HCV co-infected patients.

On the other hand, antiretroviral-related liver toxicity could have further contributed to liver damage in our HIV population^[7]. Mitochondrial toxicity of nucleoside analogues and glucose or lipid abnormalities, particularly common when using some protease inhibitors, may produce or enhance LF progression in HIV-seropositive patients. The correlation between use of antiretroviral drugs and LF in patients with HIV/HCV co-infection has been evaluated in different studies but with contradictory results^[21,28-30].

Macías *et al*^[21] reported that HAART regimens, including nevirapine, were associated with an increased degree of LF, while the use of protease inhibitor-based HAART was associated with less severe fibrosis and a slower progression of fibrosis in HIV/HCV co-infected patients. In contrast, Berenguer *et al*^[28] found that exposure to NNRTI was associated with a reduction in LF progression. In addition, Halfon *et al*^[29] showed that exposure to NNRTI was an independent factor in LF while Blanco *et al*^[30] highlighted that exposure to dideoxynucleosides was an independent factor associated with ALF.

In our study, no correlation was found between HAART exposure, duration of HAART exposure or cumulative exposure to any class of antiretroviral drugs and LF. In addition, we analyzed the correlation between duration of

exposure to dideoxynucleosides (in particular didanosine, stavudine, zidovudine) and LF but also in this case no correlation was observed, suggesting that these drugs could not play any role in the progression of LF.

ALF was significantly higher in HIV/HCV co-infected patients than in HCV mono-infected patients when the subset of co-infected patients with undetectable HCV-RNA were excluded from the analysis. Overall, HIV/HCV co-infected patients with undetectable HCV-RNA had either no or only mild fibrosis (F0-F1) compared to the remaining co-infected patients, suggesting that the presence of HCV is important in conditioning the progression of LF and that anti-HCV therapy is mandatory in HIV/HCV co-infected patients in order to eradicate the virus. In fact, other authors have reported that achieving HCV clearance may reduce liver-related complications and mortality^[31,32] and probably permits at least a partial regression of LF^[33]. However, in HIV-positive patients liver cirrhosis may also occur without chronic viral hepatitis, and possible causes of hepatic steatosis in patients with HIV may be due to HIV itself, pathological alcohol use, diabetes mellitus, obesity or antiretroviral medications^[34].

Evaluation of LF using the 2 biochemical scores (APRI and FIB-4) was not in full agreement with LS measurement. In fact, these 2 biochemical tests were in agreement with TE values only for high-grade LF, but not in low and moderate LF, suggesting that at least in these cases liver biopsy could be necessary to assess the precise degree of LF. In this respect, we are aware that the lack of liver biopsy, as a reference tool of LF, is a limitation of our study.

More consideration, perhaps, should be given to transaminase levels. In fact, the HCV mono-infected group had the highest levels of transaminases, which may have influenced LS values by increasing them. This result could further support our observation that co-infected patients are at highest risk of LF because of their high AST levels and the immune suppression associated with a low CD4 cell count.

Finally, also in our area, HCV genotype 3 was confirmed to be more associated with HIV-positive patients, because of their habits as drug abusers^[35].

In conclusion, in our population, HIV/HCV co-infected patients had more ALF than HCV and HIV mono-infected patients. This result was not correlated with long-term exposure to HAART but with a lower CD4 cell count, suggesting that immunologically successful HAART may protect from progression of liver damage in HIV/HCV co-infected patients. In addition, the detection of unsuspected ALF in HIV mono-infected patients confirms that FibroScan[®] is very useful in this population. HCV infection, with its different pattern of cytolysis, may condition LS values, but viral eradication is mandatory to reduce fibrosis progression. Finally, the use of these non-invasive parameters of LF should be considered with caution. In fact, from our data it emerges that both TE and the biochemical scores may be suitable only for high grades of LF. In contrast, for mild/moderate degrees of fibrosis, they could not replace liver biopsy in the correct evaluation of LF.

COMMENTS

Background

Liver disease associated with hepatitis C virus (HCV) has emerged as a significant problem in human immunodeficiency virus (HIV) patients, thanks to improved survival in the highly active anti-retroviral therapy (HAART) era. Co-infection with HIV is known to lead to a more rapid progression of HCV liver disease to cirrhosis. Other factors such as severe immune suppression and alcohol consumption accelerate the progression of HCV-related fibrosis. In addition, successful HAART slows the progression of liver fibrosis (LF), but antiretroviral-liver toxicity could contribute to hepatic damage in co-infected patients. The advent of transient elastography (TE) has demonstrated to be very helpful for the non-invasive measurement of LF.

Research frontiers

Percutaneous liver biopsy is the gold standard for assessing LF but it is an invasive technique with risk of morbidity and mortality. For these reasons new non-invasive methods for the assessment of LF have recently been developed. TE (FibroScan[®]) and biochemical markers have demonstrated to be very helpful in the non-invasive measurement of LF. In this study, using these non-invasive tools, i.e. TE plus 2 biochemical tests, aminotransferase platelet ratio index (APRI) and FIB-4, we showed that advanced LF was significantly higher in HIV/HCV co-infected patients than in mono-infected patients and that it was significantly associated with lower CD4+ cells count. The APRI and FIB-4 tests correlated only with the highest values of TE, i.e. ≥ 9.5 , suggesting that they are useful tools in diagnosing high grade liver disease, but in the case of a low or moderate degrees of LF liver biopsy remains the best means for correctly diagnosing the degree of fibrosis. Furthermore, the results showed that, overall, a greater number of HIV/HCV co-infected patients with undetectable HCV-RNA had either no or mild fibrosis (F0-F1) compared to the remaining co-infected patients with detectable HCV-RNA.

Innovations and breakthroughs

Several studies have been carried out to identify factors related to an accelerated progression of LF in HIV/HCV co-infected patients. Conflicting results have been reported in the literature about the role of antiretroviral therapy on the progression of LF. In the study, information on alcohol intake, duration of HCV infection and cumulative exposure to non-nucleoside and nucleoside reverse-transcriptase inhibitors, protease inhibitors and specific dideoxynucleoside analogues (didanosine, stavudine, zidovudine) was evaluated. The results showed that on univariate analysis liver stiffness (LS) was significantly associated with alcohol intake > 20 g/d in both HCV mono-infected and co-infected patients, but we did not find any correlations between LF and duration of HCV infection, HAART exposure, duration of HAART exposure or cumulative exposure to any class of antiretroviral drugs.

Applications

A good adherence to antiretroviral therapy, when it is indicated, is important to reduce the risk of progression of LF in co-infected patients. In addition, HCV mono- and co-infected patients should modify negative habits and lifestyles, such as alcohol consumption, which could accelerate the progression of LF. Important fields for further study could include the use and evaluation of the applicability of FibroScan[®] for repeated assessment in the monitoring of LF.

Terminology

Transient elastometry (Fibro-Scan[®]; EchoSens, Paris, France) is a rapid, reliable and well-tolerated imaging technique for the assessment of LF by measuring LS.

Peer review

The authors aimed to assess the prevalence of advanced LF (ALF) in HIV, HCV and HIV/HCV patients using TE and to identify factors associated with ALF. They concluded that HIV/HCV co-infected patients had ALF more frequently at TE than HCV and HIV mono-infected patients. The title reflects accurately the contents of the article, and the abstract delineates concisely the research.

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NKX2-3 and IRGM variants are associated with disease susceptibility to IBD in Eastern European patients

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Abstract

AIM: To investigate variants of immunity-related GT-Pase family M (IRGM) and NKX2-3 genes and genotype-phenotype in Eastern European patients with inflammatory bowel disease (IBD).

METHODS: We analyzed 1707 Hungarian and Czech subjects with Crohn's disease (CD) ($n = 810$, age: 37.1 ± 12.6 years, duration: 10.7 ± 8.4 years) and ulcerative colitis (UC) ($n = 428$, age: 43.7 ± 15.0 years, duration: 12.6 ± 9.9 years), as well as 469 healthy controls. IRGM rs13361189, NKX2-3 rs10883365 and ECM1 rs13294 polymorphisms were tested by LightCycler allele discrimination. Detailed clinical phenotypes were determined by reviewing the medical charts.

RESULTS: NKX2-3 rs10883365 variant allele was associated with increased risk for CD ($P = 0.009$, OR = 1.24, 95% CI = 1.06-1.48) and UC ($P = 0.001$, OR = 1.36, 95% CI = 1.13-1.63), whereas variant IRGM allele increased risk for CD ($P = 0.029$, OR = 1.36, 95% CI = 1.03-1.79). In contrast, ECM1 rs13294 was not associated with either CD or UC. In CD, the variant IRGM allele was associated with a colon-only location ($P = 0.02$, OR = 1.62, 95% CI = 1.07-2.44), whereas in UC, the ECM1 variant was associated with cutaneous manifestations ($P = 0.002$, OR = 3.36, 95% CI = 1.48-7.63). Variant alleles did not predict resistance to steroids or azathioprine, efficacy of infliximab, or need for surgery.

CONCLUSION: NKX2-3 and IRGM are susceptibility loci

for IBD in Eastern European patients. Further studies are needed to confirm the reported phenotype-genotype associations.

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Key words: Crohn's disease; Ulcerative colitis; NKX2-3; Immunity-related GTPase family M; ECM1; Genotype; Phenotype; Pharmacogenetics

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INTRODUCTION

Inflammatory bowel diseases (IBDs) are multifactorial with both environmental and genetic components; the latter displaying heterogeneity in terms of disease presentation as well as response to treatment^[1]. Crohn's disease (CD) has a strong genetic component, and to date, at least nine susceptibility loci have been identified^[2]. The first, and most consistently replicated critical mutations have been found in the NOD2/CARD15 gene on chromosome 16 (IBD1). Other loci encode genes that are involved in a number of homeostatic mechanisms: innate pattern recognition receptors (including NOD2/CARD15, TLR4 and CARD9), differentiation of Th17-lymphocytes (IL-23R, JAK2, STAT3, CCR6 and ICOSLG), autophagy [ATG16L1, immunity-related GTPase family M (IRGM) and LRRK2], maintenance of epithelial barrier integrity (IBD5, DLG5, PTGER4, ITLN1, DMBT1 and XBP1), and orchestration of the secondary immune response (HLA-region, TNFSF15/TL1A, IRF5, PTPN2, PTPN22, NKX2-3, IL-12B, IL-18RAP and MST1)^[3-6]. As the incidence of IBD is rapidly increasing in some parts of Eastern Europe^[1], it is of great importance to study social and environmental, as well as host-genetic factors that might underlie this trend.

The IRGM gene is located on chromosome 5q33.1, and encodes an autophagy-inducing protein and belongs to the immunity-related guanosine triphosphatases (IRGs), also known as p47 guanosine triphosphatases. IRGs play an important role in host defense against intracellular pathogens^[7]. Genetic association of the autophagy genes, autophagy-related 16-like 1 (ATG16L1) and IRGM has been suggested in adult-onset CD by genome-wide association scan studies (GWASs), but not in UC^[5,6,8-10]. Although a meta-analysis of the three index GWASs

has implicated a single nucleotide polymorphism (SNP; rs11747270) based on imputed data with an OR of 1.33^[10], other studies including a new meta-analysis^[11] have confirmed the IRGM signal on rs13361189 and rs4958847 immediately flanking IRGM.

Recently, the rs13361189 variant, upstream of IRGM, has been shown to be in perfect linkage disequilibrium with a 20-kb deletion polymorphism that affects the expression of IRGM (and cellular autophagy) in a tissue-specific manner^[9]. These results suggest that the CD association at IRGM arises from an alteration in IRGM regulation that affects the efficacy of autophagy, and identifies rs13361189 and its strongly correlated neighbors at the 5' end of IRGM, including the 20-kb deletion polymorphism as a likely causal variant.

Association between the rs10883365 variant of NK2 transcription factor related, locus 3 (NKX2-3) gene on chromosome 10q24.2 and susceptibility of CD has been reported in Western Europe, including The Wellcome Trust Case Control Consortium (WTCCC) GWA and a replication study from The Netherlands, and in Japan, with an OR of 1.2-1.6^[12-14]. In addition, a modest association ($P = 3.3 \times 10^{-4}$ in the ulcerative colitis panel and $P = 2.4 \times 10^{-6}$ using the expanded WTCCC control panel) has also been reported between rs10883365 and UC in a non-synonymous SNP scan by Fisher *et al.*^[15]. NKX2-3-deficient mice show severe defects in gut development; primarily in the epithelium of the small intestine^[16]. In addition, the lymphoid organs of these mice, including the spleen and Peyer's patches, have abnormal tissue architecture and abnormalities in the migration and segregation of B and T cells^[17], however, the exact mechanism is unknown.

ECM1, on chromosome 1q21.2, is also a plausible candidate gene for UC; it encodes extracellular matrix protein 1, a glycoprotein expressed in small and large intestine, and it interacts with the basement membrane and inhibits matrix metalloproteinase^[18]. Notably, ECM1 strongly activates nuclear factor- κ B signaling, a key immune regulator. Expression is upregulated in colorectal cancer and metastases, which implicates ECM1 in epithelial-stromal interaction^[18]. Of note, the WTCCC observed modest association between these ECM1 SNPs and ankylosing spondylitis, a related inflammatory disorder ($P = 0.0041$ and 0.0044), respectively^[13]. More recently, an association between the rs3737240 and rs13294 variants of ECM1 and UC susceptibility was reported in a GWAS by Fisher *et al.*^[15], with an OR of 1.3-1.4 for the homozygous carriage of the variant allele. rs3737240 and rs13294 encode substitutions T130M and G290S: Thr130, residing within a collagen IV binding domain, is conserved in primates, whereas Gly290 is not.

Finally, data about the pharmacogenetics of IBD are still limited. Resistance to steroids is associated with high expression of β -glucocorticoid receptors (hGR β) and over-expression of MDR1 has been found in patients who fail steroid therapy and require surgery^[19]. In contrast, according to our group's earlier results, the presence of the DLG5 Arg30Gln variant allele, but not variants in ABCG2 or MDR1 genes, predicted resistance to steroids^[20,21]. Vermeire *et al.*^[22] have reported a lack of association between the

presence of NOD2 mutations and response to infliximab therapy, and later, the same group reported an association between the presence of Fas ligand -843C/T variant and response to infliximab^[23].

In light of the lack of data in Eastern European countries, our aim was to investigate the prevalence of IRGM rs13361189, NKX2-3 rs10883365 and ECM1 rs13294 variants in large independent cohorts of Czech and Hungarian IBD patients. We also aimed to investigate a possible association between genotype and clinical phenotype, need for surgery, and response to medical therapy.

MATERIALS AND METHODS

Study population

One thousand seven hundred and seven unrelated IBD patients (CD: $n = 810$, age: 37.1 ± 12.6 years, duration: 10.7 ± 8.4 years and UC: $n = 428$, age: 43.7 ± 15.0 years, duration: 12.6 ± 9.9 years) and 469 healthy subjects (blood donors) from Hungary and the Czech Republic were investigated. The clinical data of the CD and UC patients are presented in Table 1. A detailed clinical phenotype was available in 789 CD and 422 UC patients.

The diagnosis was based on the Lennard-Jones criteria^[24]. Age; age at onset; presence of extraintestinal manifestations [arthritis: peripheral and axial; ocular manifestations: conjunctivitis, uveitis and iridocyclitis; skin lesions: erythema nodosum and pyoderma gangrenosum; and hepatic manifestations: primary sclerosing cholangitis (PSC)]; frequency of flare-ups (frequent relapses: > 1 clinical relapse/year); therapeutic effectiveness (e.g. steroid and/or immunosuppressive use, steroid resistance); need for surgery (resections); the presence of familial IBD; smoking habits; and in CD, perianal involvement, were investigated by reviewing the medical charts by the physician and completing a questionnaire. The disease phenotype (age at onset, duration, location and behavior) was determined according to the Montreal classification^[25].

The control group for mutation analysis consisted of 469 age- and sex-matched healthy blood donors (male/female: 251/218, age: 40.5 ± 11.5 years old). Control subjects did not have any gastrointestinal and/or liver diseases and were selected from consecutive blood donors in Budapest, Veszprem, Debrecen and Prague. The study protocol was approved by the Ethical and Science Committee of the Ministry of Health. Each patient was informed of the nature of the study and gave signed informed consent.

Genotyping and DNA isolation

Genomic DNA was isolated from whole blood according to the manufacturers' description with High Pure PCR Template preparation Kit (Roche, Budaors, Hungary).

Detection of IRGM (rs13361189, g.11386323T>C), ECM1 (rs13294, c.1243A>G, p.Ser415Gly, g.975342G>A) and NKX2-3 (rs10883365, g.20036290G>A) polymorphisms

Genotyping was performed using the LightCycler (Roche Diagnostics, Basel, Switzerland) allelic discrimination system. Amplification primers and hybridization probes

Table 1 Clinical characteristics of patients with inflammatory bowel diseases

	CD ($n = 810$)	UC ($n = 428$)
Male/female (n)	434/376	202/226
Age (yr)	37.1 ± 12.6	43.7 ± 15.0
Age at presentation (yr) ¹	26.5 ± 10.6	31.3 ± 13.4
Duration (yr) ¹	10.7 ± 8.4	12.6 ± 9.9
Familial IBD ¹	11.8%	7.6%
Location in CD ¹		
L1	28.2%	
L2	18.9%	-
L3	51.2%	
L4 only	1.7%	
All L4	7.9%	
Maximum extent in UC ¹		
Proctitis	-	7.8%
Left-sided		52.3%
Extensive		39.9%
Behavior in CD ¹		
B1	34.9%	
B2	34.5%	-
B3	30.7%	
Perianal disease ¹	41.2%	-
Frequent relapse in CD/chronic continuous in UC ¹	39.9%	27.6%
Arthritis ¹	38.6%	27.1%
Cutaneous ¹	7.8%	5.9%
Ocular ¹	7.7%	3.8%
PSC ¹	2.4%	3.8%
Steroid use/refractory ¹	81.1%/11.6%	66.2%/12.3%
Azathioprine use ¹	68.3%	29.3%
Anti-TNF use ¹	33.2%	10.4%
Surgery in CD/colectomy in UC ¹	50.9%	10.0%
Smoking habits ²		
No	55.1%	71.6%
Yes	31.3%	12.4%
Previous	13.6%	16.0%

¹Clinical phenotype available in 789 Crohn's disease (CD) and 422 ulcerative colitis (UC) patients; ²Available in 691 CD and 388 UC patients. L1: Ileal; L2: Colon; L3: Ileocolonic; L4: Upper gastrointestinal; B1: Inflammatory; B2: Stenosing; B3: Penetrating. IBD: Inflammatory bowel disease; TNF: Tumor necrosis factor.

were designed by the LightCycler Probe Design software (Roche Diagnostics). All oligonucleotides were synthesized by VBC Biotech (Vienna, Austria). The following amplification primers and hybridization probes were used for genotyping IRGM: IRGM-LCF: 5'-ATGGACAGT-CAGTACCCTGCAC-3', IRGM-LCR: 5'-CTCTTTAC-CATTGACTCCTTGTGCC-3', IRGM-ANC: 5'-LC Red 640-TGCTCAGCGGGTACAGTTTAGAAAGGGAA-Phosphate-3', IRGM-SENS: 5'-GAAAATCGGATG-TATATTAGTAGACCC-Fluorescein-3'.

The amplification primers and hybridization probes used for genotyping of ECM1 were: ECM1-LCF: 5'-ACCCACCACCCTTGTGT-3', ECM1-LCR: 5'-TGCTT-GGTGAGAACTCTTGGTTT-3', ECM1-ANC: 5'-LC Red 640-TCAAGATGTCCCGGTCATAGTTGGGG-TAAGGAG-Phosphate-3', ECM1-SENS: 5'-TGACTC-GACCGATGTCAAT-Fluorescein-3'.

The amplification primers and hybridization probes used for genotyping of NKX2-3 were: NKX2-LCF:

5'-CCGCATAAGACGTTACTTAAACATGT-3', NKX2-LCR: 5'-GCTATCTACTCGAAACTGTCTGC-3', NKX2-ANC-2: 5'-TCTCCCCGGGGGTCACGTTG-Fluorescein-3', NKX2-SENS-2: 5'-LC Red 610-ACAAACACCTTCAAACCGTC-Phosphate-3'.

Polymerase chain reaction (PCR) was performed by LightCycler 480 real-time PCR System (Roche), in a reaction volume of 20 μ L with 50 ng genomic DNA, 10 μ L 2 \times PCR Master Mix (Promega), and 5 pmol of the respective labeled oligonucleotides (sensor and anchor). For IRGM and NKX2-3, an asymmetric multiplex system was used for simultaneous amplification of the two fragments with 3:10 pmol forward:reverse (F:R) amplification oligonucleotides and 10:3 F:R amounts for IRGM and NKX2-3 SNPs, respectively. Similarly, for ECM1, an asymmetric PCR was applied with a 10:3 pmol F:R primer mix for amplification in a separate reaction. Cycling conditions were as follows: initial denaturation at 95°C for 3 min, followed by 35 cycles of denaturation at 95°C for 20 s, annealing at 55°C for 30 s, and extension at 72°C for 45 s, with a ramping rate of 4.4°C/s.

After amplification, a melting curve analysis was performed by cooling the samples to 40°C, followed by gradual heating to 80°C with a ramp rate of 0.04°C/s. The decline in fluorescence was continuously monitored. Melting curves were converted to melting peaks with wild-type and variant alleles showing distinct melting points. For the IRGM and NKX2-3 multiplex PCR, color compensation was performed to compensate for the fluorescence crosstalk between detection channels. Genotype calling was carried out by two independent investigators.

Statistical methods

Variables were tested for normality using Shapiro Wilk's W test. A t test with separate variance estimates, χ^2 test and χ^2 test with Yates correction were used to evaluate differences between IBD patients and controls, as well as within subgroups of IBD patients. Logistic regression was used to compare genetic and clinical data and results are expressed as OR with 95% CI. $P < 0.05$ was considered as significant. For the statistical analysis, SPSS version 15.0 (SPSS Inc., Chicago, IL, USA) was used. Statistical analysis was performed by Lakatos PL with the assistance of a statistician.

RESULTS

Association between NKX2-3, IRGM and ECM1 and disease susceptibility

All investigated polymorphisms were in Hardy-Weinberg equilibrium ($P = 0.38-0.95$). The success rate of the genotyping assays was 98%-99%. The genotype and allele frequencies are presented in Table 2. NKX2-3 rs10883365 variant allele was associated with increased risk for CD ($P = 0.018$ after Bonferroni correction, OR = 1.24, 95% CI = 1.06-1.48) and UC ($P = 0.003$ after Bonferroni correction, OR = 1.36, 95% CI = 1.13-1.63), whereas the variant IRGM allele increased the risk of CD ($P = 0.04$ after Bonferroni correction, OR = 1.36, 95% CI = 1.03-1.79). The association between NKX2-3 rs10883365 variant and IBD

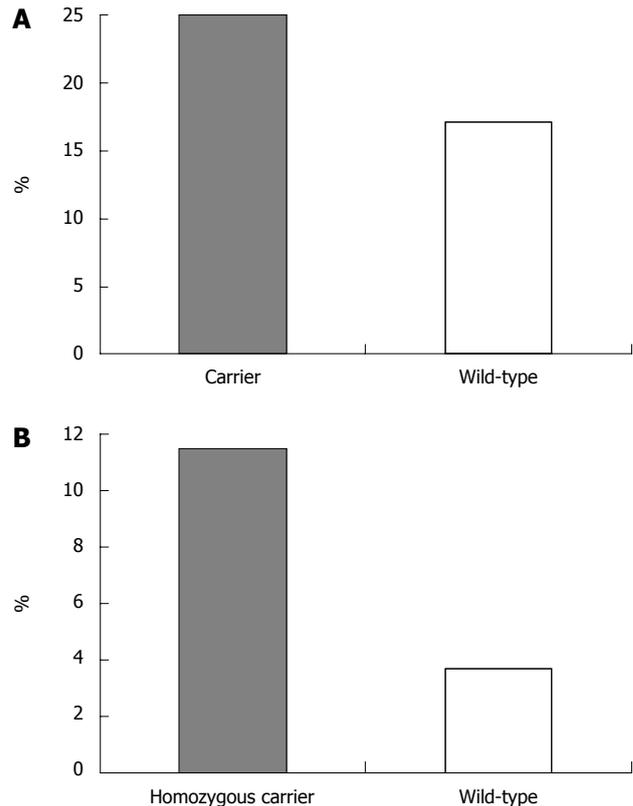


Figure 1 Association between immunity-related GTPase family, M and ECM1 and disease phenotype in patients with inflammatory bowel diseases. A: Association between the IRGM rs13361189 variant and disease location in Crohn's disease. $P = 0.04$, OR = 1.62, 95% CI: 1.07-2.44; B: Association between homozygous carriage of the ECM1 rs13294 variant allele and cutaneous manifestations in ulcerative colitis. $P = 0.004$, OR = 3.36, 95% CI: 1.48-7.63.

was also significant in the genotypic and dominant models. A similar trend was noted between IRGM and CD. In contrast, ECM1 rs13294 was not associated with either CD or UC. The combination of IRGM carrier/NKX2-3 homozygote genotype was significantly higher in CD compared to the controls (7.2% *vs* 2.1%, $P < 0.0001$ after Bonferroni correction, OR = 3.55, 95% CI = 1.80-7.01).

Role of NKX2-3, IRGM and ECM1 variants in predicting sex, familial disease, age at onset, disease location, phenotype or extraintestinal manifestations

In CD, presence of the variant IRGM allele was associated with colon-only location (in carriers: 25% *vs* wild-type: 17.1%, $P = 0.04$ after Bonferroni correction, OR = 1.62, 95% CI = 1.07-2.44, Figure 1A). In UC, homozygous carriage of the ECM1 variant allele was associated with cutaneous manifestations (11.5% in homozygotes *vs* 3.7% in patients with other genotypes, $P = 0.004$ after Bonferroni correction, OR = 3.36, 95% CI = 1.48-7.63, Figure 1B). No other significant associations were found in either CD or UC patients (data not shown).

Association between NKX2-3, IRGM and ECM1 and response to medical therapy or need for surgery

We also investigated the association between the NKX2-3, IRGM and ECM1 variants and the response to steroids,

Table 2 Association between NKX2-3, IRGM and ECM1 polymorphisms and disease susceptibility in patients with inflammatory bowel disease

	WT (%)	HET (%)	HOM (%)	<i>P</i> value	Carrier (%)	<i>P</i> value	OR (95%CI)	MAF	<i>P</i> value	OR (95%CI)
IRGM rs13361189										
All CD (<i>n</i> = 808)	636 (78.7)	156 (19.3)	16 (2.0)	0.060 ¹	172 (21.3)	0.060 ¹	-	188 (11.6)	0.029	1.36 (1.03-1.79)
Hungarian CD (<i>n</i> = 456)	355 (77.9)	89 (19.5)	12 (2.6)	NS ^{1,2}	101 (22.1)	NS ^{1,2}	-	113 (12.4)	NS ^{1,2}	-
Czech CD (<i>n</i> = 352)	281 (79.8)	67 (19.0)	4 (1.2)	NS ^{1,2}	71 (20.2)	NS ^{1,2}	-	75 (10.7)	NS ^{1,2}	-
All UC (<i>n</i> = 428)	351 (82.0)	76 (17.8)	1 (0.2)	NS ^{1,2}	77 (18.0)	NS ^{1,2}	-	78 (9.1)	NS ^{1,2}	-
Hungarian UC (<i>n</i> = 274)	221 (80.7)	52 (19.0)	1 (0.3)	NS ^{1,2}	53 (19.3)	NS ^{1,2}	-	54 (9.9)	NS ^{1,2}	-
Czech UC (<i>n</i> = 154)	130 (84.4)	24 (15.6)	0	NS ^{1,2}	24 (15.6)	NS ^{1,2}	-	24 (7.8)	NS ^{1,2}	-
All controls (<i>n</i> = 460)	382 (83.0)	75 (16.3)	3 (0.7)	-	78 (17.0)	-	-	81 (8.8)	-	-
Hungarian controls (<i>n</i> = 265)	217 (81.9)	46 (17.4)	2 (0.7)	-	48 (18.1)	-	-	50 (9.4)	-	-
Czech controls (<i>n</i> = 195)	165 (84.6)	29 (14.9)	1 (0.5)	-	30 (15.4)	-	-	31 (7.9)	-	-
NKX2 rs 10883365										
All CD (<i>n</i> = 810)	208 (25.7)	389 (48.1)	213 (26.2)	0.010 ¹	602 (74.3)	NS ^{1,2}	-	815 (50.3)	0.009	1.24 (1.06-1.48)
Hungarian CD (<i>n</i> = 457)	115 (25.2)	220 (48.1)	122 (26.7)	NS ^{1,2}	342 (74.8)	NS ^{1,2}	-	464 (50.8)	NS ^{1,2}	-
Czech CD (<i>n</i> = 353)	93 (26.3)	169 (47.9)	91 (25.8)	0.070 ¹	260 (73.7)	NS ¹	-	351 (49.7)	0.030 ¹	1.31 (1.03-1.68)
All UC (<i>n</i> = 427)	90 (21.1)	226 (52.9)	111 (26.0)	0.004 ¹	337 (78.9)	0.006 ¹	1.52 (1.13-2.08)	448 (52.5)	0.001	1.36 (1.13-1.63)
Hungarian UC (<i>n</i> = 274)	56 (20.4)	152 (55.5)	66 (24.1)	NS ^{1,2}	218 (79.6)	0.070 ¹	-	284 (51.8)	0.060	-
Czech UC (<i>n</i> = 153)	34 (22.2)	74 (48.4)	45 (29.4)	0.017 ¹	119 (77.8)	0.046 ¹	1.63 (1.01-2.65)	164 (53.6)	0.005 ¹	1.53 (1.14-2.07)
All controls (<i>n</i> = 469)	136 (29.0)	245 (52.2)	88 (18.8)	-	333 (71.0)	-	-	421 (44.9)	-	-
Hungarian controls (<i>n</i> = 271)	73 (26.9)	145 (53.5)	53 (19.6)	-	198 (73.1)	-	-	251 (46.3)	-	-
Czech controls (<i>n</i> = 198)	63 (31.8)	100 (50.5)	35 (17.7)	-	135 (68.2)	-	-	170 (42.9)	-	-
ECM1 rs13294										
All CD (<i>n</i> = 807)	139 (17.2)	392 (48.6)	276 (34.2)	NS ^{1,2}	688 (82.8)	NS ^{1,2}	-	944 (58.5)	NS ^{1,2}	-
Hungarian CD (<i>n</i> = 455)	89 (19.6)	228 (50.1)	138 (30.3)	NS ^{1,2}	366 (80.4)	NS ^{1,2}	-	504 (55.4)	NS ^{1,2}	-
Czech CD (<i>n</i> = 352)	50 (14.2)	164 (46.6)	138 (39.2)	NS ^{1,2}	302 (85.8)	NS ^{1,2}	-	440 (62.5)	NS ^{1,2}	-
All UC (<i>n</i> = 428)	77 (18.0)	225 (52.6)	126 (29.4)	NS ^{1,2}	351 (82.0)	NS ^{1,2}	-	477 (55.7)	NS ^{1,2}	-
Hungarian UC (<i>n</i> = 275)	44 (16.0)	156 (56.1)	75 (27.3)	NS ^{1,2}	231 (84.0)	NS ^{1,2}	-	306 (55.6)	NS ^{1,2}	-
Czech UC (<i>n</i> = 153)	33 (21.6)	69 (45.1)	51 (33.3)	NS ^{1,2}	120 (78.4)	NS ^{1,2}	-	171 (55.9)	NS ^{1,2}	-
All controls (<i>n</i> = 463)	90 (19.4)	222 (47.9)	151 (32.6)	-	373 (80.6)	-	-	524 (56.6)	-	-
Hungarian controls (<i>n</i> = 265)	56 (21.1)	124 (46.8)	85 (32.1)	-	209 (78.9)	-	-	294 (55.5)	-	-
Czech controls (<i>n</i> = 198)	34 (17.2)	98 (49.5)	66 (33.3)	-	164 (82.8)	-	-	230 (58.1)	-	-

¹*P* value vs controls; ²*P* value Crohn's disease (CD) vs ulcerative colitis (UC). WT: Wild-type; HET: Heterozygous carrier; HOM: Homozygous carrier; MAF: Minor allele frequency; NS: Not significant.

infiximab or azathioprine or the need for surgery in patients with CD. Two hundred and sixty-three unrelated CD patients were treated with anti-tumor necrosis factor (TNF): 259 received infiximab and four, adalimumab, two of whom were treated after secondary loss of response to infiximab therapy. Overall, there was no association between the presence of the above variants and short-term response (assessed at week 12) to infiximab induction therapy [5 mg/kg at weeks 0, 2 and 6; partial response: Crohn's disease activity index (CDAI) decreased by ≥ 70 points and/or $\geq 50\%$ decrease in the number of draining fistulas; remission: CDAI < 150 or closure of all fistulas]; steroid use/resistance; azathioprine use; or need for surgery (data not shown). Similarly, no association was found between either of the variants and steroid use/resistance, azathioprine use or need for surgery in patients with UC (data not shown).

DISCUSSION

This is the first report on the prevalence of the IRGM rs13361189, NKX2-3 rs10883365 and ECM1 rs13294 variants, in large, independent IBD cohorts from Eastern Europe. The variant NKX2-3 allele conferred a risk in both UC and CD, whereas the IRGM rs13361189 variant allele

was associated with increased risk for CD. In addition, the IRGM variant was associated with disease location in CD.

The genotype and allele frequencies for IRGM and NKX2-3 variants in CD, UC and controls reported in the present study were in line with most previous reports in Caucasian populations, whereas the frequency of the variant ECM1 rs13294 allele was approximately 10% higher in both IBD and controls, compared to that reported in previous studies^[7,8,12,13,15,26].

We confirmed that the IRGM rs13361189 variant was associated with disease susceptibility in CD in Eastern European populations. The allelic OR of 1.36 (95% CI = 1.03-1.79) was in the range reported in Caucasian populations (OR = 1.38-1.56)^[7,13] and in a recent meta-analysis (OR = 1.34)^[10]. Similar genotype distributions were observed in both the Czech and Hungarian cohort, however, due to the low variant allele frequency, the difference became significant only in the combined analysis. A similar tendency (*P* = 0.06) was observed in the genotypic and dominant model. In contrast, in the present study we failed to replicate the weak association between IRGM and UC (rs13361189 *P* = 0.0069, pooled OR = 1.16; rs4958847 *P* = 0.014, pooled OR = 1.13) that was reported recently in a Spanish meta-analysis^[10]. Of note, the present study was underpowered to detect such small

differences, however, there was even no trend for a difference between UC and controls.

In addition, in an Italian study^[27], the rs4958847 polymorphism was associated with fistulizing behavior ($P = 0.037$, OR = 1.54, CI = 1.02-2.31) and perianal fistulas ($P = 0.045$, OR = 1.55, CI = 1.01-2.38) in a logistic regression analysis. This was later partially confirmed by the Leuven group. Henckaerts *et al.*^[28] have reported in a very elegant study a significant association between the IRGM rs4958847 variant, U7 gene desert rs12704036 T-allele, NOD2/CAR15 mutation, ileal involvement at diagnosis, male sex, and time to development of non-perianal fistulas in a Cox regression analysis. In a further study from New Zealand^[29], rs13361189 variant increased the risk for ileal CD in 507 CD patients and 576 controls. The OR in ileal CD was 1.92 (95% CI = 1.27-2.96). Moreover, Peterson *et al.*^[30] have suggested an association between IRGM and pediatric disease onset (< 17 years) of CD in a North American cohort. However, only one of the two IRGM variants studied (rs13361189) was weakly associated with CD in their study (uncorrected $P = 0.03$). In the present study, we could not confirm the association between age at onset and the presence of the IRGM variant, in accordance with Canadian, Italian and Scottish results^[29,31]. In contrast, we found an association between IRGM carriage and disease location in CD; colonic location was significantly more common in carriers of the variant allele (OR = 1.62, 95% CI = 1.07-2.44). Of note, however, the rs4958847 variant was not investigated in the present study.

The association between the rs10883365 variant of NKX2-3 gene and susceptibility of IBD was first reported in CD in Caucasian patients and in a Japanese study with an OR of 1.2-1.6^[12,14]. In addition, using the UC panel and the expanded WTCCC control panel, Fisher *et al.*^[15] have reported a modest association ($P = 3.3 \times 10^{-4}$ and $P = 2.4 \times 10^{-6}$) between rs10883365 and UC. In the present study, we confirmed these findings; the rs10883365 variant was associated with UC and CD susceptibility in the allelic and genotypic models with an OR of 1.53 and 1.24, respectively. Based on our data, the association between NKX2-3 and IBD is stronger in UC compared to CD, at least in patients from Eastern Europe. In a recent Dutch study, the association between the rs10883365 variant of NKX2-3 and CD was linked to smoking status, with the risk being more pronounced in active and passive smokers^[32]. In the present study, however, we did not find an association between NKX2-3 and smoking status, and similarly, no genotype-phenotype associations were found.

In addition, Weersma *et al.*^[13] have created genetic risk profiles by combining the presence of variant alleles in IL23R, ATG16L1, IRGM, NKX2-3, 1q24, 5p13, HERC2, CCNY, 10q21 and NOD2/CARD15, and the number of risk alleles was associated with gradually increased risk for CD. Similarly, in the present study, the combination of IRGM carrier/NKX2-3 homozygote genotype was associated with an increased risk for CD, with a much higher OR compared to either of the variant alleles alone.

Recently, an association between ECM1 rs3737240 and rs13294 variants and UC has been reported in a GWAS

by Fisher *et al.*^[15], with an OR of 1.3-1.4 for the homozygous carriage of the variant allele. The association for the rs13294 variant has recently been confirmed in a Dutch study, with an OR of 1.24 in patients with UC^[33]. In contrast, no association was found in CD^[34], even though a different SNP (rs11205387) was investigated. Although the present study was powered to confirm a difference with an OR of 1.3-1.5 with adequate statistical power, we could not confirm an association between the ECM1 rs13294 variant and either UC or CD. The accidental association between homozygous carriage of the ECM1 variant allele and cutaneous manifestations ($P = 0.002$, OR = 3.36, 95% CI = 1.48-7.63, Figure 1B) requires further confirmation.

Theoretically, through influencing inflammatory responses, autophagy and epithelial-stromal interactions, polymorphisms in the above genes might be of potential importance in altering the efficacy of anti-inflammatory therapy and thereby the need for surgery. However, in the present study, none of the variant alleles was associated with the response to either steroid or infliximab therapy, or the need for surgery (resection in CD or colectomy in UC) in IBD.

In conclusion, NKX2-3 and IRGM are susceptibility loci for IBD in Eastern European patients. None of the variants investigated were associated with the need for surgery or efficacy of medical therapy. Further studies are needed to confirm the reported phenotype-genotype associations found in this study.

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COMMENTS

Background

Sequence variants in the autophagy gene immunity-related GTPase family M (IRGM) and NKX2-3 have been reported to contribute to Crohn's disease (CD) susceptibility, whereas ECM1 contributes to ulcerative colitis (UC) in genome-wide association scans in North America and Western Europe.

Research frontiers

There is a lack of data in Eastern European countries, therefore, our aim was to investigate the prevalence of IRGM rs13361189, NKX2-3 rs10883365 and ECM1 rs13294 variants. In addition, the possible association between genotype and clinical phenotype and the need for surgery is conflictive, and the association between the above genetic variants and response to medical therapy was not investigated.

Innovations and breakthroughs

In the present study, the authors showed in two well-characterized, independent

CD cohorts with strict clinical follow-up, that NKX2-3 rs10883365 variant allele was associated with increased susceptibility to CD and UC, whereas variant IRGM allele increased the risk for CD only. Our data suggest that the variant IRGM allele is associated with colon-only location, whereas in UC, the ECM1 variant was associated with cutaneous manifestations. None of the variants predicted resistance to steroids and azathioprine, efficacy of infliximab, or need for surgery.

Application

The new data presented from Eastern Europe might contribute to better understanding of genetic or environmental differences between populations and the association of those differences with disease susceptibility and phenotype.

Terminology

Vienna-Montreal classification: classification systems of disease phenotypes in CD. The classification assesses the age at presentation, disease location and disease behavior. The IRGM gene encodes an autophagy-inducing protein and plays an important role in host defense against intracellular pathogens. NKX2-3 is a member of the NKX family of homeodomain-containing transcription factors, which are implicated in many aspects of cell type specification and maintenance of differentiated tissue functions. ECM1 encodes extracellular matrix protein 1, a glycoprotein expressed in small and large intestine. Notably, ECM1 strongly activates nuclear- κ B signaling, a key immune regulator.

Peer review

The need to extend studies performed in the other parts of the world to Eastern Europe is valid, and provides a point for understanding subtle genetic or environmental differences between populations and the association of those differences with disease.

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Clinical analysis of high serum IgE in autoimmune pancreatitis

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Abstract

AIM: To clarify the clinical significance of high serum IgE in autoimmune pancreatitis (AIP).

METHODS: Forty-two AIP patients, whose IgE was measured before steroid treatment, were analyzed. To evaluate the relationship between IgE levels and the disease activity of AIP, we examined (1) Frequency of high IgE (> 170 IU/mL) and concomitant allergic diseases requiring treatment; (2) Correlations between IgG, IgG4, and IgE; (3) Relationship between the presence of extrapancreatic lesions and IgE; (4) Relationship between clinical relapse and IgE in patients treated with steroids, and (5) Transition of IgE before and after steroid treatment.

RESULTS: IgE was elevated in 36/42 (86%) patients.

Concomitant allergic disease was observed in seven patients (allergic rhinitis in three, bronchial asthma in three, and urticaria in one). There were no significant correlations between IgG, IgG4, and IgE ($r = -0.168$ for IgG, and $r = -0.188$ for IgG4). There was no significant difference in IgE in the patients with and without extrapancreatic lesions (526 ± 531 IU/mL vs 819 ± 768 IU/mL, $P = 0.163$), with and without clinical relapse (457 ± 346 IU/mL vs 784 ± 786 IU/mL, $P = 0.374$). There was no significant difference in IgE between before and after steroid treatment (723 ± 744 IU/mL vs 673 ± 660 IU/mL, $P = 0.633$).

CONCLUSION: Although IgE does not necessarily reflect the disease activity, IgE might be useful for the diagnosis of AIP in an inactive stage.

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Key words: IgE; IgG4; IgG; Autoimmune pancreatitis

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INTRODUCTION

Autoimmune pancreatitis (AIP) is a unique, benign pan-

creatic disease characterized by irregular narrowing of the pancreatic duct, swelling of the pancreas, lymphoplasmacytic infiltration and fibrosis, and favorable response to steroid therapy^[9-12]. Serologically, elevation of IgG and IgG4 is the most remarkable characteristic in this disease^[9-12]. A recent study showed that IgM and IgA were decreased in AIP^[13]. There has been no detailed clinical analysis of IgE, although some clinicians have noted elevated serum IgE in AIP or IgG4-related diseases^[14-17].

In most allergic diseases, total serum IgE levels do not reflect disease activity; however, in allergic bronchopulmonary aspergillosis, it is reported that IgE is a useful marker for therapeutic monitoring^[18-21]. The expression of T-helper type 2 (Th2) cytokines [interleukin (IL)-4, IL-5, and IL-13] are upregulated in the affected tissues of AIP^[22]. Both IgG4 and IgE production are dependent on help by Th2; therefore, all IgG4-inducing antigens are also efficient IgE inducers^[23]. As IgG4 reflects the disease activity of AIP^[12], it is reasonable to expect that IgE is also related to the disease activity of AIP and could become a clinically useful marker. Thus, we decided to clarify whether IgE is related to the disease activity of AIP from various viewpoints.

MATERIALS AND METHODS

Patients

Between 1997 and 2009, 67 patients were diagnosed as having AIP at the University of Tokyo hospital and affiliated hospitals. All the patients fulfilled the diagnostic criteria of AIP proposed by the Mayo Clinic^[3] or the revised criteria by the Japan Pancreas Society^[4]. Serum IgE was measured in 48 patients before steroid treatment. As the method of measurement was different in six patients, these patients were excluded. Thus, 42 patients whose IgE level was measured by the same method before steroid treatment were enrolled in this study. Of the 42 patients, 33 were men and nine were women. The mean age of onset was 65 years old. Thirty-seven patients received steroid treatment. Prednisolone at an initial dose of 30-40 mg/d was administered for 2-4 wk in most cases. It was then tapered by 5 mg every 2-6 wk until 10 mg/d, and 2.5-7.5 mg/d was continued as maintenance therapy in principle.

This retrospective study was approved by the review board of our institute.

Methods

Serum IgE was measured by fluorescence enzyme immunoassay. To evaluate the relationship between IgE levels and disease activity, we examined (1) frequency of high IgE (> 170 IU/mL) and concomitant allergic diseases requiring treatment; (2) correlations among IgG, IgG4, and IgE; (3) relationship between the presence of extrapancreatic lesions and IgE; (4) relationship between clinical relapse and IgE in patients treated with steroids; and (5) transition of IgE before and after steroid treatment.

With regard to allergic diseases, only diseases that required treatment during follow-up were counted. There are many extrapancreatic lesions in AIP; however, in this

study, only representative and definite lesions, including sclerosing cholangitis^[7,8,24], retroperitoneal fibrosis^[8,25], sclerosing sialadenitis^[17], interstitial pneumonia^[26], and tubulointerstitial nephritis^[27] were counted. With regard to the number of extrapancreatic lesions, we used the number of extrapancreatic lesions that were observed when IgE was measured. We do not regard intrapancreatic biliary stricture as an extrapancreatic lesion, because it is influenced by pancreatic edema^[24]. We defined "clinical relapse" as AIP-related symptomatic unfavorable events; i.e. obstructive jaundice from distal bile duct stenosis due to exacerbated pancreatitis with pancreatic swelling, increased levels of biliary enzymes caused by sclerosing cholangitis (in which extrapancreatic biliary strictures were confirmed on imaging findings), retroperitoneal fibrosis, interstitial pneumonia, and interstitial nephritis (for which simple observation seemed very inadequate and remission induction therapy was introduced). Concerning clinical relapses and IgE, we analyzed patients whose follow-up after the initiation of steroid treatment was more than 6 mo. With regard to the transition of IgE, IgE measured before steroid treatment and during maintenance steroid treatment (2.5-7.5 mg prednisolone/d) were compared.

Statistical analysis

Categorical variables were compared by the χ^2 or Fisher exact test, where appropriate. Continuous variables were reported as mean \pm SD and compared by the Student *t* test, Welch *t* test, or paired *t* test, where appropriate. A *P* value of < 0.05 was considered statistically significant. Statistical analyses were performed by the statistical software JMP 7.0.1 (SAS Institute Inc., Cary, NC, USA).

RESULTS

Frequency of high IgE and concomitant allergic diseases

The clinical profiles of 42 patients with AIP are summarized in Table 1. Serum IgE was elevated in 36/42 (86%). The average value of IgE was 679 \pm 675 IU/mL (range, 67-3000 IU/mL). No patient had concomitant parasitosis. Concomitant allergic diseases were observed in seven patients, comprising allergic rhinitis in three, bronchial asthma in three, and urticaria in one. There was no significant difference between the average IgE values of these seven patients and those of the other 35 patients (970 \pm 775 IU/mL *vs* 621 \pm 650 IU/mL, *P* = 0.216). The frequency of high IgE was 100% (7/7) in these patients, and 63% (29/35) in the others; however, this difference was not statistically significant (*P* = 0.567).

Correlations between IgG, IgG4, and IgE

The values of IgG and IgG4, which were measured at the same time as IgE before steroid treatment, were used in this analysis. Elevation of IgG and IgG4 were observed in 20 (47%) and 39 (93%) patients, respectively. The correlation coefficient of IgG and IgE was -0.168 (not significant, *P* = 0.290). The correlation coefficient of IgG4 and IgE was -0.188 (not significant, *P* = 0.235). The correla-

Table 1 Clinical profiles of 42 patients with autoimmune pancreatitis

Patient	Sex	Age	IgE (< 171 U/mL)	IgG (870-1800 mg/dL)	IgG4 (< 135 mg/dL)	Total bilirubin (0.3-1.3 mg/dL)	Concomitant allergic diseases	Extrapancreatic lesion associated with AIP
1	F	58	670	2542	592	0.6	AR	-
2	M	63	650	2055	691	3.0	AR	-
3	F	53	500	1527	143	7.9	AR	SA
4	M	64	490	2457	670	0.5	BA	-
5	M	56	1800	1712	436	0.5	BA	-
6	F	43	340	1036	223	0.9	BA	-
7	M	74	2339	1481	98	0.9	Urticaria	RF
8	F	70	480	2190	133	5.8	-	-
9	M	57	120	3793	1420	10.6	-	RF
10	M	55	480	1419	320	1.7	-	-
11	M	61	270	1878	410	0.4	-	SC
12	M	66	1200	1620	310	0.5	-	SA
13	M	79	170	1585	420	3.3	-	SC
14	M	73	290	1647	360	5.4	-	-
15	M	79	410	1404	554	0.7	-	-
16	M	76	1000	1728	65	14.1	-	SC
17	F	72	650	2384	1400	1.6	-	SA
18	F	65	190	1511	374	0.6	-	-
19	M	68	290	1656	253	2.0	-	SC
20	M	61	940	1448	578	1.6	-	-
21	F	61	640	2177	354	0.4	-	-
22	M	58	2289	1973	481	6.9	-	-
23	M	71	1915	2318	470	0.6	-	-
24	M	61	69	2215	974	0.5	-	SA
25	M	65	91	3032	1260	5.4	-	SC, RF
26	M	64	330	1730	361	0.4	-	SC
27	M	66	1330	1849	270	4.7	-	-
28	F	64	328	2898	456	12.8	-	SC
29	M	69	440	1875	270	8.7	-	-
30	M	73	70.3	2395	393	0.4	-	RF
31	M	67	660	1683	230	0.6	-	-
32	M	72	3000	1579	455	0.5	-	-
33	M	61	467	1301	331	2.9	-	-
34	M	40	320	1996	650	1.0	-	RF
35	M	62	480	1368	236	0.5	-	SC, SA
36	M	71	267	1827	458	1.3	-	-
37	M	59	625	1876	139	0.5	-	RF
38	M	73	302	2834	1800	0.5	-	SA
39	F	76	426	1458	543	0.9	-	RF
40	M	76	943	1840	431	0.7	-	SC
41	M	59	67	1338	140	0.7	-	-
42	M	64	198	1709	232	10.2	-	-

AIP: Autoimmune pancreatitis; AR: Allergic rhinitis; BA: Bronchial asthma; SA: Sialadenitis; RF: Retroperitoneal fibrosis; SC: Sclerosing cholangitis.

Table 2 Correlations between IgG, IgG4, and IgE

	Correlation coefficient	P value
IgG and IgE	-0.168	0.290
IgG4 and IgE	-0.188	0.235
IgG and IgG4	0.698	< 0.0001

tion coefficient of IgG and IgG4 was 0.698, which was significant ($P < 0.0001$) (Table 2).

Relationship between the presence of extrapancreatic lesions and IgE

Extrapancreatic lesions were observed in 20 patients (48%). Two patients had two lesions, and 18 patients had one lesion. Sclerosing cholangitis, retroperitoneal fibrosis, and sclerosing sialadenitis, were observed in nine,

Table 3 Comparison of IgE, IgG, and IgG4 between patients with and without extrapancreatic lesions

	Patients with extrapancreatic lesions ($n = 20$)	Patients without extrapancreatic lesions ($n = 22$)	P value
IgE (IU/mL)	526 \pm 531	819 \pm 768	0.163
IgG (mg/dL)	2065 \pm 644	1775 \pm 396	0.093
IgG4 (mg/dL)	588 \pm 505	392 \pm 161	0.110

seven, and six patients, respectively. The IgE levels of the patients with and without extrapancreatic lesions were compared, and the same analysis was performed for IgG and IgG4. The results are shown in Table 3. IgG tended to be related to the presence of extrapancreatic lesions, although statistical significance was not attained ($P = 0.093$). No such tendency existed for IgE.

Table 4 Comparison of IgE, IgG, and IgG4 between patients with and without clinical relapses

	Patients with clinical relapses (n = 5)	Patients without clinical relapses (n = 28)	P value
IgE (IU/mL)	457 ± 346	784 ± 786	0.374
IgG (mg/dL)	1898 ± 424	1915 ± 579	0.953
IgG4 (mg/dL)	266 ± 157	558 ± 429	0.148

Table 5 Transition of IgE, IgG, and IgG4 before and after steroid treatment

	Before	After	P value
IgE (IU/mL) (n = 29)	723 ± 744	673 ± 660	0.633
Proportion of high IgE	26/29	23/29	0.470
IgG (mg/dL) (n = 30)	1891 ± 566	1155 ± 315	< 0.0001
Proportion of high IgG	14/30	1/30	0.0002
IgG4 (mg/dL) (n = 28)	557 ± 429	229 ± 112	0.0002
Proportion of high IgG4	27/28	20/28	0.0248

Normal range, IgE: < 171 IU/mL, IgG: 870-1800 mg/dL, IgG4: < 135 mg/dL.

Relationship between clinical relapse and IgE in the patients treated with steroids

There were 33 patients whose follow-up period was more than 6 mo. The mean follow-up period was 52 mo (range, 8-141 mo). Clinical relapse was observed in five patients. The style of clinical relapse was pancreatitis in two, interstitial pneumonia in two, and sclerosing cholangitis in one. Their relapses occurred 16 mo after the initiation of steroid therapy on average (range, 3-26 mo). The mean follow-up period was the same between the patients with and without clinical relapse (53.0 mo *vs* 51.8 mo, *P* = 0.929). IgE levels of the patients with and without clinical relapse were compared, and the same analysis was performed for IgG and IgG4. The results are shown in Table 4. Neither IgE, IgG nor IgG4, were related to later clinical relapses.

Transition of IgE before and after steroid treatment

IgE measured before steroid treatment and during maintenance therapy could be compared in 29 patients (Figure 1). IgE increased in 10, and decreased in 18. There was no significant difference in IgE between before and after steroid treatment (723 ± 744 IU/mL *vs* 673 ± 660 IU/mL, *P* = 0.633). Abnormally high IgE (> 170 IU/mL) was observed in 90% (26/29) before steroid treatment, and in 79% (23/29) after steroid treatment (*P* = 0.470). By contrast, IgG and IgG4 did show significant differences before and after steroid treatment (Table 5).

DISCUSSION

High IgE in AIP has been frequently documented^[14-17], but its frequency and clinical significance were unknown. Kamisawa *et al.*^[14] reported that elevation of IgE was observed in 34% (12/35) of patients, and that all the patients with high IgE had present and/or past histories of allergic diseases, although none of the patients with normal IgE had such histories. In the present study, the

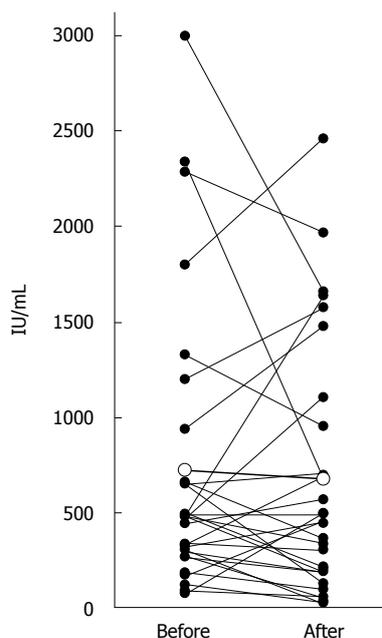


Figure 1 IgE levels measured before steroid treatment (Before) and during maintenance therapy (After) were compared in 29 patients. White circles show average values.

frequency of high IgE was surprisingly high at 86% (36/42), which might be equal to frequency of high IgG4 (73.3%-94.3%)^[12]. On the other hand, unlike the previous report, there seemed no definite relationship between IgE and allergic diseases. It seemed unreasonable to count allergic diseases that occurred decades ago. In addition, it is difficult to accurately judge past histories of mild allergic diseases. Thus, we included only concomitant allergic diseases. For reference, there were at least eight patients who had past histories of allergic diseases, but no concomitant ones. Comparison between patients with (*n* = 15) and without (*n* = 27) present and/or past histories of allergic diseases showed no significant difference in mean IgE values (654 ± 605 IU/mL *vs* 693 ± 721 IU/mL, *P* = 0.860) and frequency of high IgE (93% *vs* 81%, *P* = 0.395); therefore, the presence of past allergic disease did not affect the results.

From the results shown in Table 3, IgE levels appear to be unrelated to disease activity from the viewpoint of extrapancreatic lesions. On the contrary, it is possible that high IgE is associated with lower disease activity, when considering the higher IgE levels in the group without extrapancreatic lesions, and the negative correlation coefficient of IgG (IgG4) and IgE. It is difficult to analyze the results shown in Table 4 because of the small number of patients with clinical relapses. Nevertheless, it is likely that high IgE is not a risk factor for later clinical relapses, especially considering the higher IgE levels in the group without clinical relapses. IgG4 seems a little high in the group without clinical relapses (Table 4), which is similar to previous reports^[8,28].

It was of great interest whether IgE could become a useful marker for therapeutic monitoring in AIP, like IgG and IgG4. From the results shown in Table 5, we

cannot help but conclude that IgE is not a useful marker. However, this phenomenon is not strange in other allergic diseases. For example, Gunnar *et al*^[18] reported that steroid treatment did not alter IgE levels in patients with atopic dermatitis. Kumar *et al*^[19] showed that changes in serum IgE are not related to severity of asthma or allergic rhinitis. Exceptionally, in allergic bronchopulmonary aspergillosis, it is reported that the response of IgE (35% or more reduction) to steroid treatment is a sensitive marker in the management^[20].

Although IgE does not seem to reflect disease activity, we speculate that this feature might be useful for the diagnosis of inactive AIP. Indeed, three patients in the present series showed low IgG4 (65, 98, and 133 mg/dL) at the diagnosis, but all of them showed high IgE (1000, 2339 and 480 IU/mL). When patients with a past history suggestive of AIP, such as voluntarily improved jaundice, do not show high IgG and IgG4, IgE should be measured. If IgE is also low, the possibility that their diagnosis is AIP will be low. If IgE is high, it might indicate AIP in an inactive stage.

In summary, the elevation of serum IgE is very frequent in AIP. It is also observed even in patients without other allergic diseases. IgE might not reflect the disease activity; however, it might be useful for the diagnosis of AIP in an inactive stage.

COMMENTS

Background

It is known that elevation of serum IgE is frequently observed in autoimmune pancreatitis (AIP). However, its clinical significance has not yet been clarified.

Research frontiers

This study demonstrated the frequency of high IgE in AIP, and investigated whether IgE is related to the presence of extrapancreatic lesions and later clinical relapses. In addition, the transition of IgE before and after steroid treatment was investigated to confirm whether IgE can become a marker for therapeutic monitoring.

Innovations and breakthroughs

This study confirmed the high frequency of elevated serum IgE in AIP, although IgE does not seem to be related to the disease activity.

Applications

Measuring IgE might be useful for the diagnosis of AIP especially in an inactive stage.

Peer review

These data about IgE were not positive, which means that IgE is not considered as a useful marker for AIP. However, the author revealed that many (86%) AIP patients have IgE elevation and some AIP patients with low IgG4 have a high level of IgE. IgE should be considered as one of the supportive parameters for diagnosis of AIP and the authors succeeded in clarifying that.

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Segmental gastrectomy with radical lymph node dissection for early gastric cancer

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Abstract

AIM: To describe a new surgical technique and evaluate the early results of segmental gastrectomy (SG) with modified D2 lymph node (LN) dissection for early gastric cancer (EGC).

METHODS: Fourteen patients with EGC underwent SG with modified D2 dissection from 2006 to 2008. Their operative results and postoperative courses were compared with those of 17 patients who had distal gastrectomy (DG) for EGC during the same period.

RESULTS: Operating time, blood loss, and hospital stay were similar between the 2 groups. Postoperative complications developed significantly more frequently in the DG group than in the SG group. Mean number of dissected LNs per each station in the SG group was comparable with that in the DG group. Postoperative recovery of body weight was significantly better in the SG group than in the DG group. The incidence of reflux esophagitis and gastritis after surgery was less frequent in the SG group than in the DG group.

CONCLUSION: SG with modified D2 LN dissection may be a new function-preserving gastrectomy that is feasible for treatment of EGC with possible LN involvement.

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Key words: Gastrectomy; Early diagnosis; Gastric cancer; Lymph node; Metastasis; Gastrointestinal surgical procedures

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INTRODUCTION

Less invasive surgery for early gastric cancer (EGC) has been more commonly employed in Japan^[1-4]. Segmental gastrectomy (SG), which was originally applied for peptic ulcers, is one type of limited gastrectomy available for treating EGC^[5]. SG for EGC is generally accompanied only by dissection of the lymph nodes (LNs) adjacent to tumors, although only a few studies regarding the application of SG in EGC have been reported^[1-4]. To establish SG with adjacent LN dissection as a valid option for surgical treatment of EGC, it is necessary to demonstrate intraoperatively that there is no lymph node metastasis (N0). However, at present, it is difficult to determine the status of LN metastasis intraoperatively, even using the sentinel node (SN) navigation method^[6-8].

The superiority of limited gastrectomy over conven-

tional D2 gastrectomy for EGC in terms of postoperative quality of life seems apparent, as previously reported^[1,4,9,10]. In 1995, Sawai *et al*^[11] developed pylorus-preserving gastrectomy (PPG) with D2 dissection by preservation of the infrapyloric artery as a function-preserving gastrectomy. Although this technique is considered to be applicable to submucosal or undifferentiated gastric cancer, there remains a risk of adverse events such as postoperative gastric stasis and reduced capacity of the remnant stomach.

We developed SG with modified D2 dissection and have applied it to EGC that do not meet endoscopic treatment criteria. We report the technique here and evaluate the early results of SG with modified D2 dissection for EGC.

MATERIALS AND METHODS

Between April 2006 and November 2008, 35 patients with EGC in the middle or lower third of the stomach which did not meet endoscopic treatment criteria underwent gastrectomy at our institution: 17 patients who underwent SG and 18 patients who underwent conventional distal gastrectomy (DG) with D2 dissection. The criteria for endoscopic treatment is EGC with differentiated histology, invasion limited to the mucosal layer, a diameter smaller than 2 cm, and no ulcer findings. In this study, SG was distinguished from PPG by defining that the remaining pyloric cuff needed to be more than 4 cm in SG. When the distance from the distal edge of the resection to the pylorus was < 4 cm, DG was performed instead of PPG.

A total of 14 patients received SG with modified D2 dissection. The remaining 3 patients who were excluded from this study received SG only with adjacent LN dissection because of intraoperative determination of apparent mucosal cancer with no LN metastasis.

In 3 out of 18 patients in the DG group, SG was converted to DG based on intraoperative findings including suspected T2 tumor or positive LN metastasis.

Patients were followed every 3 mo after surgery. The follow-ups also included an endoscopy and computed tomography 1 year after surgery. The operative and postoperative results were compared between the SG and DG groups.

Operative procedures

To make it possible to locate the tumor intraoperatively, proximal and distal margins of the tumor were marked by endoscopic clipping before surgery. After laparotomy, we explored the abdominal cavity and determined if the preoperative diagnosis was correct. If a T2 or T3 tumor was suspected or LN metastases were apparent, DG or total gastrectomy (TG) with D2 dissection was performed. Swollen and/or hard palpable LNs located adjacent to the tumor were excised and immediately examined by frozen section analysis. Infrapyloric LNs (station 6) and those along the common hepatic artery (CHA; station 8a) were also routinely subjected to frozen section analysis. DG or TG with D2 dissection was performed if LN metastasis

was proved by frozen section analysis, however, if T1N0 was confirmed SG with modified D2 dissection was carried out.

The resection line of the stomach was made 2 cm and 5 cm away from the tumor margin with differentiated and undifferentiated histology, respectively. The greater omentum was preserved, and the gastrocolic ligament corresponding to the resection area of the stomach was dissected, after separation, at least 3 cm away from the gastroepiploic vessels. For dissection of LNs located in station 6 and along the greater curvature (station 4d), right gastroepiploic vessels were skeletonized, allowing excision of adjacent LNs, and divided at the distal resection line of the stomach (Figure 1A). The suprapyloric LNs (station 5) were dissected in the same manner. The right gastric artery was skeletonized and divided distally to the second or third branch (Figure 1B). The left halves of LNs along the proper hepatic artery (station 12a) were removed, and the hepatic and pyloric branches of vagus nerves were preserved. Right paracardial LNs (station 1), LNs along the lesser curvature (station 3), and the left gastric artery (LGA) (station 7) were dissected by dividing the LGA at its origin. The celiac branch of the vagus nerve was also dissected. Dissection of the upper portion of station 1 LNs was occasionally omitted in order to preserve the origin of the hepatic branch of the vagus nerve and the anterior branch of the Latarjet nerve. LNs along the CHA (station 8a, 8p), around the celiac axis (station 9), and along the proximal splenic artery (station 11p) were routinely dissected. LNs along the left gastroepiploic artery (LGEA) (station 4sb) were dissected by dividing the last few branches of the LGEA. After transection of the stomach, the surgical margins were subjected to intraoperative histological examination by frozen section analysis. Reconstruction was performed using hand-sewn end-to-end anastomosis (Figure 1C).

Statistical analysis

Statistical analysis was performed using either the χ^2 test or Student's *t*-test. A *P*-value < 0.05 was considered significant.

RESULTS

There were no differences between the 2 groups in terms of sex, age, and tumor characteristics, with the exception of tumor location (Table 1). In 1 patient of the DG group and 2 patients of the SG group, LN metastasis was proven to be positive.

Operative data are shown in Table 2. Operating time, blood loss, and hospital stay were similar between the two groups. However, postoperative complications developed significantly more frequently in the DG group than in the SG group. There were no instances of anastomotic leakage, hemorrhage, gastric stasis, wound infection or operative death in either group.

The mean number of dissected LNs per station was comparable between the 2 groups (Table 3).

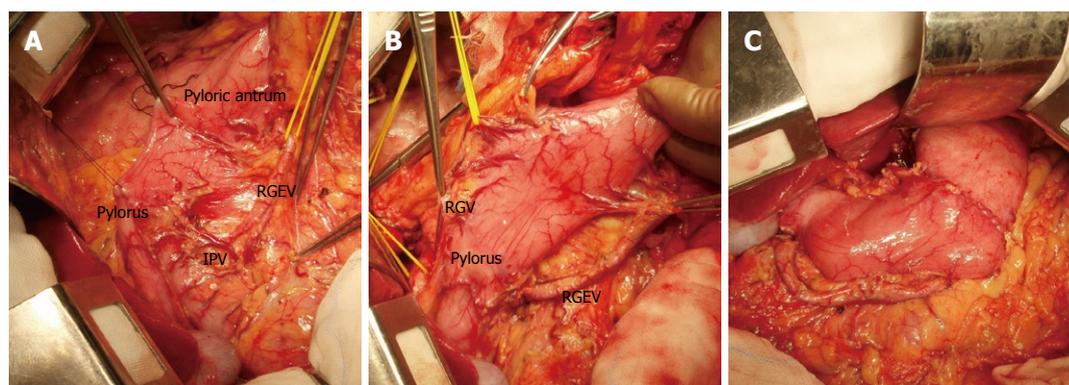


Figure 1 Photographs during surgery. A: The right gastroepiploic vessels were skeletonized allowing excision of adjacent lymph nodes (LNs) (stations 6 and 4 d). The surrounding nerve plexuses were preserved; B: For dissection of the suprapyloric LNs (station 5), the right gastric artery was skeletonized and divided distally to the 3rd branch; C: Reconstruction was performed using hand-sewn end-to-end anastomosis. RGEV: Right gastroepiploic vessels; IPV: Infrapyloric vessels; RGV: Right gastric vessels.

Table 1 Comparison of clinicopathological characteristics between the 2 groups

	SG (n = 14)	DG (n = 18)	P
Age (yr, mean ± SD)	63.9 ± 9.6	60.0 ± 12.9	0.204
Sex (M/F)	9/5	7/11	0.154
Location of tumor			0.002
Upper	0	0	
Middle	13	7	
Lower third of the stomach	1	11	
Depth of invasion			0.589
Mucosa	4	8	
Submucosa	8	9	
Muscularis propria	1	1	
Subserosa	1	0	
Histological type			0.358
Differentiated	10	11	
Undifferentiated	4	7	
Lymph node metastasis			0.401
No	12	17	
Yes	2	1	

SG: Segmental gastrectomy; DG: Distal gastrectomy.

Table 2 Operative results (mean ± SD)

	SG (n = 14)	DG (n = 18)	P
Operating time (min)	273 ± 65	262 ± 46	0.589
Blood loss (mL)	206 ± 124	179 ± 101	0.511
Hospital stay (d)	14.9 ± 2.6	16.7 ± 5.0	0.227
Complications	0	5	0.032
Wound infection	0	0	
Anastomotic leakage	0	0	
Hemorrhage	0	0	
Cholecystitis	0	2	
Pancreatitis	0	1	
Pancreatic fistula	0	1	
Adhesive ileus	0	1	
Operative death	0	0	1.000

SG: Segmental gastrectomy; DG: Distal gastrectomy.

The postoperative course is summarized in Table 4. Postoperative recovery of body weight was significantly better in the SG group than in the DG group. The inci-

Table 3 Numbers of dissected lymph nodes according to each station (mean ± SD)

Lymph node station	SG (n = 14)	DG (n = 18)	P
Right paracardial (1)	2.0 ± 1.3	3.1 ± 1.2	0.068
Left paracardial (2)	1.1 ± 1.5	0.7 ± 1.6	0.462
Along the lesser curvature (3)	8.7 ± 4.7	10.8 ± 7.3	0.362
Along the LGEA (4sb)	1.2 ± 2.1	1.4 ± 1.9	0.754
Along the RGEA (4d)	9.2 ± 4.9	11.7 ± 4.9	0.155
Suprapyloric (5)	0.3 ± 0.6	0.6 ± 0.9	0.286
Infrapyloric (6)	3.7 ± 3.7	5.6 ± 2.6	0.118
Along the LGA (7)	3.7 ± 2.4	4.3 ± 2.7	0.473
Along the CHA (8)	2.7 ± 1.2	3.3 ± 1.5	0.232
Along the celiac axis (9)	2.8 ± 1.6	3.3 ± 2.0	0.442
Along the proximal SA (11p)	1.5 ± 1.5	2.0 ± 1.7	0.412
Along the PHA (12a)	0.5 ± 1.0	0.2 ± 0.5	0.246
Along the SMV (14v)	-	1.2 ± 2.1	-

SG: Segmental gastrectomy; DG: Distal gastrectomy; LGEA: Left gastroepiploic artery; RGEA: Right gastroepiploic artery; LGA: Left gastric artery; CHA: Common hepatic artery; SA: Splenic artery; PHA: Proper hepatic artery; SMV: Superior mesenteric vein.

Table 4 Postoperative course (mean ± SD)

	SG (n = 14)	DG (n = 18)	P
Gastric stasis	0	0	1.000
Dumping syndrome	1	1	0.854
Body weight change ratio (%)	96.8 ± 6.1	90.4 ± 7.0	0.012
Laboratory data			
Lymphocytes (/mm ³)	2007 ± 437	1977 ± 646	0.885
Total protein (g/dL)	6.8 ± 0.3	7.0 ± 0.3	0.156
Total cholesterol (mg/dL)	215 ± 34	192 ± 32	0.063
Endoscopic examination			
Reflux gastritis	1	5	0.138
Reflux esophagitis	0	4	0.059

SG: Segmental gastrectomy; DG: Distal gastrectomy.

dence of reflux esophagitis and gastritis after surgery was less frequent in the SG group than in the DG group.

No recurrence or death was observed in either group during a median follow-up period of 32.8 mo. One patient in the SG group developed colon cancer during the

follow-up period and subsequently underwent curative resection.

DISCUSSION

SG has not been previously used to treat EGC, since it was first reported by Wangenstein *et al*^[5] as an operation for peptic ulcer. In 1999, Ohwada *et al*^[2] modified the procedure and reported its use for treatment of EGC of the middle third of the stomach. However, previous studies concerning the use of SG for the treatment of EGC are limited, primarily due to difficulty in diagnosing LN metastasis accurately during surgery, and it being performed with very limited LN dissection. Deterioration of the radicality caused by omitting or limiting LN dissection should be avoided, because EGC can be treated with conventional D2 gastrectomy with excellent prognosis. Therefore, SG with limited LN dissection is not recommended unless T1N0 is confirmed.

On the other hand, a method for accurate intraoperative diagnosis of LN metastasis has yet to be established. Recently, SN biopsy has been used to assist intraoperative diagnosis of LN metastasis during surgical treatment of EGC. The SN concept seems feasible for treatment of EGC as described previously, however, several important issues including optimal tracer, method of injection, and false negative cases, still need to be resolved^[6-8].

Our modified D2 dissection was considered to be comparable with conventional D2 dissection, because dissected stations in our SG corresponded with those in conventional D2 dissection. The mean number of dissected LNs of station 1 tended to be smaller in the SG group than in the DG group. This will be because dissection of the upper half of station 1 was occasionally omitted in order to preserve the anterior branches of the vagus nerve along the lesser curvature of the proximal remnant stomach, which may help maintain postoperative motility of this portion. The influence of limited dissection of station 1 on the oncological outcome is unclear, however, tumor recurrence resulting from incomplete dissection of station 1 has not been seen so far. Even in 3 patients whose LN metastasis was positive in the DG or SG group, no recurrence has been observed. In 1 of 2 patients whose LN metastasis was positive in the SG group, positive LN metastasis was proved after surgery in station 7 which belongs to the second tier. In the other 2 patients, LN metastasis was positive in station 3. These results may support the quality and effectiveness of our modified D2 dissection and the impact of D2 dissection.

In our procedures, 2-5 LNs were subjected to frozen section analysis. Station 8a was routinely examined by frozen section analysis. The frequency of LN metastasis in station 8a is relatively high even in EGC, and stations 7, 8a, and 11p are sometimes SN stations although they belong to the second tier^[6,8,12-14]. Once the tumor advances to stage T2 or T3, lymphatic vessels can be obstructed by cancerous invasion, and metastasis in distant LNs can occur even in the absence of involvement of LNs adjacent to tumors. In the case where station 7 LN was proved

positive after SG, intraoperative frozen section analysis detected no metastasis of stations 3 and 8a. Therefore, it is not recommended to limit LN dissection even if frozen section analysis reveals no LN involvement. Frozen section analysis with LN sampling was performed by us in order to rule out patients with positive LN metastasis rather than to confirm N0.

Unexpectedly, postoperative gastric stasis has not been observed in our patient population thus far. The precise mechanisms of development of gastric stasis after limited gastrectomy such as PPG remain unclear^[15-18]. The main causes of gastric stasis are generally thought to include damage to the vagus nerve, insufficient blood supply to the pyloric region, or tonic and phasic contractions of the pylorus. In our procedure, not only the blood supply but also the venous drainage of the pyloric region is more sufficient than in PPG. These findings may have contributed to good maintenance of pyloric motility.

The present study demonstrated the safety and effectiveness of our procedures. This procedure could be a new function-preserving gastrectomy that is feasible for treatment of EGC with possible LN involvement. However, further studies including a larger number of patients and longer follow-up periods are essential for a more definitive conclusion.

COMMENTS

Background

Less invasive surgery for early gastric cancer (EGC) has been more commonly employed based on the background of an increase in EGC. Although it has been reported that pylorus-preserving gastrectomy can be performed with D2 dissection, there has been no report on segmental gastrectomy with D2 dissection.

Research frontiers

A sentinel node navigation method has been developed for accurate intraoperative determination of lymph node (LN) metastasis during surgery for EGC.

Innovations and breakthroughs

This is the first report to demonstrate that segmental gastrectomy can be performed with D2 dissection for treatment of EGC.

Applications

The superiority of function-preserving gastrectomy over conventional D2 gastrectomy for EGC in terms of postoperative quality of life is apparent. However, limited LN dissection accompanying function-preserving gastrectomy may reduce the radicality of gastrectomy for EGC. This procedure may be applicable to EGC with possible LN involvement.

Terminology

Segmental gastrectomy is one of the limited gastrectomies in which the central one third portion of the stomach is resected. The sentinel node is generally defined as the lymph node which receives the lymphatic flow first from the tumor.

Peer review

This is an interesting small series and I think it has value. I would like more information concerning the pathological outcomes before accepting the conclusions and suggestions in the discussion.

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Predictive factors for lymph node metastasis in early gastric cancer

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Abstract

AIM: To analyze the predictive factors for lymph node metastasis (LNM) in early gastric cancer (EGC).

METHODS: Data from patients surgically treated for gastric cancers between January 1994 and December 2007 were retrospectively collected. Clinicopathological factors were analyzed to identify predictive factors for LNM.

RESULTS: Of the 2936 patients who underwent gastrectomy and lymph node dissection, 556 were diagnosed with EGC and included in this study. Among these, 4.1% of patients had mucosal tumors (T1a) with LNM while 24.3% of patients had submucosal tumors

with LNM. Univariate analysis found that female gender, tumors ≥ 2 cm, tumor invasion to the submucosa, vascular and lymphatic involvement were significantly associated with a higher rate of LNM. On multivariate analysis, tumor size, lymphatic involvement, and tumor with submucosal invasion were associated with LNM.

CONCLUSION: Tumor with submucosal invasion, size ≥ 2 cm, and presence of lymphatic involvement are predictive factors for LNM in EGC.

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Key words: Early gastric cancer; Lymph node metastasis; Endoscopic treatment; Endoscopic submucosa dissection; Depth of tumor invasion

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Sung CM, Hsu CM, Hsu JT, Yeh TS, Lin CJ, Chen TC, Su MY, Chiu CT. Predictive factors for lymph node metastasis in early gastric cancer. *World J Gastroenterol* 2010; 16(41): 5252-5256 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v16/i41/5252.htm> DOI: <http://dx.doi.org/10.3748/wjg.v16.i41.5252>

INTRODUCTION

The term early gastric cancer (EGC) describes gastric cancers involving the mucosa or submucosa irrespective of the presence of lymph node metastasis (LNM). Radical surgery including lymph node dissection has been the

standard treatment for early gastric cancer; however, LNM has only been associated with approximately 8% to 20% of EGC cases^[1-3]. Unnecessary surgery could be avoided and endoscopic treatment might be a consideration in patients with EGC with negligible risk of LNM. Prior studies have demonstrated that the presence of LNM is the most significant factor for survival in patients with EGC^[4,5] and usually constitutes the watershed between radical and endoscopic surgery. Identification of LNM cannot be achieved *via* endoscopic ultrasonography or computed tomography because the lymph node size is not a reliable parameter for detection of metastasis^[1,2]. Many retrospective studies on EGC have established an indication for endoscopic treatment^[6] and the probability of LNM in EGC has been estimated based on macroscopic-endoscopic tumor characteristics and histopathological findings.

According to the treatment guidelines for gastric cancer in Japan^[7] the indication for endoscopic treatment such as endoscopic mucosal resection (EMR) or endoscopic submucosal dissection (ESD) are patients with non-ulcerated tumors < 2 cm. Several investigators are currently attempting to extend the indication for endoscopic treatment to include: differentiated type, intramucosal cancer without ulcer, > 2 cm in size; differentiated type, intramucosal cancer, ≤ 3 cm in size if ulcerated; and, undifferentiated type, intramucosal tumor without ulcer, ≤ 2 cm in size (Table 1).

While endoscopic treatment for EGC is widely adapted in Japan and Korea using various criteria^[4,8-10], it remains uncertain whether these guidelines for EMR/ESD are applicable to patients in areas outside of Japan and Korea. Japan and Korea have the highest gastric cancer rate in the world^[11,12] and between 30% and 70% of all gastric cancers are diagnosed as EGCs. In other countries, EGCs account for only about 5% to 15% of all gastric cancers^[13,14]. Japan and Korea have national screening programs in which the use of chromoendoscopy could increase the detection rate of EGC. Race, diet, and other factors such as pathologic diagnosis may explain differences in the diagnosis of EGC between Japan and other countries^[15,16]; however, comparable data about EGC from other countries is rare or only involve a small case series^[17]. The purpose of this study was to identify factors related to LNM in EGC and to elucidate which subgroup of EGC patients could be treated with EMR or ESD instead of radical surgery.

MATERIALS AND METHODS

Between January 1994 and December 2007, 2936 patients underwent gastrectomy for gastric cancer in the Department of Surgery, Chang Gung Memorial Hospital, Taipei, Taiwan, China. Clinicopathological data were obtained from a retrospectively constructed medical database, which had been reviewed by IRB, Chang Gung Memorial Hospital. In total, 556 of these patients were diagnosed with primary EGC and were included in this

Table 1 Extended indications for endoscopic mucosal resection/endoscopic submucosal dissection according to the treatment guidelines for gastric cancer in Japan

Differentiated type, mucosal cancer, ulcer (-), > 2 cm
Differentiated type, mucosal cancer, ulcer (+), ≤ 3 cm
Undifferentiated type, mucosal cancer, ulcer (-), ≤ 2 cm

Additional lymph node resection is not necessary when lymphovascular invasion is absent and also when it is not deeper than SM1 (-500 μm).

study. There were 330 men and 226 women with a median age of 62 years (range: 21-89 years).

Poorly differentiated adenocarcinomas, signet ring cell carcinomas, and mucinous adenocarcinomas were classified as undifferentiated tumors. Well and moderately differentiated tubular adenocarcinoma and papillary adenocarcinoma were grouped together as differentiated tumors. Associations between the various clinicopathological factors and the presence of LNM were analyzed to identify risk factors of LNM. These factors included: gender; age (< 65 years or ≥ 65 years), carcinoembryonic antigen (CEA, < 5 ng/mL or ≥ 5 ng/mL), gross appearance, presence of an ulcer, histological type, depth of invasion (mucosa or submucosa), lymphatic involvement, and vascular involvement. Endoscopic macroscopic appearance was evaluated based on the Japanese Classification of Gastric Carcinoma established by the Japanese Research Society for Gastric Cancer^[18]. Gross tumor findings were classified into five groups: type I (protruded); II a (superficially elevated); II b (flat); II c (superficially depressed); or III (excavated). Macroscopic findings were defined as elevated types (type I, II a, and combined I or II a with II b), flat type (type II b), or depressed types (type II c, III, and any combination of II b, II c or III). When both elevated and depressed types were observed in one lesion, the lesion was defined as mixed type. An ulcer was identified based on the presence of an ulcer or ulcer scar defined endoscopically as converging folds and recognized histologically as a deformity of the muscularis propria or fibrosis in the submucosal layer^[19].

Specimens were fixed in 5% formaldehyde and the tumor area and surrounding normal tissue were completely embedded in paraffin. The size (largest diameter) of each carcinoma was measured by the pathologist after fixation. From each block, 2 μm thick sections were cut and stained with hematoxylin and eosin. The depth of infiltration was measured at the deepest point of penetration of the cancer cells^[20]. The pT1 category was confirmed as well as the subdivision in pT1a (limited to the mucosa or muscularis mucosa) and pT1b (submucosa).

All dissected lymph nodes were analyzed microscopically for metastatic disease. When necessary, additional lymph node sections were analyzed and special staining was applied. Immunohistochemistry for micrometastasis was not performed.

Statistical analysis

Calculations were performed using SPSS for Windows

Table 2 Clinicopathological features of 556 patients diagnosed with early gastric cancer and univariate analysis of potential risk factors of regional lymph node metastasis

Variables	Positive rate of lymph node metastasis (%)	P value
Age (yr)		0.876
< 65	40/288 (13.9)	
≥ 65	36/268 (13.4)	
Gender		0.012
Male	35/330 (10.6)	
Female	41/226 (18.1)	
Size (cm)		< 0.001
< 2	34/352 (9.7)	
≥ 2	42/204 (20.6)	
Endoscopic appearance		0.993
Elevated	9/65 (13.8)	
Depressed	43/307 (14.0)	
Flat	16/123 (13.0)	
Mixed	8/61 (13.1)	
Serum CEA (ng/mL)		0.152
< 5	43/336 (12.8)	
≥ 5	7/32 (21.9)	
Depth of invasion		< 0.001
T1a	12/293 (4.1)	
T1b	64/263 (24.3)	
Histology differentiation		0.759
Differentiated	41/309 (13.3)	
Undifferentiated	35/247 (14.2)	
Vascular invasion		< 0.001
Absence	68/546 (12.5)	
Presence	8/10 (80.0)	
Lymphatic involvement		< 0.001
Absence	44/517 (8.5)	
Presence	32/39 (8.2)	
Ulcer		0.449
Absence	22/182 (12.1)	
Presence	54/374 (14.4)	

(version 11.5K, Chicago, Illinois). The χ^2 test was used to assess potential risk factors of LNM by bivariate comparisons of the categorical variables. Significant factors noted by univariate analysis were subsequently entered into a multivariate logistic regression model for analysis. *P* values < 0.05 were considered to be statistically significant.

RESULTS

EGCs were diagnosed in 18.9% of the gastric cancer cases (556 cases). Of these 556 diagnosed with EGC, 76 (13.7%) had LNM. As shown in Table 2, 293 (52.7%) were intramucosal tumors and 4.1% of these had LNM. In addition, 263 lesions (47.3%) penetrated the submucosa and 24.3% of submucosal tumors had LNM.

Univariate analysis identified that female gender, size ≥ 2 cm, tumor invasion to the submucosa, presence of lymphatic involvement, and presence of vascular involvement were significantly associated with a higher rate of LNM (Table 2). Tumor size ≥ 2 cm (*P* < 0.008), deep penetration into the submucosa (*P* < 0.001), and lymphatic involvement (*P* < 0.001) remained significant in multivariate analysis (Table 3).

Table 4 demonstrates the incidence of LNM of our

Table 3 Multivariate analysis of potential risk factors for regional lymph node metastasis

Variables	Odds ratio (95% CI)	P value
Gender (female/male)	1.49 (0.35-1.1)	0.163
Tumor size (≥ 2 cm/< 2 cm)	2.28 (1.20-4.17)	0.008
Vascular invasion (yes/no)	1.86 (0.23-12.65)	0.598
Lymphatic invasion (yes/no)	27.2 (10.3-74.8)	< 0.001
Depth of invasion (T1b/T1a)	4.91 (2.44-9.89)	< 0.001

Table 4 Incidence of lymph node metastasis in our patients fulfilled the criteria used in endoscopic treatment for early gastric cancer in Japan

Criteria	Patient number with lymph node metastasis/total patient	Incidence (%)
Non-ulcerated, differentiated, intramucosal tumor without lymphovascular invasion, ≤ 2 cm	0/42	0
Non-ulcerated, differentiated, intramucosal tumor without lymphovascular invasion, any size	0/77	0
Ulcerated, intramucosal tumor, without lymphovascular invasion, ≤ 3 cm	0/78	0
Non-ulcerated, undifferentiated intramucosal tumor without lymphovascular invasion, ≤ 2 cm	3/35	8.6

patients fulfilled the criteria used for endoscopic treatment in EGD Japan^[7]. In patients without lymphovascular invasion, 42 (tumor size ≤ 2 cm) and 77 (any tumor size) patients with differentiated intramucosal cancers and no ulceration did not have LNM; intramucosal lesions with ulcer, size ≤ 3 cm were found in 78 patients, who had no LNM; 3 of 35 patients with undifferentiated intramucosal tumors, no ulceration and size ≤ 2 cm had LNM.

DISCUSSION

The incidence of LNM in EGC ranges from 2.6% to 4.8% in mucosal cancers and 16.5% to 23.6% in submucosal cancers^[21,22]. In this study the positive rates of LNM in intramucosal and submucosal lesions were 4.1% and 24.3%, respectively, in line with the previous reports^[21,22]. Endoscopic treatment for gastric cancer not only preserves gastric function but also helps maintain the patient's quality of life. For patients with EGC, "early" treatment is advocated as the best option for obtaining a complete cure. At present, a correct diagnosis of LNM is impossible during either EMR or ESD. This means that if LNM exists at the time of EMR or ESD, recurrence is very likely. For this reason, multiple patient- and tumor-related variables are currently under investigation as predictors of lymph node involvement^[23], particularly in Japan and Korea. Many investigators have suggested possible extended criteria for local treatment^[4].

In areas outside of Japan and Korea, the possibility

of using the above-described criteria remains problematic. Japan and Korea have the highest rate of gastric cancer rate in the world^[11,12] and that in these countries, between 30% and 70% of all gastric cancers are diagnosed as EGCs. In other areas or countries, EGCs account for only about 5% to 15% of all gastric cancers^[13,14,24].

National screening programs and chromoendoscopy could improve the detection rate of EGC; however, race, diet, and other factors such as pathological diagnosis may explain differences in the diagnosis of EGC between Japan and other countries. For example, there are some intestinal-type mucosal cancers in Japan that are not regarded as cancer in Western countries^[15,16]. Hölscher *et al.*^[17] reported that the rate of LNM in mucosal cancer in one European series (6.5%) is higher than reported in Asian countries (2.7%). These differences are even greater if study data are limited to Japan and Korea; however, no difference in submucosal cancer exists (23.9% *vs* 22.1%). Therefore, whether the standard treatment employed in Japan and Korea can be used in other countries remains unknown. Compared with the data generated in this study, the rate of EGC was 18.9%, which is lower than that previously reported in Japan and Korea and similar to the reports from the United States and Europe. Our results revealed that the rate of LNM in intramucosal cancer was 4.1%, higher than the value published from Japan and Korea^[17]. This might be explained due to the bias of histology criteria employed in our study (similar to those used in Western countries) and Japan and Korea.

In this study, various clinicopathological factors including gender, age, CEA levels, gross appearances, histological type, invasion depth, lymphatic involvement, and vascular involvement were analyzed for LNM in EGC. Our results showed that female gender was a significant factor in univariate analyses, but was not evident in multivariate analyses. Other research teams reported that being female was associated with LNM in both depressed EGCs and differentiated submucosally invasive EGC^[10,25], possibly related to estrogen level^[26]. At present, the precise link between gender and LNM remains unclear and further biologic studies are required to explain this effect.

Many studies suggest that serum CEA is an independent risk factor for hematogenous recurrence of gastric carcinoma^[27]. Ikeda *et al.*^[28], for example, reported that stage II and III gastric cancer patients with higher preoperative CEA levels had frequent liver metastasis. This analysis, however, included all stages of gastric cancer. In the subgroup analysis of EGC in our studies, serum CEA levels were not a significant risk factor for LNM. Whether increased CEA levels have any impact on survival in patients with EGC needs further study.

Some studies have indicated that histological differentiation and ulceration had no significant association with LNM^[25,26,29-31]. In contrast, Gotoda *et al.*^[4] performed a large study including 5265 patients with EGC. They reported that undifferentiated EGC and ulceration were independent factors. Moreover, Ye *et al.*^[32] assessed 591 patients with undifferentiated EGC and found that poorly differentiated EGCs had higher rates of LNM ($P < 0.001$). In

the current study, histological differentiation was not a predictor of LNM, consistent with previous reports^[25,26,29-31]. Nonetheless, our results showed that 3 of 35 cases (8.6%) with undifferentiated intramucosal tumors, which were not ulcerative and ≤ 2 cm in size, had LNM. It is well accepted that in the presence of LNM, only radical gastrectomy provided a chance for curing patients with EGC. Therefore, we suggest that surgical resection with lymphadenectomy instead of endoscopic management should be the treatment choice for undifferentiated EGC.

Many researchers have accepted that depth of tumor invasion is the major factor relating to regional LNM^[4,26,30,31] and endoscopic treatment is considered in EGC even if there is minimal submucosal invasion. Nonetheless, some of these researchers still advise against the use of extended criteria even if minimal submucosa invasion is present because rare cases had LNM that met the extended criteria for EMR/ESD^[33].

In summary, tumor with submucosal invasion, size ≥ 2 cm, and presence of lymphatic involvement appear to be significant factors for LNM. Endoscopic treatment might be an alternative in carefully selected EGC patients without predictors for LNM.

COMMENTS

Background

Endoscopic treatment for early gastric cancer (EGC) has been widely adapted in Japan and Korea to avoid unnecessary gastric resection. However, the presence of lymph node metastasis (LNM) which affects patient survival is considered a contraindication of endoscopic management in this situation. This study was designed to analyze the predictive factors for LNM in early gastric cancer.

Research frontiers

Studies have established an indication for endoscopic treatment for EGC and the probability of LNM in EGC is extremely low based on endoscopic and histopathological findings.

Innovations and breakthroughs

Guidelines for endoscopic mucosal resection (EMR) or endoscopic submucosal dissection (ESD) remains uncertain in areas outside of Japan and Korea. The authors identify the predictive factors related to LNM in EGC and test the guideline.

Applications

Endoscopic treatment might be an alternative in carefully selected EGC patients without risk factors for LNM.

Terminology

EMR is an endoscopic technique of resection of a lesion that requires the separation of the submucosa using normal saline solution. ESD is a new method of resection, allowing the dissection of the lesion within the thickness of the submucosa or the interface between the submucosa and the muscularis propria.

Peer review

Excellent contribution highlighting the appropriate selection indicators for endoscopic treatment of early gastric cancer indicating that not all early cancers are the same.

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Staging systems for predicting survival of patients with hepatocellular carcinoma after surgery

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Abstract

AIM: To compare the staging systems for stratifying and predicting the prognosis of patients with hepatocellular carcinoma (HCC) after partial hepatectomy (PH).

METHODS: Clinical data about 438 HCC patients who underwent PH from January 1991 to December 2004 at our hospital were retrospectively analyzed. Tumor stage was evaluated following the Chinese tumor node metastasis (TNM) and barcelona clinic liver cancer (BCLC) staging systems, respectively. Survival curves for the HCC patients were plotted using the Kaplan-Meier method and differences were compared by the log-rank test. The accuracy of each system for predicting death of HCC patients was evaluated by calculating the area under the receiver operating characteristic curve.

RESULTS: The HCC patients were classified into stag-

es I-III, stages I-IV and stages A-C, according to the 3 staging systems, respectively. Log-rank test showed that the cumulative survival rate was significantly different for the HCC patients at 3 Chinese system stages, TNM stages I and II, TNM stages III and IV, and 3 BCLC stages ($P < 0.05$). However, no significant difference was found in the HCC patients at TNM stages II and III. The accuracy of the Chinese and BCLC staging systems was higher than that of the TNM staging system for predicting the survival rate of HCC patients.

CONCLUSION: The Chinese and BCLC staging systems are better for stratifying and predicting the prognosis of HCC patients after PH than the TNM staging system.

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Key words: Hepatocellular carcinoma; Tumor staging; Prognosis; Survival; Hepatectomy

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INTRODUCTION

Hepatocellular carcinoma (HCC), one of the most common cancers in the world, especially in Eastern Asia, with a poor prognosis^[1], is the first leading cause of cancer-related death in the southeast of China^[2]. Treatment modalities for HCC are strongly dependent on tumor stage

and the underlying liver diseases. Surgical intervention is the only potentially curative modality for it at present. However, the long-term prognosis of HCC patients remains dismal even after radical excision or liver transplantation^[3].

Staging systems are used to define the prognosis of HCC and its treatment^[4]. Generally, a better clinical staging system can stratify patients according to their survival time, and is reliable and useful for comparing the curative effects on HCC. Several HCC staging systems have been proposed, such as the Okuda staging system^[5], tumor node metastasis (TNM) staging system of the American Joint Committee on Cancer (AJCC)^[6], cancer of the liver Italian program (CLIP) scoring system^[7], Barcelona clinic liver cancer (BCLC) staging classification^[8], Japan integrated staging (JIS) score^[9], and Tokyo score^[10]. However, no worldwide consensus has been reached on the use of any given HCC staging systems. Therefore, more accurate classification of HCC patients with a homogeneous prognosis would at minimum improve the application of currently available treatment modalities.

The Chinese staging system, established by the Chinese Society of Liver Cancer (CSLC) in 1999^[11,12], combines the tumor-related factors and liver function reserve. However, its application in stratifying and predicting the prognosis of HCC patients remains to be defined. This study was to evaluate and compare the Chinese staging system, the AJCC TNM staging system (7th edition) and the BCLC staging system for stratifying and predicting the prognosis of a large cohort of Chinese HCC patients after partial hepatectomy (PH).

MATERIALS AND METHODS

Patients

Four hundred and thirty-eight patients with HCC who underwent PH from January 1991 to December 2004 at our hospital were included in this study. The diagnosis of HCC was pathologically confirmed. Clinicopathological features and survival rates of the patients were analyzed. The study was approved by the Ethical Committee of Sun Yat-Sen Memorial Hospital and in accordance with the Helsinki Declaration of 1975. Written informed consent was obtained from the patients or their guardians.

Tumor stage

HCC was divided into different stages following the criteria for the Chinese, TNM and BCLC staging systems, respectively. The detailed definition and criteria for the Chinese staging system are listed in Table 1.

Treatment

All patients underwent non-anatomical resection. According to the Couinaud's nomenclature for liver segmentation, minor hepatectomy (1-2 segments), major hepatectomy (≥ 3 segments), and wedge resection were performed in 179 (40.9%), 47 (10.9%), and 212 (48.2%) patients, respectively. Of the 438 patients, 24 (5.5%) with

Table 1 Definition and criteria of Chinese staging system for hepatocellular carcinoma (1999)

Stage	Tumor	Thrombi	CLN metastasis	Distant metastasis	Child-Pugh score
I a	Solitary ≤ 3 cm	No	No	No	A
I b	Solitary or two ≤ 5 cm in single lobe	No	No	No	A
II a	Solitary or two ≤ 10 cm in single lobe, or two ≤ 5 cm in bilateral lobes	No	No	No	A
II b	Solitary or two > 10 cm in single lobe, or two > 5 cm in bilateral lobes	No	No	No	A
III a	Any	PV-branch, HV or BD	No	No	A
	Any	No	No	No	B
	Any	PV-trunk or IVC	Yes/No	Yes/No	A/B
	Any	Yes/No	Yes	Yes/No	A/B
III b	Any	Yes/No	Yes/No	Yes	A/B
	Any	Yes/No	Yes/No	Yes/No	C

CLN: Celiac lymph nodes; PV: Portal vein; HV: Hepatic vein; BD: Bile duct; IVC: Inferior vena cava.

unresectable HCC underwent surgery after trans-catheter hepatic arterial chemoembolization (TACE, down-staged). Moreover, HCC patients with inoperable intrahepatic recurrence or extrahepatic metastases received combined therapies, including TACE, radiofrequency ablation (RFA), microwave coagulation therapy (MCT), percutaneous ethanol injection (PEI), and biotherapy or traditional Chinese therapy.

Follow-up

During the first 6 mo after operation, the patients were re-examined every 1-2 mo followed by every 3-6 mo. The clinical, laboratory and radiological (abdominal computed tomography scan and chest X-ray) data were collected at each follow-up. Three hundred and ninety-two (89.5%) HCC patients were followed-up until the end of January 2005 or death, while 46 (10.5%) HCC patients were lost during the follow-up. The median follow-up time was 21 mo (range 1-156 mo).

Statistical analysis

Statistical analysis was conducted with the SPSS software package (version 13.0, SPSS, Chicago, IL). Quantitative data were presented as mean \pm SE. Survival curves for the HCC patients were plotted using the Kaplan-Meier method and examined by the log-rank test. The accuracy of each system for predicting the 1-, 3-, and 5-year rates of HCC patients was evaluated by calculating the area under the receiver operating characteristic curve. Patients censored before 1, 3 and 5 years were excluded from the analysis. $P < 0.05$ was considered statistically significant.

Table 2 Characteristics of hepatocellular carcinoma patients enrolled in this study

Characteristics	n (%)
Sex	
Male	380 (86.8)
Female	58 (13.2)
Age (yr)	
≤ 50	235 (53.6)
> 50	203 (46.4)
Child-Pugh score	
Class A	391 (89.3)
Class B	47 (10.7)
Tumor number	
Single	374 (85.4)
Two	29 (6.6)
Multiple	35 (8)
Tumor size (cm)	
≤ 5	166 (37.9)
> 5	272 (62.1)
Tumor location	
Single lobe	389 (88.8)
Bilateral lobes	49 (11.2)
Capsular invasion	
With	346 (79)
Without	92 (21)
Vascular invasion	
With	84 (19.2)
Without	354 (80.8)
Lymph node metastasis	
With	11 (2.5)
Without	427 (97.5)
Extra-hepatic metastasis	
With	7 (1.6)
Without	431 (98.4)
Histological grade	
G1	129 (29.5)
G2	188 (42.9)
G3	121 (27.6)

Table 3 Overall survival rates of hepatocellular carcinoma patients according to their tumor stage

Tumor stage	n	Survival rate (%)		
		1-yr	3-yr	5-yr
CS				
I	132	0.916	0.760	0.693
II	265	0.622	0.426	0.281
III	41	0.330	0.126	0.126
TNM				
I	271	0.825	0.652	0.548
II	67	0.521	0.354	0.216
III	82	0.437	0.235	0.153
IV	18	0.278	/	/
BCLC				
A	178	0.870	0.678	0.602
B	165	0.756	0.574	0.402
C	95	0.375	0.182	0.142

CS: Chinese staging; TNM: Tumor node metastasis; BCLC: Barcelona clinic liver cancer.

Table 4 Accuracy of three staging systems for the death of hepatocellular carcinoma patients 1, 3 and 5 years after partial hepatectomy

System	AUC (95% CI)		
	1-yr death	3-yr death	5-yr death
CS	0.709 (0.658-0.761)	0.703 (0.645-0.761)	0.720 (0.648-0.791)
TNM	0.718 (0.662-0.774)	0.702 (0.646-0.759)	0.695 (0.629-0.760)
BCLC	0.730 (0.675-0.785)	0.701 (0.644-0.757)	0.710 (0.645-0.776)

AUC: Area under the receiver operating characteristic curve; CI: Confidence interval; CS: Chinese staging; TNM: Tumor node metastasis; BCLC: Barcelona clinic liver cancer.

RESULTS

Clinicopathological features and survival of HCC patients

The general characteristics of the 438 HCC patients are summarized in Table 2. The mean and median ages of the patients were 50.0 ± 0.6 years and 49.0 years (range: 35-68 years), respectively. By the end of follow up, 223 HCC patients (50.9%) died. The 1-, 3- and 5-year postoperative overall survival rates were 72.2%, 53.5% and 43.3%, respectively, for the patients after PH.

Prognosis stratification according to the three clinical staging systems

The 438 HCC patients were classified into stages I-III, stages I-IV and stages A-C according to the Chinese, TNM and BCLC staging systems, respectively. The log-rank test showed that the cumulative survival rate was significantly different for the HCC patients at 3 Chinese system stages, TNM stages I and II, TNM stages III and IV, and 3 BCLC stages (Table 3 and Figure 1, *P* < 0.05). However, no significant difference was found in the HCC patients at TNM stages II and III (*P* > 0.05).

Accuracy of the three clinical staging systems for predicting survival rate of HCC patients

The accuracy of 3 staging systems for predicting the survival rate of HCC patients 1, 3 and 5 years after PH is summarized in Table 4. The accuracy of the Chinese and BCLC staging systems was higher than that of the TNM staging system for predicting the survival rates of HCC patients (Figure 2).

DISCUSSION

HCC is the second most lethal cancer after pancreatic ductal adenocarcinoma, leading to about 600 000 deaths every year worldwide, with nearly 55% of the deaths occurred in China alone^[3]. The long term prognosis of HCC patients is extremely dismal and the incidence of HCC is continuously growing globally^[1,13,14]. In the southeast of China, HCC is the leading cause of cancer-related death despite aggressive conventional therapies^[2]. Surgery remains the most effective treatment of HCC with a curative potential^[15,16]. However, HCC patients even after curative resection of the tumor often have a high rate of relapse.

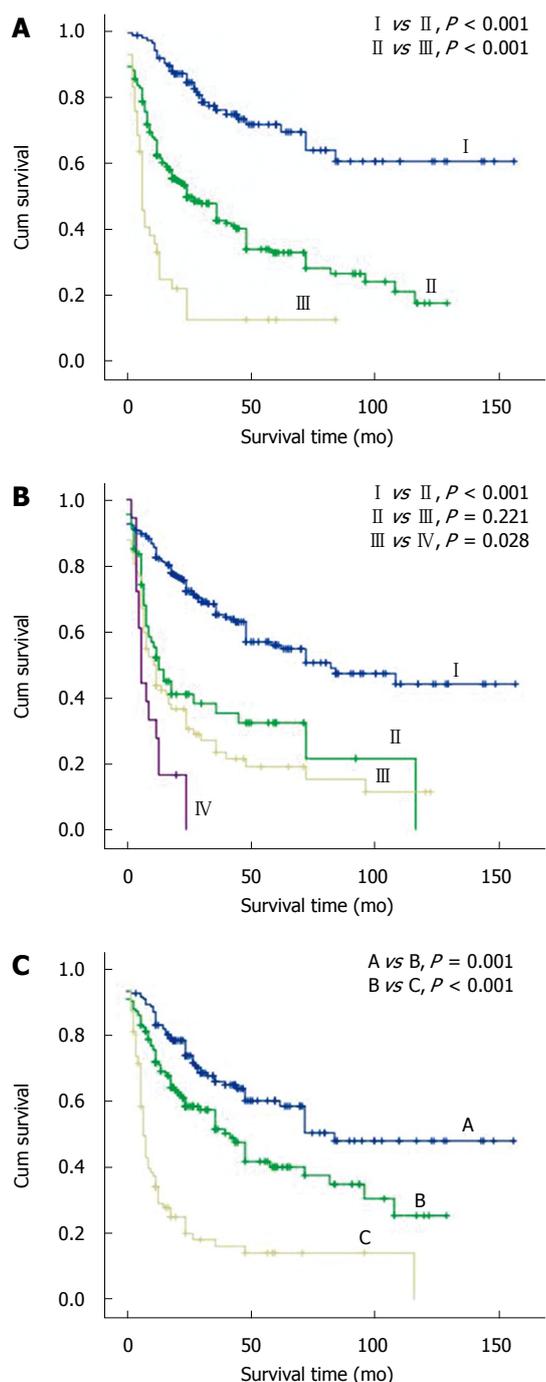


Figure 1 Survival curves for hepatocellular carcinoma patients according to the Chinese staging system (A), tumor node metastasis staging system (B), barcelona clinic liver cancer staging system (C).

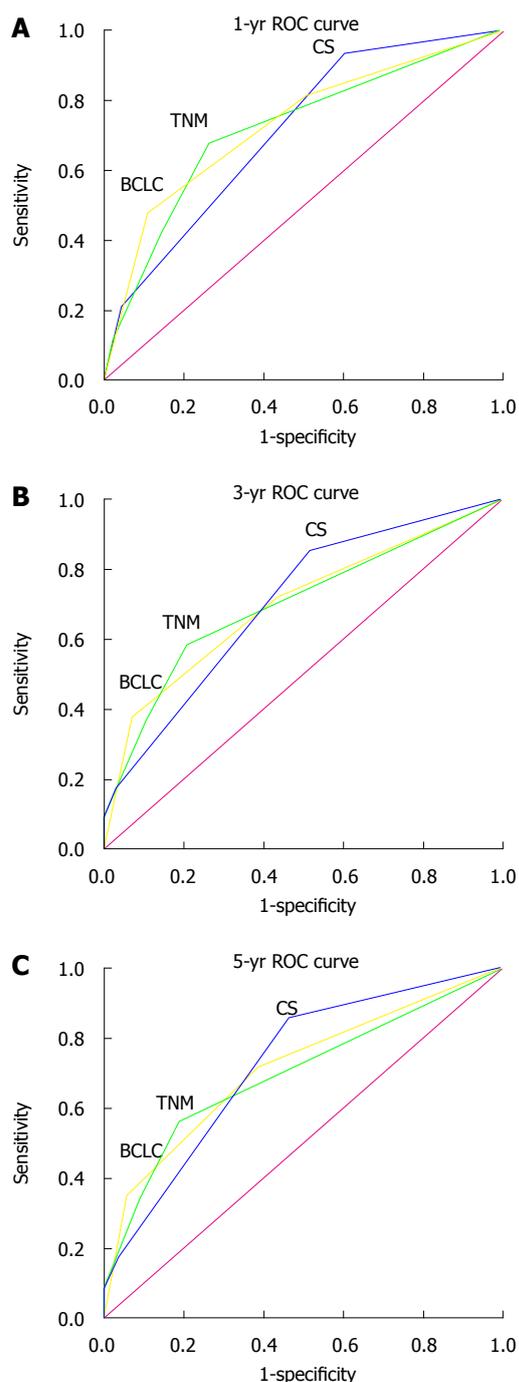


Figure 2 Accuracy of the three staging systems for predicting the 1-year (A), 3-year (B), 5-year (C) survival rates of hepatocellular carcinoma patients. ROC: Receiver operating characteristic curve; CS: Chinese staging; TNM: Tumor node metastasis; BCLC: Barcelona clinic liver cancer.

Therefore, tools that can be used to stratify the prognosis of HCC patients after therapy are urgently needed. Gene-expression analysis has led to the successful molecular classification of HCC according to its prognosis, aetiology and intra-hepatic recurrence^[17]. However, it has not been widely accepted due to its high cost.

Staging systems are often used to select primary and adjunctive therapies and to assess their outcome. Generally, a well defined clinical staging system not only can classify HCC patients and predict their survival time, but

also can be generally applied globally. Increasing evidence shows that liver function reserve and tumor-related factors can also significantly influence the prognosis of HCC patients^[4]. Chen *et al*^[18] reported that a better staging system can provide more valid tumor-related factors and liver function parameters. Therefore, both tumor-related features and liver function reserve should be included in the clinical staging systems for HCC^[19].

Several clinical staging systems are available for pre-

dicting the prognosis of HCC patients after PH at present. However, no worldwide consensus has been reached on which staging system is the best for predicting the prognosis of HCC patients after surgery^[20]. Although the Okuda staging system^[5], CLIP scoring system^[7], JIS score^[9], and Tokyo score^[10] are widely used, they have been mostly applied to unresectable HCC, and none is universally accepted^[21]. The TNM staging system is the most widely used system worldwide at present^[21]. However, the AJCC TNM staging system does not include any measurement of liver functions and is thus not widely used^[20]. Llovet *et al.*^[22] reported that the AJCC TNM staging system fails to adequately stratify HCC patients and predict their prognosis. Lu *et al.*^[23] also reported that the TNM staging system provides inadequate information for the prognosis of HCC patients.

In the present study, application of the CS system in stratifying and predicting prognosis of a large cohort of Chinese HCC patients ($n = 438$) after PH was investigated and compared to that of the AJCC TNM and BCLC staging systems. The log-rank test showed that the cumulative survival rate was significantly different for HCC patients at Chinese system stages, TNM stages I and II, TNM stages III and IV, and 3 BCLC stages, while no significant difference was found in the cumulative survival rate of HCC patients at TNM stages II and stage III. The accuracy of the Chinese and BCLC staging systems was higher than that of the TNM staging system for predicting the long-term survival (3- and 5-year) rates of HCC patients after PH, indicating that the Chinese and BCLC staging systems are better than the TNM staging system for stratifying and predicting the prognosis of HCC patients after PH. In our study, the AJCC TNM staging system could not accurately stratify the HCC patients with multiple nodules or vascular/peripheral invasion.

In conclusion, the Chinese and BCLC staging systems are better than the AJCC TNM staging system for stratifying and predicting the prognosis of HCC patients after PH. Further studies are needed to establish a single, worldwide staging system that can stratify and predict the prognosis of HCC patients after PH.

COMMENTS

Background

Staging systems are used to define the prognosis and treatment of hepatocellular carcinoma (HCC) patients. Several staging systems are available for predicting the prognosis of HCC patients, but no worldwide consensus has been reached on the use of any given HCC staging systems. Therefore, more accurate classification of HCC patients with homogeneous prognosis is urgently needed.

Research frontiers

Although the Okuda and cancer of the liver Italian program scoring systems, Japan integrated staging score, and Tokyo score are widely used, they have been mostly applied to unresectable HCC patients. The tumor node metastasis (TNM) staging system for HCC does not include any measurement of liver functions and is thus not widely used. The Chinese staging system for stratifying and predicting the prognosis of HCC patients remains to be defined.

Innovations and breakthroughs

The Chinese staging system was studied for stratifying and predicting the prognosis of HCC patients. Furthermore, the applicability of the Chinese staging system was compared with other staging systems for stratifying and predicting the prognosis of HCC patients after partial hepatectomy.

Applications

The results of this study demonstrate that the Chinese staging system can be used for predicting the prognosis of HCC patients after partial hepatectomy.

Peer review

The authors evaluated and compared the Chinese, American Joint Committee on Cancer (AJCC) TNM and Barcelona clinic liver cancer (BCLC) staging systems for stratifying and predicting the prognosis of a large cohort of Chinese HCC patients after partial hepatectomy. The results reveal that the Chinese and BCLC staging systems are better than AJCC TNM staging system for stratifying and predicting the prognosis of HCC patients after partial hepatectomy.

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Primary malignant liver mesenchymal tumor: A case report

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Abstract

Primary malignant liver mesenchymal tumor is a rare condition defined as a tumor with vascular, fibrous, adipose, and other mesenchymal tissue differentiation. We report a case of primary malignant liver mesenchymal tumor in a 51-year-old male with anemia, weight loss and hepatomegaly. Finally unconventional liver biopsy and histological manifestation led to the definitive diagnosis.

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Key words: Hepatic mesenchymal tumor; Liver biopsy; Hepatic leiomyosarcoma; Hepatic schwannoma

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INTRODUCTION

Primary malignant liver mesenchymal tumor is a very rare tumor, accounting for less than 1% of all hepatic malignancies^[1]. Hepatic angiosarcoma, leiomyosarcoma, embryonal sarcoma, schwannoma and lymphoma are the more common mesenchymal tumors. The diagnosis is dependent on histological imaging. However, some cases of multiple nodular lesions can only be diagnosed by percutaneous liver biopsy (PLB) without surgery. We present a case of malignant liver mesenchymal tumor in an adult and its diagnosis and treatment were discussed.

CASE REPORT

A 51-year-old Chinese male was referred to our hospital with a 2-mo history of mild abdominal pain, an abdominal mass in the upper quadrant, fatigue and progressive weight loss. His symptoms gradually worsened with fatigue 1 wk after onset of the disease. He had no fever, cough or skin lesions in the past 2 mo and no family history of liver and autoimmune diseases. Physical examination revealed mild pale conjunctiva and skin, and enlargement of the liver without percussion pain.

His complete blood hemoglobin was 58 g/L. Stool occult blood test was negative. Liver functional test showed that his alanine aminotransferase, aspartate aminotransferase, alkaline phosphatase, γ glutamyl transpeptidase, total bilirubin, direct bilirubin, and albumin were 81 U/L, 86 U/L, 224 U/L, 73 U/L, 23.55 μ mol/L, 11.74 μ mol/L, 30.5 g/L, respectively. Series hepatitis markers (hepatitis A virus, hepatitis B virus, hepatitis C virus, hepatitis D virus, hepatitis E virus, Epstein-Barr virus, and cucumber mosaic virus) were negative. α -fetoprotein, carcinoembryonic antigen and CA19-9 concentrations were also normal. Human immunodeficiency virus and syphilis antibodies were negative. Coagulation profile was normal.



Figure 1 Axial fat-suppressed T2-weighted turbo spin echo magnetic resonance imaging showing two large lesions (A) and several small cyst-like lesions (B) in liver, and coronal and transverse T1-weighted imaging showing thickened wall of lesions with a ragged appearance (C) and enhancement (D) in liver.

Ultrasound and magnetic resonance imaging (MRI) were used as the initial diagnostic tools. Abdominal ultrasound revealed a solid mass in the liver with a low echo, a sharp border, a rich blood supply and liquefaction necrosis. The maximum diameter of the mass was 13.9 cm. Abdominal MRI showed multiple diffuse abnormal signals suggestive of a possible malignant tumor. Axial fat-suppressed T2-weighted turbo spin echo imaging showed two larger and several smaller well-margined cyst-like lesions in the liver (Figure 1A and B). Coronal and transverse T1-weighted imaging demonstrated thickened wall of lesions with a ragged appearance and enhancement (Figure 1C and D). Endoscopy showed duodenal ulcer (S2 stage), normal colon and rectum.

PLB was performed under ultrasonography (US) guidance using a Bard biopsy gun (18-gauge cut needle) to make a final diagnosis of the lesions in liver. During biopsy, bloody liquid was observed in the lesion. Microscopic examination confirmed that the bloody liquid contained a large number of erythrocytes. However, pathology of the liver only showed a spindle cell tumor. The possible reasons are as follows. First, the liver specimen was too small because the lesion contained only fluid and was surrounded by a very thin wall. Second, the location of tumor and its hardness limited the adjustable puncture angle.

To confirm the diagnosis of this patient, another unconventional liver biopsy was performed with gastroscopic biopsy forceps as follows.

At beginning of the procedure, a local anesthetic agent (5% lidocaine) was injected subcutaneously through

a 25-gauge needle. Next, a 15 cm long 18 gauge puncture needle was passed into the cyst under US guidance. After the local skin and subcutaneous tissue were dilated, a PTC exchange stainless steel guide wire with a flexible tip was introduced into the cyst cavity through the needle, and then the needle was withdrawn. A 5-French catheter was plated into the cyst using the Seldinger technique. Finally, gastroscopic biopsy forceps was passed into the cyst through the catheter to get the liver tissue sample. The histological results indicated that spindle-shaped tumor cells were well-oriented, arranged in bundles and clustered in some part of the regional tumor. Nuclei with rare mitosis were elongated in a rod-like shape with different sizes and blunt ends. The final diagnosis was established as a low grade malignant liver mesenchymal tumor (Figure 2).

The patient was suggested to receive hepatic arterial chemoembolization. Selective digital subtraction angiography in the early and later phases showed lesions surrounded by abnormal tortuous tumor arteries (Figure 3A) and patchy enhancement (Figure 3B), respectively, in different areas. Then, 5-Fu (750 mg), mitomycin (5 mg), pyrazine imidacloprid Star (30 mg), and super-liquid iodized oil (5 mL) were infused into the tumor arteries. After treatment, liver function of the patient was improved and his hemoglobin level increased (Table 1). The patient died 2 years after treatment.

DISCUSSION

In this paper, we presented a case of multiple nodular cyst-

Table 1 Changes in serum biochemical index before and after treatment

	WBC ($\times 10^9/L$)	HGB (g/L)	PLT ($\times 10^{12}/L$)	ALT (U/L)	AST (U/L)	TBIL ($\mu\text{mol}/L$)	ALB (g/L)
Diagnosis	10.44	58	294	81	86	23.55	30.5
Treatment	6.24	86	241	17	24	20.74	34.1

WBC: White blood cell count; HGB: Hemoglobin; PLT: Platelet count; ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; TBIL: Total bilirubin; ALB: Albumin.

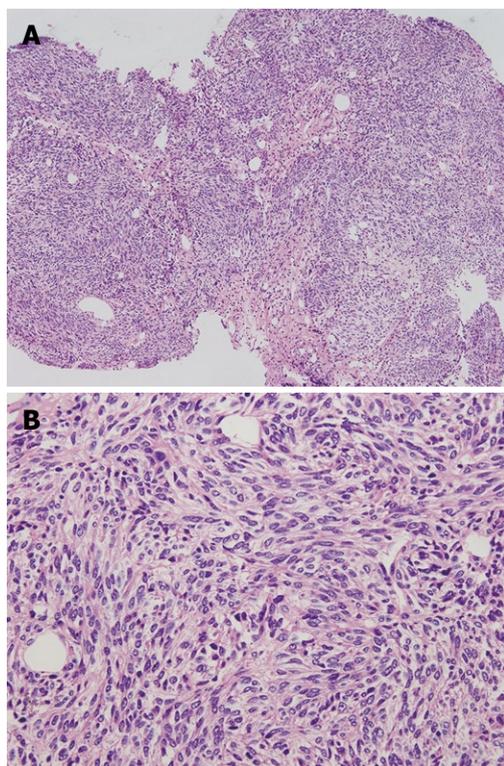


Figure 2 Hematoxylin and eosin staining showing a low grade malignant liver mesenchymal tumor under the magnification $\times 10$ (A) and $\times 40$ (B).

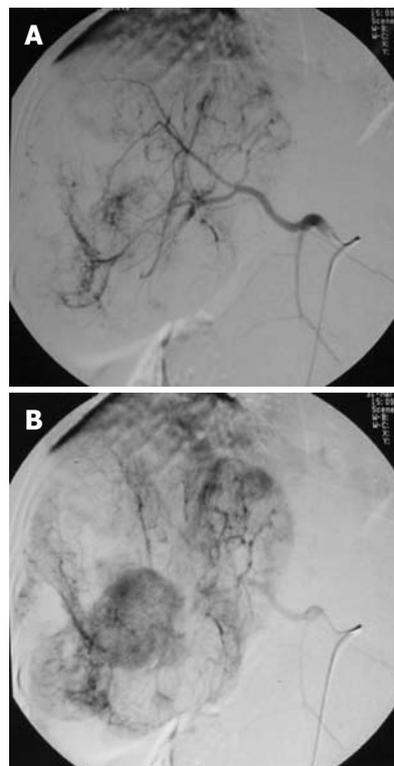


Figure 3 Selective digital subtraction angiography showing abnormal tortuous arteries in the early phase (A) and patchy enhancement in later phase (B) in different areas.

tic lesions in liver. The final diagnosis was established as a low grade malignant liver mesenchymal tumor. However, HE staining could not show the source of mesenchymal cells. Further immunohistochemistry staining with Vimentin, Desmin and α -SMA was performed, which could not still show the source of mesenchymal cells.

Primary malignant liver leiomyosarcoma and schwannoma are both rare tumors in the liver. Primary liver leiomyosarcoma is a rare malignancy involving the liver, occurring as a primary liver sarcoma in patients without any underlying disorder, and its incidence increases as a primary tumor in immunodeficiency patients^[2]. Its usual clinical presentation is painful hepatomegaly or epigastric mass^[3]. Malignant liver schwannoma is the most common soft tissue sarcoma in adults, but primary liver schwannoma is extremely rare. Only 12, 8, and 1 cases of benign, malignant, and semimalignant liver schwannoma are available from the literature worldwide^[4-12]. Hepatic schwannoma is usually associated with neurofibromatosis. However, two cases of malignant liver schwannoma without neurofibromatosis have been reported^[9,11].

Unfortunately, it is difficult to make the diagnosis of malignant liver mesenchymal tumor because both its clinical presentation and imagine are nonspecific.

The common symptoms and signs of patients with malignant liver mesenchymal tumor include abdominal pain, weight loss, weakness, loss of appetite, vomiting, enlargement of the liver, ascites, and jaundice, which lack of specificity in differential diagnosis between benign and malignant mesenchymal tumors.

Furthermore, imaging studies, such as MRI scan, computed tomography (CT) scan and angio photography are the commonly used methods to identify the characteristics of liver tumor. However, imaging findings of liver mesenchymal tumors, including leiomyosarcoma and schwannoma, are nonspecific and infrequently reported^[13-19]. It is quite difficult for MRI and CT scan to differentiate primary liver mesenchymal neoplasms from other liver malignancies, although they should be included in differential diagnosis when MRI or CT scan demonstrates hepatic lesions without characteristics of hepatocellular carcinoma,

especially in patients with no extrahepatic primary malignancies.

The diagnosis of malignant liver mesenchymal tumor depends on histological change in either needle or open biopsy, while metastatic status is facilitated by the presence of extrahepatic primary tumor.

Liver biopsy is an important diagnostic tool and helps make therapeutic decision for liver tumor. Open biopsy is a major surgical procedure for liver tumor. PLB under ultrasound or CT guidance is a safe and almost painless procedure for lesions with a soft tissue component or located close to vital structures^[20]. Most reported cases of cystic liver mesenchymal tumor were diagnosed by open liver biopsy. In this case, uncommon PLB method was used instead of the routine PLB to make the final diagnosis, avoiding injury and complications of open biopsy. Minimally invasive treatment devices, such as gastroscopic biopsy forceps and catheters used in liver cancer intervention, make the new PLB method possible, which is safe and reliable and can thus be used in diagnosis of cystic liver lesions.

In conclusion, mesenchymal liver tumor is rare in adults and cross-sectional findings are varied, which can be diagnosed with the uncommon PLB method.

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 26th Pakistan Society of
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 18th Annual Meeting of Indian
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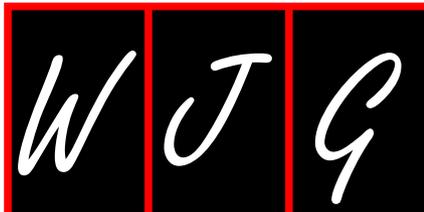
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In press

- 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

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- 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.00000035706.28494.09]

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- 5 **Vallancien G**, Emberton M, Harving N, van Moorseelaar 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]

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

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

Books

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

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

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

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- 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

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- 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>

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- 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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