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Locoregional therapy response in patients with hepatocellular cancer waiting for liver transplantation: Only selection or biological effect?

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Abstract

Locoregional treatments (LRT) represent a broad strategy used for reducing the risk of drop-off and contextually improving the survivals in patients with hepatocellular cancer receiving a liver transplantation (LT). However, it is not sufficiently clear if LRT are only a surrogate of tumor aggressiveness or if they consent a real benefit in terms of tumor stabilization. A recent study by Pommergaard *et al* reported the results from the European Liver Transplant Registry. Patients receiving LRT before LT had better 5-year survival rates respect to no-LRT cases (69.7% vs 65.8%; $P < 0.001$). When the number of LRT was tested, one-to-two treatments were connected with improved survivals respect to no treatment [hazard ratio (HR) = 0.85 and 0.71, respectively]. The efficacy of LRT was also reported in the presence of larger tumors (HR = 0.78) and micro-macrovascular invasion (HR = 0.71). The results observed in the present study are partially in discordance with other analyses showing a detrimental effect of LRT. The main problem in the interpretation of these results is connected with the possible initial selection biases present in the studies. The most recent guidelines suggest to perform LRT before the transplant, but the level of evidence is typically low due to the absence of prospectively designed studies.

Key words: Allocation; Recurrence; Trans-arterial chemo-embolization; Radiofrequency ablation; Model for end-stage liver disease

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Core tip: The role of locoregional treatments in the setting of hepatocellular cancer and liver transplantation is controversial. On one side, neoadjuvant approaches should consent a selection of tumor aggressiveness. On the other side, a real survival improvement thanks to the tumor ablation should be achieved. Recent evidences report an effective beneficial role of locoregional strategies in terms of survival and recurrence. However, several biases must be taken into account in these studies, due to the heterogeneous characteristics of treated *vs* untreated subjects. Further studies are need with the intent to clarify this important topic.

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INTRODUCTION

Liver transplantation (LT) represents the gold-standard treatment in patients with unresectable hepatocellular cancer (HCC) developed on underlying cirrhosis^[1]. Unfortunately, LT represents a scarce resource, mainly due to the limited number of available donors^[2]. Thus, in patients awaiting LT, disease burden may progress beyond the conventional LT criteria while on the waiting list^[3]. Several strategies have been adopted with the intent to alleviate the risk of drop-out due to tumor progression: for example, Model for End-Stage Liver Disease (MELD) exception points are routinely used in several regions in the presence of T2 HCCs^[4]. Another widespread strategy is the use of locoregional treatments (LRTs) as a neo-adjuvant strategy with the intent to bridge patients to LT^[5] or downstage patients initially outside transplantation criteria^[6].

Response to LRT has been correlated with improved post-LT survival rates in several studies^[7,8]. However, it is not sufficiently clear if LRTs are only a surrogate of tumor aggressiveness, efficaciously selecting patients with favorable tumor biology, or if they are beneficial concerning tumor stabilization, mainly in case of complete or partial response.

STUDY ANALYSIS

In a recent Issue on Transplant International, Pommergaard *et al*^[9] reported the results of a multicentric study based on the European Liver Transplant Registry (ELTR) and focused on the use of LRT in HCC patients undergoing LT. A total of 4978 patients (no LRT = 1406, 28.2%; LRT = 3572, 71.8%) were enrolled. As expected, the median waiting time was longer in the LRT group

(4 mo *vs* 1.7 mo; $P < 0.001$) and the median MELD score was higher in the directly transplanted subjects (12 *vs* 10; $P < 0.001$). Overall, patients receiving LRT before LT had better 5-year survival rates respect to no-LRT cases (69.7% *vs* 65.8%; $P < 0.001$). When the different treatment types were investigated, the use of radiofrequency ablation (RFA) had the strongest association with an improved overall survival [hazard ratio (HR) = 0.51]. The beneficial effect was also observed in case of the combination of RFA and trans-arterial chemo-embolization (TACE) (HR = 0.74). Several sub-analyses were also done. As for the number of LRT performed, one-two treatments were connected with improved survivals respect to no treatment (HR = 0.85 and 0.71, respectively). On the opposite, three or more treatments showed no association (HR = 1.11).

When a subclass of HCCs being larger (> 3 cm) or with more nodules (> 5 lesions) was examined, LRT maintained their protective role for the risk of death (HR = 0.78). In this context, RFA, TACE or combined RFA + TACE all were significantly associated with improved survival (HR = 0.54, 0.81, and 0.60, respectively).

Stratifying the entire population according to the underlying liver status (cirrhosis *vs* non-cirrhotic liver), in case of HCC on cirrhosis LRT were also protective (HR = 0.86).

In the presence of pathological micro-macrovascular invasion, the effect of LRT was strong (HR = 0.71). Both RFA and TACE (HR = 0.54 and 0.69, respectively) were associated with improved survival.

PERSPECTIVE

The role of LRT in the setting of HCC and LT has not been fully clarified, mainly in light of the potential detrimental effects of repetitive treatments. For example, a recent meta-analysis performed on 1122 TACE patients showed an increased risk of post-LT hepatic artery complications (odds ratio = 1.57; $P = 0.02$)^[10]. Another study from the US performed on 3601 patients all meeting the Milan Criteria, showed that the increasing number of LRT significantly predicted post-LT recurrence (3 LRTs: HR = 2.1; $P < 0.001$; 4 + LRTs: HR = 2.5; $P < 0.001$)^[5]. Interestingly, LRT patients achieving complete response had superior 5-year recurrence-free survivals when compared with untreated cases or LRT subjects not achieving complete response (72% *vs* 69% *vs* 67%; respectively)^[5]. The here described study performed on a large population of European HCC cases showed the beneficial role of LRT, mainly in case of RFA use. Moreover, the repetitive number of treatments was not connected with worse results. LRT maintained their protective role for the risk of death even when larger tumors or harmful clinical conditions like vascular invasion were investigated. It is difficult to definitively clarify if the LRT only select low-risk HCC, or if their ability of tumor burden zeroing should also have some impact regarding survival improvement. It is clear that

the response after LRT is a robust predictor of post-LT course. A recent large multicentric European study based on 2103 HCC patients identified the poor radiological response after LRT as one of the most important predictors for the risk of low intention-to-treat benefit after transplant^[11]. Another multicentric European study performed on 276 cases all treated with LRT showed that an HCC-related remaining vital tissue in the main lesion ≥ 2 cm at pathological assessment after LT was a strong independent risk factor for post-LT recurrence (HR = 5.6; $P < 0.001$)^[12]. All of these results have been positively recognized by the recent European Association for the Study of the Liver (EASL) guidelines, in which it is stated that "in LT candidates with HCC, the use of pre-transplant (neoadjuvant) loco-regional therapies is recommended if feasible, as it reduces the risk of pre-LT drop-out and aims at lowering post-LT recurrence - particularly when complete or partial tumour response are achieved"^[13]. Unfortunately, although the strength of recommendation for this statement is strong, the scientific evidence is low, clearly underlining the lack of prospectively designed studies. More researchers are needed, with the intent to better explore the role of LRT concerning intention-to-treat survivals.

Moreover, we should remember the critical impact that local allocation rules and waiting time duration may play on the role and the effect of LRT. As an example, in the United States most HCC patients wait for at least six months from the diagnosis before having the opportunity to be transplanted. More studies also focused on these aspects are surely needed.

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Helicobacter pylori: A foodborne pathogen?

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Abstract

Helicobacter pylori (*H. pylori*) is an organism that is

widespread in the human population and is sometimes responsible for some of the most common chronic clinical disorders of the upper gastrointestinal tract in humans, such as chronic-active gastritis, duodenal and gastric ulcer disease, low-grade B-cell mucosa associated lymphoid tissue lymphoma of the stomach, and gastric adenocarcinoma, which is the third leading cause of cancer death worldwide. The routes of infection have not yet been firmly established, and different routes of transmission have been suggested, although the most commonly accepted hypothesis is that infection takes place through the faecal-oral route and that contaminated water and foods might play an important role in transmission of the microorganism to humans. Furthermore, several authors have considered *H. pylori* to be a foodborne pathogen because of some of its microbiological and epidemiological characteristics. *H. pylori* has been detected in drinking water, seawater, vegetables and foods of animal origin. *H. pylori* survives in complex foodstuffs such as milk, vegetables and ready-to-eat foods. This review article presents an overview of the present knowledge on the microbiological aspects in terms of phenotypic characteristics and growth requirements of *H. pylori*, focusing on the potential role that foodstuffs and water may play in the transmission of the pathogen to humans and the methods successfully used for the detection of this microorganism in foodstuffs and water.

Key words: *Helicobacter pylori*; Viable but nonculturable state; Foodborne pathogen; Food; Water; Animal reservoirs; Culture methods; Molecular methods

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Core tip: To date, the transmission routes and reservoirs of *Helicobacter pylori* (*H. pylori*) are topics of debate. Epidemiological evidence and the occurrence of *H. pylori* in foods of animal origin, vegetables and water corroborate the hypothesis advanced by numerous authors that *H. pylori* may be a foodborne pathogen. The present review is focused on the

evidence supporting the role of foods and water in the transmission of *H. pylori* to humans and on the methods for detecting the pathogen in foodstuffs and water.

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INTRODUCTION

The first isolation of *Helicobacter pylori* (*H. pylori*) in 1982 by Marshall and Warren^[1,2] marked a turning point in understanding gastrointestinal microbial ecology and disease^[3]. Following the initial scepticism regarding the aetiologic importance of this organism, it is now recognized that infections with *H. pylori* are linked to some of the most common chronic clinical disorders of the upper gastrointestinal tract in humans^[4]. In fact, *H. pylori* has been acknowledged as a major cause of chronic-active gastritis and is associated with duodenal and gastric ulcer disease, low-grade B-cell mucosa-associated lymphoid tissue lymphoma of the stomach (MALToma)^[5], and gastric adenocarcinoma, which is the third leading cause of cancer death worldwide^[4,6,7]. Furthermore, *H. pylori* has been linked to a variety of extra-gastric disorders, including coronary heart disease, dermatological disorders such as rosacea and idiopathic urticaria, autoimmune thyroid disease, thrombocytopenic purpura, and iron deficiency anaemia^[8].

Human infection by *H. pylori* is a great public health hazard because *H. pylori* colonizes the gastric mucosa of approximately half of the world's population^[9-12]. The infection is usually acquired in infancy and early childhood, and it is long lasting, often remaining for the entire lifespan^[13]. The prevalence of *H. pylori* shows large geographical variation, with infection rates much higher in developing countries (in some areas > 85%) than in Europe and North America (approximately 30%-40%)^[14,15]. In various developing countries, more than 80% of the population is *H. pylori* positive, even at young ages^[16]. The prevalence of *H. pylori* in industrialized countries generally remains under 40% and is considerably lower in children and adolescents than in adults and elderly people. A comparison of prevalence rates by age suggests that the acquisition of *H. pylori* is decreasing in recent cohorts, and this finding is most apparent in developed countries and may be linked to improvements in hygiene practices. Furthermore, it has been estimated that between two and 20 percent of people infected with *H. pylori* develop peptic ulcer disease^[17].

Although *H. pylori* can cause severe illnesses with a high rate of morbidity and mortality, the complex interactions between this microbe and humans,

particularly its transmission pathways to humans and reservoirs, are largely unknown, although multiple routes of transmission have been suggested^[3,18-20]. The current literature suggests that the transmission of *H. pylori* occurs from person to person *via* the oral-oral, faecal-oral, and gastric-oral routes and that the infection dose for humans is low^[6,21]. *H. pylori* may be a sex-transmitted pathogen^[22,23] and may lead to fibrocystic breast changes^[24]. The oral cavity can be primarily colonized by *H. pylori*, and this can be linked to later gastric infection^[25]. Faecal-oral transmission has more important implications than oral-oral transmission because *H. pylori* may occur in food and water supplies subsequent to faecal contamination^[26]. Furthermore, several authors have considered *H. pylori* to be a foodborne pathogen because of its microbiological and epidemiological characteristics^[6,10,27-31]. Information on the distribution of *H. pylori* in water, vegetables and foods of animal origin is critical in determining its potential transmission in foods.

This review article presents a brief overview of the present knowledge on the microbiological characteristics of *H. pylori* in terms of its phenotypic characteristics and growth requirements, focusing on the potential role that foodstuffs and water may play in the transmission of this pathogen to humans and the methods for isolating and detecting this microorganism in foodstuffs and water.

LITERATURE SEARCH

A PubMed search was conducted using the following keywords and phrases: "*Helicobacter pylori*, *Helicobacter pylori* and food, *Helicobacter pylori* and milk, *Helicobacter pylori* and water, VBNC, survival of *Helicobacter pylori*". In addition, we performed a manual review of the reference lists of the primary and review articles to ensure identification of all relevant articles.

MICROBIOLOGICAL CHARACTERISTICS

Phenotypic characteristics

H. pylori was originally thought to be a species belonging to the genus *Campylobacter* and was first named *Campylobacter pyloridis*, which was later corrected to *Campylobacter pylori* (*C. pylori*)^[32]. Because subsequent 16S rRNA sequence analysis showed that the distance between the species belonging to the genus *Campylobacter* and *C. pylori* was sufficient to exclude *C. pylori* from this genus^[33], it was renamed *Helicobacter pylori*^[34], the first member of the new genus *Helicobacter*.

H. pylori organisms are spiral or curved bacilli ranging from 0.3 to 1.0 μm in width and 1.5 to 10.0 μm in length; they are gram-negative and assume a rod-like shape when cultured on solid medium^[34]. Furthermore, after prolonged *in vitro* culture and under adverse environmental conditions, such as an insufficient supply of nutrients, desiccation, lack of protection against oxygen, and exposure to antimicrobial agents, *H. pylori* can survive entering the viable but non-culturable

(VBNC) state, changing its rod-like shape to a coccoid shape^[35-37].

When this morphological change occurs, *H. pylori* is unable to grow on agar plates using conventional cultivation methods^[38-40].

Bacteria in the VBNC state maintain their metabolic activity, pathogenicity and ability to return to active regrowth conditions^[41,42]. For *H. pylori*, the ability to return to active regrowth conditions has not yet been proven. Nevertheless, the aptitude of *H. pylori* to overcome stressed conditions is very significant for public health^[29], even if the role of VBNC in the transmission of *H. pylori*, especially by food and water, is still controversial.

H. pylori is motile and usually possesses four to six unipolar-sheathed flagella, which may be an adaptation to survive in gastric juices^[3,43].

Growth requirements

Since the discovery of *H. pylori*, bacterial culture has been used as a routine diagnostic test and is considered the gold standard. *H. pylori* culture is recommended for performing antibiotic susceptibility testing if primary resistance to clarithromycin is higher than 20% or after failure of second-line treatment^[44]. Despite the long use of bacterial culture, to date, there are no defined media for the selective culture of *H. pylori* because of its fastidious nature with particular growth requirements of atmosphere, nutrient-rich media, high humidity (98%), and long incubation time (5-7 d)^[3,44].

H. pylori is a capnophilic organism that requires an atmosphere with a high level of CO₂ (from 5% to 10%). It has been considered a microaerophile, but the concentration of O₂ required for its growth is still a topic of discussion^[44].

H. pylori requires a complex culture substrate (solid or liquid) with some forms of supplementation, such as whole sheep or horse blood, haemoglobin, serum, coal, yeast, or yolk emulsion^[45,46], which may serve as nutritional substrates. These supplements also detoxify the medium and protect the microorganism^[7].

Furthermore, if isolation is attempted from samples with basic microbial flora, it is necessary to make the media selective through supplementation of several antibiotics^[47].

Growth in liquid media is enhanced by agitation, which allows gas dispersion and incubation in a CO₂-rich atmosphere^[31,47].

H. pylori grows within a temperature range of 30 °C to 37 °C, with optimum growth at 37 °C, but is not able to grow at 25 °C^[43]. At 42 °C, growth is variable^[29].

Similar to *C. jejuni*, *H. pylori* survives longer at 4 °C than at room temperature, and it grows within a pH range of 4.5 to 7.3, with optimum at pH 5.5. *H. pylori* grows well in the presence of 0.5% and 1% NaCl but not of 2% NaCl. The minimum water activity (a_w) for growth is between 0.96 and 0.98. These data suggest that this microorganism is most likely not able to grow in many types of food^[47].

H. pylori is catalase and oxidase positive; it is also

characterized by strong urease activity and is negative for hippurate and nitrate reduction, characteristics that discriminate it from species belonging to the genus *Campylobacter*^[29].

EVIDENCE SUPPORTING THE ROLE OF FOODS IN TRANSMISSION OF *H. PYLORI* TO HUMANS

Since 1997, when the transmission of *H. pylori* through water and foods was hypothesized for the first time, several studies have evaluated the survival and the presence of this microorganism in different foodstuffs (Tables 1 and 2).

One of the most important topics supporting this thesis was the phylogenetic proximity of *H. pylori* to *C. jejuni*, which led to the hypothesis that the transmission pathways described for the latter could also be applied to *H. pylori*^[27]. Several investigators have also considered *H. pylori* a foodborne pathogen based on some of its epidemiological characteristics^[27,28,30] such as the high prevalence of infection within closed family groups and among individuals living in institutions^[48]. These aspects suggest that in addition to direct transmission, this bacterium may be transmitted indirectly through a common source, such as through consumption of the "same foods at the same table"^[26]. The finding that the prevalence of *H. pylori* infection is greater in geographical areas in which the hygienic conditions of life are poor also supports this hypothesis^[30,49].

Additional indirect evidence of the transmission of *H. pylori* to humans through foods of animal origin has been provided by epidemiological studies on the presence of antibodies in slaughterhouse workers and in veterinary workers. The incidence rates in these workers were positive and were greater than those in workers who had no direct contact with carcasses^[50,51] (Figure 1).

Foods presenting intrinsic factors, such as a_w higher than 0.97 and pH ranging from 4.9 to 6.0, could theoretically provide conditions for *H. pylori* survival^[30,52].

Therefore, data on survival ability may be more important than concerns about the growth of the microorganism in foods when determining the role of foods in *H. pylori* transmission to humans^[53].

Survival of *H. pylori* in foodstuffs

Several studies have demonstrated the survival of *H. pylori* in water, milk, ready-to-eat foods, vegetables, pasteurized apple and orange juices, ground beef and dry fermented sausages^[26,53-60] (Table 1).

H. pylori is able to survive in artificially contaminated milk stored at 4 °C for several days (from 5 to 9 d in pasteurized milk and from approximately 6 to 12 d in sterile milk)^[26,53,54,56]. These findings corroborate the hypothesis that post-processed contaminated milk may play a more effective role than other foods in the transmission of *H. pylori* infection due to the intrinsic

Table 1 Studies evaluating the survival of *Helicobacter pylori* in artificially contaminated foods

Year	Food	Method	Observations	Ref.
1998	Sterilized milk	Bacterial count on chocolate agar	10 d at 4 °C 3 d at 25 °C	Fan <i>et al.</i> ^[54]
2001	Pasteurized milk water tofu, tofu, yogurt, lettuce and chicken	Bacterial count on tryptic soy agar, non-selective Wilkins-Chalgren Anaerobe blood agar and selective Wilkins-Chalgren Anaerobe blood agar	from 5 to 7 d in pasteurized milk, tofu and water tofu at 4 °C for up to 2 d in lettuce and raw chicken at 4 °C for up to 1 d in yogurt at 4 °C	Poms <i>et al.</i> ^[26]
2000	Ground beef packaged in vacuum and air	Bacterial count on <i>H. pylori</i> special peptone agar	6 d in ground beef packaged in air at 4 °C 3-6 d in ground beef packaged in vacuum at 4 °C 3 d in ground beef packaged in air and in vacuum at -18 °C	Stevenson <i>et al.</i> ^[55]
2002	Ground beef, sterile milk, and apple and orange juices	Bacterial count on brain heart infusion agar and horse serum	7 d in ground beef at 4 °C 11 d in irradiated ground beef at 4 °C 6 d in sterile milk at 4 °C 1 d in apple and orange juice at 4 °C and 25 °C	Jiang <i>et al.</i> ^[56]
2004	Lettuce and carrots	Bacterial count on <i>Helicobacter</i> special peptone agar and Columbia blood agar	3 d in lettuce at 8 °C 5 d in sterilized carrot at 8 °C 3 d in sanitized carrot at 8 °C	Gomes <i>et al.</i> ^[57]
2007	Sterile milk and pasteurized milk	Bacterial count on Wilkins-Chalgren anaerobe agar	12 d in sterile milk at 4 °C 9 d in pasteurized milk at 4 °C	Quaglia <i>et al.</i> ^[53]
2010	Spinach	Bacterial count on brucella blood agar, Wilkins-Chalgren anaerobe blood agar	6 d at 8 °C	Buck <i>et al.</i> ^[58]
2011	Traditional Turkish fermented sausage (<i>sucuk</i>)	Bacterial count on Wilkins-Chalgren anaerobe blood agar	7 d	Guner <i>et al.</i> ^[59]
2017	Spring onion, cabbage, lettuce and spinach	Bacterial count on non-selective Blood base agar with 5% horse blood	3 d in spring onion, lettuce and spinach 4 d in cabbage stored at 4 °C	Ng <i>et al.</i> ^[60]

characteristics of this organism^[53]. It is well known that *H. pylori*'s ability to survive in an acidic pH environment is urea dependent^[3], and because urea is present in milk^[61], the urea-dependent acid resistance of *H. pylori* may account for the long-term survival of *H. pylori* in this foodstuff^[47]. Moreover, the microorganism is able to survive in milk for longer than the best-before date on an open milk package, making milk a possible source of transmission of this microorganism to humans. In fact, although the *H. pylori* load contaminating milk under natural conditions is unknown (although it is presumably lower than that used *in vitro*), the infection dose for humans is low; thus, even a small number of *H. pylori* cells surviving in foods may represent a potential health hazard for consumers^[53].

Other studies have been conducted on the survival of microorganisms in other more complex foodstuffs. *H. pylori* survives for approximately 7 d in ground beef at 4 °C, up to 3 d at -18 °C^[55,56] and for only 2 d in prepacked boneless, skinless chicken thighs^[26]. Vacuum packaging has no impact on survival time. However, if the high level of background bacteria present in the ground beef is eliminated, survival time increases to an undetectable level (< 10 cfu/g) within 11 d^[55]. The fate of *H. pylori* during the fermentation process of a traditional Turkish fermented sausage (*sucuk*) was investigated. The results of this study showed that the microorganism could survive and grow during the

fermentation process of *sucuk* (22 °C for 7 d). A possible explanation is that some fermentation products, such as protein degradation compounds and CO₂, might have been used by this pathogen and that indigenous bacteria might have created a microenvironment suitable for *H. pylori* growth^[59]. In contrast, *H. pylori* is not able to survive in yogurt^[26] or pasteurized fruit juice^[56] because its growth is hampered by the acidic pH and organic acids from lactic acid bacteria growth^[62,63].

Survival time in vegetables is shorter: 3 d in sanitized lettuce and carrot stored at 8 °C, 4 d in sterilized carrot and 5 d in carrot packaged in a modified atmosphere^[57]. A possible explanation could be the not-robust nature of this bacterium that on the surface of vegetables is exposed to oxygen and desiccation as opposed to what happens in liquid food and the presence of a high load of natural bacterial flora. Moreover, *H. pylori* is able to survive in contaminated vegetables despite the abovementioned adverse conditions, as it is able to form biofilms^[60]. However, a study on the survival of *H. pylori* in artificially contaminated spinach showed that this bacterium is able to survive for up to 6 d in VBNC forms that are still viable and can maintain its virulence factors despite its lack of cultivability^[58].

Occurrence of *H. pylori* in foodstuffs

Based on these findings, several studies have attempted to prove the occurrence of *H. pylori* in foodstuffs (Table

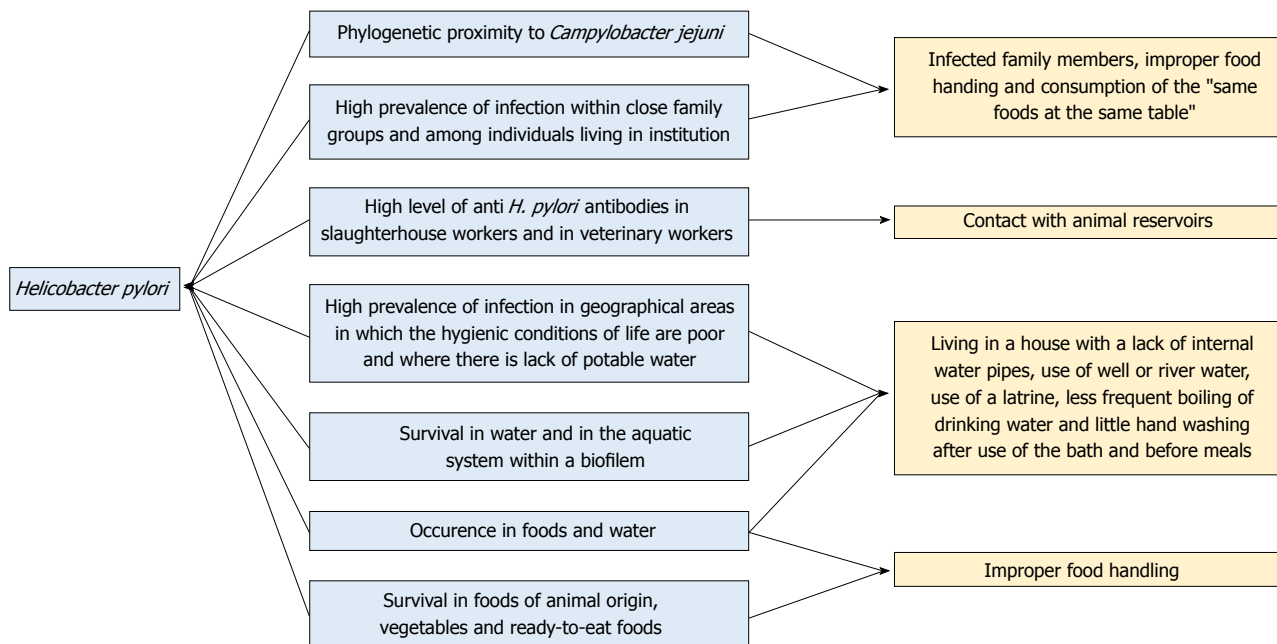


Figure 1 Evidence supporting the role of foods and water in the transmission of *Helicobacter pylori* to humans. In light blue is the epidemiological evidence supporting the hypothesis that *H. pylori* is a foodborne and/or a waterborne pathogen; in orange are the risks factors for *H. pylori* infection. *H. pylori*: *Helicobacter pylori*.

2). To the best of our knowledge, the first report about the presence of *H. pylori* in sheep milk was prompted by the observation that Sardinian shepherds with direct animal contact had a higher prevalence of infection than did their same-household siblings^[64]. *H. pylori* was isolated in 1 out of 38 PCR-positive raw sheep milk samples and in one out of 6 PCR-positive sheep gastric tissue samples^[65].

After these findings, *H. pylori* has rarely been isolated from raw milk samples^[66-69]. Bacteriological isolation of *H. pylori* occurred in one sample of raw cow milk out of 13 PCR-positive samples during a survey conducted in Japan^[66]. It was also isolated in 4 samples of raw cow milk out of 20 samples analysed in Greece^[67] and in Iran in 2 samples of raw sheep milk out of 11 PCR-positive samples and in 1 raw buffalo milk out of 15 PCR-positive samples^[68]. Afterward, Mousavi *et al*^[69] and Saedi *et al*^[70] reported a higher prevalence of *H. pylori* in raw cow, sheep, goat, buffalo and camel milks in Iran than that previously mentioned.

Furthermore, only a few studies have been carried out on the occurrence of *H. pylori* in dairy products other than milk. For example, in the survey of Mousavi *et al*^[69], 30% of Iranian traditional cheese, 15% of cream, 5% of butter and 27% of ice cream samples all made from unpasteurized milk were positive for *H. pylori*.

Compared to the few bacteriological isolations, the prevalence of *H. pylori* DNA is higher depending on the sensitivity of the method employed and the target gene^[65,66,68,71-73]. Conversely, these findings were not confirmed in the studies conducted by Jiang and Doyle^[56], Turutoglu *et al*^[74] and Bianchini *et al*^[75], which

failed to detect *H. pylori* in cow and sheep raw milk in the United States, Turkey and Italy, respectively, by PCR and bacteriological analysis.

The attempts to culture *H. pylori* from the majority of PCR-positive samples may have been unsuccessful for several reasons: the low number of contaminating bacteria in milk samples, the presence of VBNC forms that are not detectable by conventional microbiological culture-based protocols, and the relatively long period of storage before analysis, which could have affected the vitality of the few *H. pylori* cells present in the contaminated samples^[37,67,71].

Studies on the detection of *H. pylori* in food products other than milk are quite rare. *H. pylori* was isolated in 25%, 37%, 22%, 28% and 14% of cow, sheep, goat, buffalo and camel meat samples^[70] and in 1.42% and 12.5% of hamburger and minced beef samples, respectively^[76]. *H. pylori* DNA was detected in 36% and 44% of raw chicken and ready-to-eat raw tuna meat samples, respectively^[77]. Furthermore, Hemmatinezhad *et al*^[78] analysed 550 samples of ready-to-eat foods, detecting *H. pylori* in 74% of samples; olive salad (36%), restaurant salad (30%), fruit salad (28%) and soup (22%) were the most commonly contaminated. Additionally, Ghorbani *et al*^[79] recovered *H. pylori* in 60 out of 300 ready-to-eat food samples (20%), including ready-to-eat fish (15%), ham (8.33%), chicken sandwiches (5%), vegetable sandwiches (18%), meat sandwiches (10%), and minced meat (32%).

Few reports have addressed the occurrence of *H. pylori* in vegetables. In two surveys conducted in Iran, many of the vegetables analysed were positive for the presence of this microorganism: 13.72%^[80]

Table 2 Studies evaluating the occurrence of *Helicobacter pylori* in foods

Year	Food	Method	Number of samples <i>n</i>	Observations	Ref.
2001	Raw sheep milk	Culture and PCR	63 raw sheep milk	60% PCR positive samples 2.6% culture positive samples	Dore <i>et al</i> ^[65]
2002	Raw and pasteurized cow milk	Semi nested PCR, culture method and electron microscopy	18 raw cow milk 20 pasteurized milk	Raw milk: 72.2% semi-nested PCR positive samples; 1 culture positive sample Pasteurized milk: 55% semi-nested PCR positive samples	Fujimura <i>et al</i> ^[66]
2002	Raw sheep milk	Culture	440 raw sheep milk	0% positive samples	Turutoglu <i>et al</i> ^[74]
2008	Raw goat, sheep, and cow milks	Nested-PCR	160 raw goat milk 130 raw sheep milk 110 raw cow milk	25.6% positive goat milk 33% positive sheep milk 50% positive cow milk	Quaglia <i>et al</i> ^[71]
2008	Raw chicken and ready-to-eat raw tuna	Multiplex PCR	11 raw chicken 18 ready-to-eat raw tuna	36% positive raw chicken 44% positive ready-to-eat raw tuna	Meng <i>et al</i> ^[77]
2011	Raw cow milk	FISH	20	20% positive samples	Angelidis <i>et al</i> ^[67]
2012	Raw cow, sheep, goat, buffalo and camel milks	PCR	75 raw cow milk 58 raw sheep milk 42 raw goat milk 20 raw buffalo milk 15 raw camel milk	16.00% positive cow milk 13.79% positive sheep milk 4.76% positive goat milk 13.33% positive camel milk 20.00% positive buffalo milk	Rahimi <i>et al</i> ^[68]
2014	Milk and traditional dairy products	Culture and PCR	120 raw cow milk 100 raw goat milk 100 raw sheep milk 80 raw buffalo milk 60 raw camel milk 60 raw donkey milk 100 cheese 100 butter 100 cream 100 ice cream	16.6% positive cow milk 28% positive goat milk 35% positive sheep milk 15% positive buffalo milk 13.3% positive camel milk 0% positive donkey milk 30% positive cheese 15% positive cream 5% positive butter 27% positive ice cream	Mousavi <i>et al</i> ^[69]
2014	Vegetables and salad	Culture and PCR	60 salad 40 basil 40 radish 40 leek 80 spinach 80 lettuce 120 parsley	16.6% positive salad 12.5% positive basil 7.5% positive radish 20% positive leek 6.25% positive spinach 13.75% positive lettuce 6.6% positive parsley	Atapoor <i>et al</i> ^[81]
2014	Washed and unwashed vegetables	Culture and PCR	430 washed and unwashed vegetable	13.72% positive vegetables and salads	Yahaghi <i>et al</i> ^[80]
2015	Raw cow, sheep, goat, buffalo and camel milks	PCR	75 raw cow milk 58 raw sheep milk 42 raw goat milk 20 raw buffalo milk 15 raw camel milk	16.00% positive cow milk 13.79% positive sheep milk 4.76% positive goat milk 13.33% positive camel milk 20.00% positive buffalo milk	Talaei <i>et al</i> ^[72]
2015	Raw cow milk	Culture and nested PCR	50 raw cow milk	22% positive cow milk	Osman <i>et al</i> ^[73]
2015	Raw cow milk	Culture and nested PCR	163 raw cow milk	0% positive cow milk	Bianchini <i>et al</i> ^[75]
2016	Raw cow, sheep, goat, buffalo and camel milks and meats	Culture and PCR	420 raw milk 400 raw meat	21.90% positive raw milk 26.25% positive meat	Saedi <i>et al</i> ^[70]
2016	Ready-to-eat food	Culture and PCR	550 ready-to-eat food	13.45% positive ready-to-eat food	Hemmatinezhad <i>et al</i> ^[78]
2016	Ready-to-eat food and minced meat	Culture and PCR	60 ready-to-eat fish 60 ham 40 chicken sandwich 40 vegetable sandwich 50 meat sandwich 50 minced meat	15% positive ready-to-eat fish 8.33% positive ham 5% positive chicken sandwich 45% positive vegetable sandwich 20% positive meat sandwich 32% positive minced meat	Ghorbani <i>et al</i> ^[79]
2017	Hamburger and minced meat	Culture and nested PCR	80 hamburger 70 minced-meat	1.42% positive hamburger 12.5% positive minced-meat	Gilani <i>et al</i> ^[76]

and 9.56%^[81] of the vegetables and traditional salads analysed.

The high prevalence of *H. pylori* in ready-to-eat foods, meats, milks and vegetables could be due to post-

processing contamination. In fact, the high prevalence of *H. pylori* in healthy human carriers^[11] suggests that foodstuff contamination due to poor hygiene management during milking, chilling and storage and during the handling, preparation and packaging of ready-to-eat foods may occur. Furthermore, *H. pylori* strains isolated from foods showed genotypes of *vacA* alleles similar to those in isolates from human clinical samples, endorsing the hypothesis that foods can be the source of *H. pylori* transmission to humans^[76,78-80].

However, the existence of animal reservoirs of the microorganism cannot be excluded^[65,66]. In addition, the histopathology of lesions by *H. pylori* in humans differs from that of many other gastric helicobacters, causing mild or absent inflammatory responses in their natural hosts^[82]. These data suggest that *H. pylori* may have not originally evolved as a human pathogen but was likely introduced into the human population from a mammalian reservoir sometime in the distant past^[65]. This hypothesis is further supported by evidence of *H. pylori* in the gastric mucosa of calves, pigs and horses^[83] and its isolation from sheep gastric tissue and milk^[65,84]. Furthermore, in the studies of Papiez *et al.*^[85] and Dore *et al.*^[65], *H. pylori* prevalence was higher in shepherds with direct animal contact than in controls without contact with sheep. Considering the 100% positive 13C-urea breath test in sheep, it may be reasonable to assume that these animal species may act as reservoirs and spreaders of *H. pylori*^[85,86]. However, further epidemiological and experimental studies are needed to corroborate these few data.

EVIDENCE SUPPORTING THE ROLE OF WATER IN THE TRANSMISSION OF *H. PYLORI* TO HUMANS

In the last Joint Monitoring Report (JMP) of 2017, "Progress on Drinking Water, Sanitation and Hygiene" by WHO and UNICEF^[87], the first global assessment of safe drinking water and sanitation services was reported. In 2015, approximately 2.1 billion people did not manage water safely, and among them, 844 million did not even have basic drinking water services, spending more than 30 min per trip to collect water from external sources, and some of them still drank untreated water from surface water sources such as streams and lakes. Globally, at least 2 billion people use a stool-contaminated source of drinking water. Contaminated water can transmit diseases such as diarrhoea, cholera, dysentery, typhoid and polio^[87].

It has been estimated that *H. pylori* colonizes more than half of the world's population, and contaminated water is mentioned as one of major causes^[60,88-91].

Bellack *et al.*^[92] developed a conceptual model of the role of water in *H. pylori* transmission. The hypothesis is that both humans and animals are long-term hosts and that water is a relatively short-term reservoir. *H. pylori*

may survive in water for a period before it is ingested as drinking water, accidentally during bathing, or through other pathways involving food. The infected person will spread *H. pylori* through faeces; through direct faecal-oral transmission, an infected person can infect another person or contaminate water bodies through direct contamination with faeces or indirectly with wastewater that comes into contact with the water used to drink. Animal contamination of water reserves may occur by defecating directly in surface waters or by faeces penetrating groundwater. The type of soil and heavy rain events can play an important role because they can facilitate the penetrability of manure containing bacteria in groundwater^[92].

Several epidemiological studies have been conducted on the transmission of *H. pylori* through water, and several risk factors have been highlighted, such as living in a house with a lack of internal water pipes, the use of well or river water, the use of a latrine, less frequent boiling of drinking water and little hand washing after use of the bath and before meals^[93-96] (Figure 1).

In 1991, a survey carried out on 407 Peruvian Lima children aged 2 mo to 12 years from families with different socioeconomic statuses showed an overall *H. pylori* prevalence of 48%. The children underwent the 13C-urea breath test, and the results showed a higher incidence among the children of low-income families than among those of high-income families (56% vs 32%). An important risk factor was the water supply; incidence increased three-fold when the water sources were outside the home compared to those whose homes had internal water sources. Furthermore, the municipal water supply seemed to be an important source of infection among Lima children from families of both low and high socioeconomic status because children from high-income families whose homes had municipal water were 12 times more likely to be infected than were those from high-income families whose water supplies came from community wells^[97].

The poor basic hygiene conditions and the lack of potable water have been reported as the cause of *H. pylori* infection in an epidemiological study of a population in a rural area of the state of Mato Grosso in Brazil. The survey was conducted on 40 children and adolescents and 164 adults. *H. pylori* antibodies were detected in 31 (77.5%) children and adolescents and in 139 (84.7%) adults. The most important identified risk factor is using untreated water that could be contaminated by wastewater due to the lack of a sewage system^[98].

Nurgalieva *et al.*^[49] conducted a similar study on 233 adults and 55 children in Kazakhstan. The overall prevalence of *H. pylori* was 86% among adults and 64% among children. The prevalence of *H. pylori* infection was inversely correlated with the index of clean water (CWI) (boil water before consumption, frequency of recovery and reuse of water and frequency of bath and shower). Infection was significantly lower among those

with a high CWI (56%) than those with a moderate (79%) or low (95%) CWI. Moreover, the prevalence of *H. pylori* was inversely related to socioeconomic status. Those living in a family in which the levels of education and study were low had a higher rate of *H. pylori* infection (90%) than did those from a higher socioeconomic group (69%)^[49].

In another epidemiological survey conducted in Germany on 3347 children from cities and rural areas, 179 children (119 from cities and 60 from rural areas) were infected by *H. pylori*. Among the children from rural areas, positivity significantly increased with the consumption of water from non-municipal sources^[99].

Fujimura *et al.*^[100] studied the presence of *H. pylori* in 4 Japanese rivers and in 224 children who lived near one river using the stool antigen test for *H. pylori* prevalence.

The results of this study showed that *H. pylori* DNA was frequently present in river water from the middle and downstream reaches in which the human biosphere is embedded. The author concluded that river water in the natural environment could be a risk factor for *H. pylori* transmission.

Occurrence of *H. pylori* in water

Despite the several epidemiological studies that support the hypothesis that *H. pylori* is a waterborne pathogen, the real role of water in the spread of the pathogen remains a topic of discussion. As with foodstuffs, the fastidious nature of the bacterium and the difficulties in isolating it from environmental sources do not provide unequivocal evidence about the role of water as a source of transmission of this microorganism.

Culture methods, immunological methods and molecular methods have been employed to detect *H. pylori* in the aquatic environment.

Several studies on the occurrence of *H. pylori* in sewage and drinking water samples have been carried out worldwide using molecular methods. In many of these surveys, it was not possible to isolate the bacterium using culture methods (Table 3).

Based on the findings that there is an association between water sources and the prevalence of *H. pylori* infection in Peruvian children^[97], *H. pylori* DNA was detected in drinking water samples from different locations near Lima (Peru) in two different surveys using molecular methods. These results provided evidence of the presence of *H. pylori* DNA in drinking water in Peru and were consistent with conclusions from a previous epidemiological study of the same population^[101,102]. In addition, other studies have highlighted the presence of *H. pylori* DNA in samples of tap water, well water^[103], aquatic systems located in Mexico City^[104], trucks for water transport and lake water^[105], further supporting the hypothesis of the transmissibility of *H. pylori* through water.

Despite the high incidence of *H. pylori* DNA in water, only a few studies have reported bacteriological isolation

of this microorganism. Bacteriological isolation of *H. pylori* occurred in the study of Lu *et al.*^[106], who analysed untreated municipal wastewater samples using a series of steps beginning with immunomagnetic separation and cell culture.

In a survey carried out in Iraq, out of 198 samples of treated municipal drinking water, 10 strains of *H. pylori* were isolated and identified. The low concentration of chlorine in the water samples and the ability to form biofilms in water pipes^[107,108] were the reasons that *H. pylori* was isolated^[109].

H. pylori was also isolated in tap water, dental unit water, and bottled mineral water in Iran. Out of 200 water samples collected in Iran, 5 cultures were positive. Two out of 50 tap water samples (4%), 2 out of 35 dental unit water samples (5.8%), and 1 out of 40 samples (2.5%) from water coolers in public places were found to be contaminated with *H. pylori*^[110]. Ranjbar *et al.*^[111] examined 450 bottled mineral water samples and confirmed the presence of *H. pylori* in bottled mineral water.

Survival studies in water samples showed that *H. pylori* could be cultured from 48 h up to 20 d in autoclaved distilled water. An increase in survival occurs at low temperatures; in fact, high temperature causes loss of culturability^[89,91,112-118]. Shahamat *et al.*^[118] used an autoradiographic method to detect the metabolic activity of *H. pylori* VBNC in water. Four *H. pylori* strains were studied using 72-h cultures in water and incubated with [3H] thymidine for 24-72 h. After being exposed to the Kodak NTB2 emulsion for 3-28 d, the organism was vital and culturable under these conditions for up to 48 h and, in some cases, 20 to 30 d (Table 3).

One factor in support of *H. pylori* infection being waterborne or related to poor health practices is the association, which some authors claim, of *H. pylori* with free-living amoebae (FLA), such as *Acanthamoeba*, *Naegleria*, *Vermamoeba* or *Balamuthia*, which are ubiquitous protozoa commonly found in water^[119-122].

Several studies have also shown that *H. pylori* can be present as a biofilm on the pipes of the drinking water system with the ability to adhere to different hydraulic materials, such as copper and stainless steel^[121,123,124]. As a result, *H. pylori* is likely to survive in an aquatic system within a biofilm rather than in the planktonic state^[39,125].

H. pylori cells were able to survive for short periods in chlorinated drinking water in the VBNC form, which would allow them to reach final consumption points and, at the same time, enable them to be undetectable by culture methods^[115].

Moreover, in biofilms, the resistance of *H. pylori* to chlorine increases significantly^[120,126]. Therefore, it is possible that if the organism enters a distribution system, it may survive disinfection treatment within the biofilm matrix^[115]. This characteristic may be based on the lack of isolation in some surveys of *H. pylori*. In fact, in water samples treated with suitable potabilization

Table 3 Studies evaluating the occurrence and survival of *Helicobacter pylori* in water

Year	Water and study type	Method	Observations	Ref.
1993	Survival of <i>H. pylori</i> in artificially contaminated sterile river water	Culture	Culture up to 48 h	Shahamat <i>et al</i> ^[118]
1996	Occurrence of <i>H. pylori</i> in 48 water samples: 30 from municipal water system, 14 from community taps, 4 from brick tanks or plastic barrels of different households	Autoradiography IMS and PCR	50% PCR positive samples	Hulten <i>et al</i> ^[101]
1997	Study on <i>H. pylori</i> resistance to chlorination	Culture	<i>H. pylori</i> were readily inactivated by free chlorine	Johnson <i>et al</i> ^[117]
1999	Occurrence of <i>H. pylori</i> in water from rivers and ponds	IMS and nested PCR	<i>H. pylori</i> -specific DNA was detected in samples	Sasaki <i>et al</i> ^[103]
1999	Occurrence of <i>H. pylori</i> in water from delivery truck and two lakes	Nested PCR and Southern blot hybridization	PCR positive samples from truck PCR positive samples from two lakes	McKeown <i>et al</i> ^[105]
2001	Occurrence of <i>H. pylori</i> in 10 seawater samples, 10 river water samples, 10 tap water samples, 6 well water samples	IMS, real-time PCR and nested PCR	2 PCR positive samples of well water	Horiuchi <i>et al</i> ^[127]
2001	Occurrence of <i>H. pylori</i> in 139 ground water samples	PCR and Southern blot hybridization	69% positive samples	Mazari-Hiriart <i>et al</i> ^[104]
2002	Occurrence of <i>H. pylori</i> in raw municipal wastewater	IMS, culture and PCR	23 out of 37 isolated strains were confirmed to be <i>H. pylori</i> 11 out of 23 strains of <i>H. pylori</i> demonstrated <i>vacA</i> gene heterogeneity	Lu <i>et al</i> ^[106]
2002	Study on the susceptibility of <i>H. pylori</i> to chlorine, monochloramine, and ozone compared to that of <i>Escherichia coli</i>	Culture	<i>H. pylori</i> was more resistant than <i>E. coli</i> to chlorine and ozone but not monochloramine	Baker <i>et al</i> ^[116]
2004	Occurrence of <i>H. pylori</i> in water and biofilms: 11 samples from domestic proprieties, 7 samples from educational properties and from hydrants, and samples from reservoirs and water meters of 3 water utilities	Culture, IMS and PCR	All cultures were negative 26% PCR positive sample with the highest frequency in biofilm	Watson <i>et al</i> ^[120]
2004	Occurrence of <i>H. pylori</i> in seawater	Nested-PCR	<i>H. pylori</i> DNA only detected in fractionated water samples containing zooplanktonic organisms	Cellini <i>et al</i> ^[130]
2005	Occurrence of <i>H. pylori</i> in seawater	Filtration (200 mm, filter), culture and PCR	<i>H. pylori</i> was only isolated from fractionated water samples containing large zooplanktonic organisms	Cellini <i>et al</i> ^[131]
2005	Occurrence of <i>H. pylori</i> in 36 seawater samples	Culture and PCR	30 positive samples	Carbone <i>et al</i> ^[132]
2006	Study on the ability of <i>H. pylori</i> to adhere on different water-exposed abiotic surfaces	Scanning electron microscope	<i>H. pylori</i> was able to adhere to all substrates tested	Azevedo <i>et al</i> ^[123]
2007	Study on the ability of <i>H. pylori</i> to adhere to stainless steel 304 in different environmental conditions	Epifluorescence microscopy	<i>H. pylori</i> was able to adhere to stainless steel 304	Azevedo <i>et al</i> ^[124]
2007	Study on the resistance of <i>H. pylori</i> to chlorination	Culture, FISH, PCR and RT-PCR	Culture until 5 min FISH viable cells until 3 h PCR samples positive after 24 h RT-PCR positive after 24 h	Moreno <i>et al</i> ^[115]
2007	Survival of <i>H. pylori</i> in spiked bottled mineral water (drinking water)	Culture epifluorescence microscopy and PCR	Culture until 5 d Cell viability until 14 d	Queralt <i>et al</i> ^[114]
2007	Survival of <i>H. pylori</i> in spiked chlorinated filtered water (drinking water)	Culture, FISH and PCR	Culture until 5 min FISH viable cells until 3 h PCR positive after 24 h RT-PCR after 24 h	Monero-Mesonero <i>et al</i> ^[115]
2009	Occurrence of <i>H. pylori</i> in 75 drinking and environmental water samples and 21 natural water biofilms samples	Real-time PCR	0% positive samples	Janzon <i>et al</i> ^[129]
2010	Occurrence of <i>H. pylori</i> in 198 drinking water samples	Culture	10 out of 469 isolated strains were confirmed <i>H. pylori</i>	Al-Sulami <i>et al</i> ^[109]
2011	Occurrence of <i>H. pylori</i> in 137 seawater samples	PCR	21% of the samples were positive for <i>H. pylori</i>	Twing <i>et al</i> ^[134]

2013	Occurrence of <i>H. pylori</i> in 50 tap water samples, 35 dental units' water samples, and 40 bottled mineral water samples	Culture and PCR	2 positive tap water samples 2 positive water from dental unit samples 1 positive water coolers sample	Bahrani <i>et al.</i> ^[110]
2013	Occurrence of <i>H. pylori</i> in 31 seawater samples	Culture and PCR	4 positive samples	Holman <i>et al.</i> ^[135]
2016	Occurrence of <i>H. pylori</i> in 450 bottled mineral water samples	Culture and PCR	8 positive samples	Ranjbar <i>et al.</i> ^[111]
2018	Occurrence of <i>H. pylori</i> in 241 drinking water samples	PCR	49 positive samples	Boehnke <i>et al.</i> ^[102]

H. pylori: *Helicobacter pylori*.

systems, the lack of isolation can be caused by the formation of the biofilm or by the conversion of *H. pylori* in the form of VBNC^[127-129].

Some important clues have emerged from Italian research on the presence of bacteria in seawater. Work by Cellini *et al.*^[130,131] and subsequent investigations^[132] suggest that a significant reservoir for the microorganism is seawater, in which *H. pylori* can occur both in a free-living form and in association with plankton. Plankton-related *H. pylori* cells were detected in both summer and winter months depending on the flowering of Copepods and Cladocerans. The authors supposed that zooplankton organisms represent a sort of protected niche for survival of the microorganism. The finding of *H. pylori* attached to planktonic organisms is particularly interesting for the role of the latter in the seafood chain and its subsequent potential role in the spread of *H. pylori* infection^[130-132]. More generally, the presence of *H. pylori* in seawater could also be a health hazard for swimmers and others using those waters for work or pleasure^[133].

Moreover, *H. pylori* DNA has been isolated in 21% of samples from freshwater, estuarine and beach sites in Delaware (United States)^[134] and in seawater sampled from 31 locations in Georgia, Trinidad and Puerto Rico^[135]. In both reports, no correlation between the occurrence of *H. pylori* and faecal indicator bacteria was found, suggesting that standard water quality tests are ineffective in predicting the presence of this pathogen in natural waters, confirming the potential risk for *H. pylori* presence in marine waters.

METHODS FOR THE DETECTION OF *H. PYLORI* IN FOODS AND WATER

The isolation of *H. pylori* from food samples, particularly when they present high loads of accompanying microflora, is demanding and time consuming because it requires the use of selective media with numerous antibiotics, microaerophilic conditions and long incubation periods (7 d)^[55,71]. The detection of *H. pylori* in food samples and water by means of conventional microbiological techniques generally employed for clinical specimens, which are unable to detect the VBNC, may yield false negative results and thus underestimate the presence of the bacterium in food; furthermore, the presence of *H. pylori* in VBNC state in food and water represents a

potential microbiological risk for consumers, especially as a source of virulence factors^[37,136,137].

Several solid and liquid culture media for the selective isolation of *H. pylori* from foods have been tested. The culture media most suitable for *H. pylori* growth often contain defibrinated horse or sheep blood acting as a reducing agent^[29]. Furthermore, to achieve replication of *H. pylori* in broth culture, agitation is mandatory to provide good dispersion of gases throughout the liquid^[31].

Brain heart infusion broth (BHIB) with growth supplement and selective agents has been evaluated^[26,56]. BHIB with horse serum supplemented with porcine stomach mucin (0.3%), ferrous sulphate and sodium pyruvate (5%) or urea, along with the adjustment of the pH to 5.5 or 4.5, enhances the survival and possibly enables the growth of *H. pylori* in enrichment medium with fresh ground beef. In particular, pH 5.5 greatly enhances the growth and detectability of *H. pylori* in foods and should be considered an important factor for the detection of *H. pylori* in enrichment culture^[56]. Stevenson *et al.*^[55] compared the growth of *H. pylori* in several liquid and solid media. None of the media tested presented an outstanding performance; only *H. pylori* special peptone agar offered the advantage of allowing the formation of the largest *H. pylori* colonies, and it was suitable for recovering *H. pylori* from environmental samples likely to be contaminated with large numbers of competing microorganisms^[31,55].

Poms and Tatini^[26] evaluated the efficacy for the *in vitro* isolation of *H. pylori* from foods of two solid media containing tryptic soy agar and Wilkins-Chalgren anaerobe agar supplemented with 5% defibrinated horse blood. The latter, to which several antibiotics (30 mg/L colistinmethanesulphonate, 100 mg/L cycloheximide, 30 mg/L nalidixic acid, 30 mg/L trimethoprim, and 10 mg/L vancomycin) were added, was found to be highly selective for the recovery of *H. pylori* from foods, but it lacked sufficient sensitivity to detect very low numbers of the bacterium.

Many authors have successfully used Wilkins-Chalgren anaerobe-agar or the broth developed by Poms *et al.*^[26] for the isolation of *H. pylori* in foods, both supplemented as described above^[70,76,78-80].

However, there are still no standardized isolation protocols that are able to isolate the few *H. pylori* cells

present in samples rich in microbial flora such as food. Furthermore, the pathogen is able to enter a VBNC state that remains metabolically active but fails to develop into colonies when cultured on routine media^[40]. Consequently, molecular assays have been conducted to detect *H. pylori* DNA in water and foodstuffs.

Immuno-separation (IMS) followed by PCR has been successfully used by several investigators^[138-140]. The advantage of using this protocol is that it offers excellent specificity using the IMS able to concentrate the pathogen from foods, followed by high sensitivity of the molecular methods^[29]. Nevertheless, it appears expensive, exacting and time consuming. Autoradiography and ATP bioluminescence have been successfully used for the detection of *H. pylori* from water, human stools and pure cultures but have never been tested on food^[29,118]. In addition, the ATP bioluminescence assay does not allow for distinguishing among ATP from different cell sources when applied to a complex system such as a foodstuff^[141].

A multiplex touchdown PCR (MT-PCR) method for the identification (16S rRNA gene) and genotyping (*vacA*- s1/m1, s1/m2, and s2/m2- and *cagA* genes) of *H. pylori* directly from artificially contaminated sheep milk was developed^[142]. The characterization of the genes encoding virulence factors provides important information with respect to the sanitary assessment of food items because of the greater pathogenicity of certain *H. pylori* genotypes. Hence, for public health purposes, the evaluation of a food containing *H. pylori* will thus have to include the genotyping of isolates. This rapid, sensitive (15 cfu/mL) and specific molecular method presents the advantage of detecting and genotyping *H. pylori* from microbiologically complex foodstuffs in a single step^[142]. A nested PCR approach has been employed for the detection of the *H. pylori glmM* gene from seawater and sheep, goat and cow milks^[71,130,141]. The sensitivity of the nested PCR technique was 3 cfu/mL in all types of milk and 62 cfu/mL in seawater samples, and therefore, compared to the previously described MT-PCR, it was more sensitive for the detection of *H. pylori* from foods (3 cfu/mL vs 15 cfu/mL) with the same specificity^[141]. Osman *et al.*^[73] employed nested PCR in 50 cow milk samples, and 22% were positive for the presence of the *H. pylori glmM* gene.

H. pylori, as with many other bacteria, is able to form biofilms within which it can survive due to the different protection mechanisms that the biofilm offers. Quantitative real-time PCR was developed for the detection of *H. pylori* in drinking water biofilms of different ages. The target gene was the *ureA* subunit of the *H. pylori urea* gene, which showed high specificity and sensitivity^[143].

As is well known, the main limit of PCR assays is their inability to distinguish live organisms from dead organisms. PCR techniques can, however, be used to screen water and foodstuffs, thus making it necessary to use conventional isolation methods only on those samples that test positive by PCR.

In a study by Buck *et al.*^[58], mRNA of known virulence factor (*vacA*) was detected in VBNC *H. pylori* cells using RT-PCR. This method exploits the unstable nature of bacterial mRNA to infer pathogenic viability when *H. pylori* becomes non-cultivable^[144]. The half-life of mRNA of *E. coli* and *Vibrio vulnificus* cells is approximately 3-8 min and less than 60 min, respectively^[145,146]. Thus, mRNA can be an excellent indicator of viability when *H. pylori* occurs in the VBNC state. Moreover, detection of transcripts from the *vacA* virulence gene may deduce continued virulence activity of *H. pylori* when present in the VBNC state^[58]. This molecular technique offers significant promise for the detection of microorganisms in water and foodstuff and is a valid alternative to culture methods.

The fluorescence in situ hybridization (FISH) assay with the rRNA-direct molecular method has been applied for the specific detection of *H. pylori* in river and wastewater samples^[147] and in raw bulk tank bovine milk^[67] and for the assessment of its survival in chlorinated drinking water^[115,148]. The authors concluded that FISH was a rapid method for the direct detection and specific identification of viable bacteria in food^[67].

CONCLUSION

Several studies report the presence and survival of *H. pylori* in foods and water, especially in milk and in ready-to-eat products, suggesting that they can be sources of infection for humans.

Although many of the findings reported in the literature are based on indirect evidence of *H. pylori* in food and water through molecular methods and there are only in a few cases on the bacteriological isolation of this microorganism, the possibility that food and water can be routes of transmission among others cannot be ruled out.

Most of the bacteriological isolations of the pathogen in foods and water have been obtained in work conducted in Iran; a possible explanation could be the greater prevalence of the disease in this geographical area than in other areas. Moreover, the discrepancy in the prevalence of *H. pylori* in the different surveys could be related to the type and number of samples tested, sampling method, experimental methodology and climate differences in the regions from which the samples were collected.

However, to confirm a definite foodborne and waterborne role of *H. pylori* transmission, more surveys are needed on the presence of *H. pylori* in other foods of animal origin, particularly in seafood, and on the survival ability of this microorganism in dry fermented sausages and dairy products. Further investigations on the possible role of humans and animals as reservoirs of the microorganism are also required to clarify the faecal-oral route of transmission and the method of food and water contamination. Finally, the development of molecular biology methods and, above all, bacteriological isolation methods of *H. pylori* from

water and food would add provide data that could confirm or deny the role of *H. pylori* as a foodborne and waterborne pathogen.

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Hepatitis B virus infection: Defective surface antigen expression and pathogenesis

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Abstract

Hepatitis B virus (HBV) infection is a global public health concern. HBV causes chronic infection in patients and can lead to liver cirrhosis, hepatocellular carcinoma, and other severe liver diseases. Thus, understanding HBV-related pathogenesis is of particular importance for prevention and clinical intervention. HBV surface antigens are indispensable for HBV virion formation and are useful viral markers for diagnosis and clinical assessment. During chronic HBV infection, HBV genomes may acquire and accumulate mutations and deletions, leading to the expression of defective HBV surface antigens. These defective HBV surface antigens have been found to play important roles in the progression of HBV-associated liver diseases. In this review, we focus our discussion on the nature of defective HBV surface antigen mutations and their contribution to the pathogenesis of fulminant hepatitis B. The relationship between defective surface antigens and occult HBV infection are also discussed.

Key words: Hepatitis B surface protein; Defective surface antigen mutants; Endoplasmic reticulum stress; Fulminant hepatitis B; Occult hepatitis B virus infection; Pathogenesis

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Core tip: Defective surface antigen mutation is a type of mutation with great clinical relevance. Many previous publications have explored the association of defective surface antigen mutation with the development of hepatitis B virus (HBV)-associated hepatocellular carcinoma. However, there are no reviews available that elaborate on the relationship between defective surface antigen mutation and HBV-associated fulminant hepatitis (FH), as well as occult hepatitis B virus infection (OBI). This review will focus on these two aspects to discuss the nature of defective HBV surface antigen mutations and their contribution to the pathogenesis of FH. The relationship between defective surface antigens and OBI are also discussed.

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INTRODUCTION

Hepatitis B virus (HBV) is an important human pathogen that has caused chronic infections worldwide^[1]. Recent data obtained from a modeling study has shown that the global prevalence of hepatitis B surface antigen (HBsAg) was 3.9% in 2016, corresponding to an estimated 290 million infections worldwide^[2]. HBV mainly infects hepatocytes and causes a wide spectrum of clinical manifestations, ranging from an asymptomatic carrier state to acute or chronic hepatitis, with progression to liver cirrhosis, hepatocellular carcinoma (HCC), and other severe liver diseases^[3,4]. Currently, interferon- α and nucleotide analogs are used to treat chronic HBV (CHB) infections; however, the outcome is far from satisfactory^[5,6]. Prophylaxis using the current HBV vaccines has no impact on existing infections. Therapeutic vaccines of chronic HBV infection are under investigation, but further development is still required^[7]. Therefore, understanding the molecular pathogenesis of HBV infection will provide opportunities for the development of better therapies and vaccines.

HBV belongs to the family *Hepadnaviridae* and is a small, enveloped virus with a partially double-stranded DNA genome approximately 3.2 kb in size^[8]. During the life cycle of HBV, pre-genomic RNA (pgRNA) is transcribed from covalently closed circular DNA (cccDNA) and serves as the template for HBV DNA replication through a viral polymerase-mediated reverse transcription^[9,10]. Because viral polymerase lacks a proof-reading function, the HBV genome evolves with an estimated rate of nucleotide substitutions of 1×10^{-3} to 1×10^{-6} per replication cycle, according to various

investigators^[11]. Although HBV genome replication involves a step of reverse transcription, which is similar to retroviral replication, the complex HBV genome structure with overlapping open reading frames and regulatory sequences apparently limits the spectrum and rate of mutations^[3,12]. Nevertheless, this unique replication strategy leads to the great diversity of HBV genomes, thus resulting in the occurrence of various genotypes, subtypes, mutants, recombinants, and even viral quasi-species in the context of long-term HBV evolution^[13,14]. Several reports have suggested that the emergence of HBV variants plays important roles in the progression of HBV-associated liver diseases^[11,15-18]. Defective surface antigen mutation is a type of mutation with great clinical relevance^[11,15,19]. In this review, we report the current information on HBV surface antigen mutations. Further, we focus our discussion on the contribution of defective surface antigen mutations on the pathogenesis of HBV-associated liver diseases.

BIOLOGY OF HBV SURFACE ANTIGEN

Three viral envelope/surface proteins - large surface antigens (LHBs), middle surface antigens (MHBs), and small surface antigens (SHBs) - are expressed from a single open reading frame (S-ORF)^[20,21], but they are translated from two different mRNAs. LHBs are encoded by the 2.4 kb subgenomic RNA, and MHBs and SHBs are encoded by the 2.1 kb subgenomic RNA^[3]. Subgenomic RNAs of 2.4 kb and 2.1 kb are driven by preS1 and preS2/S promoters, respectively, allowing variable regulation of protein expression^[3]. The preS1 promoter is situated within the upstream region of the S-ORF, whereas the preS2 promoter corresponds to the preS1 domain^[21]. Therefore, the transcription of the 2.1 kb subgenomic RNA is also regulated by the preS1 domain^[11] (Figure 1).

The three surface proteins share the same carboxy-terminal region and only differ in length due to their amino-terminal regions. As a result, the LHBs contain the preS1 + preS2 + S [389 or 400 amino acid (aa) residues], MHBs contain the preS2 + S (281 aa residues), and SHBs contain the S domain (226 aa residues) alone^[3,20,22] (Figure 1). Additionally, a truncated and mutated preS2/S (the LHBs and truncated MHBs) can be produced by integrated viral sequences that are defective for replication^[23,24]. LHBs, MHBs, and SHBs are important for HBV structure and life cycle. Besides mediating HBV entry through binding to HBV receptors, the sodium taurocholate co-transporting polypeptide (NTCP) on hepatocytes, via the preS1 2-48 aa domain (numbering for HBV-genotype D) and subsequent infection, LHBs are indispensable for the formation and budding of virions^[3,25-29]. It has been proposed that LHBs rearrange their structure during the maturation of HBV virions and thereby regulate the release and infectivity of virions^[30-32]. The exact role of MHBs in the HBV life cycle remains an enigma.

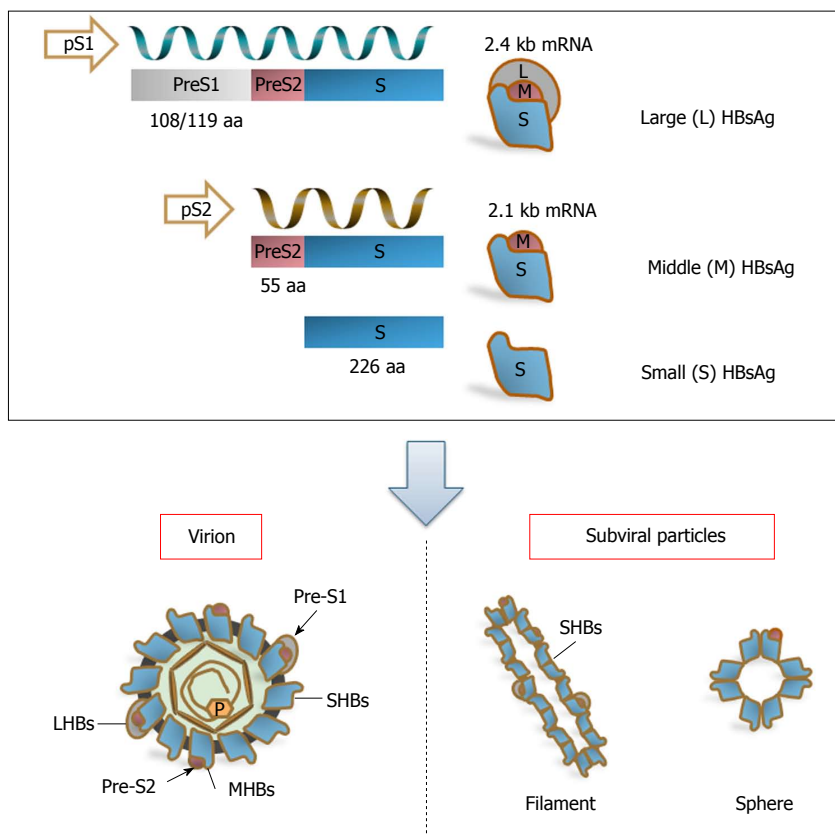


Figure 1 The transcription and expression of hepatitis B virus surface proteins. The three HBV surface proteins, LHBs, MHBs, and SHBs, are translated from two different mRNAs: LHBs are encoded by the preS1 promoter-initiated 2.4 kb subgenomic RNA; MHBs and SHBs are encoded by the preS2 promoter-initiated 2.1 kb subgenomic RNA. The 2.4 and 2.1 kb subgenomic RNAs share the same 3' end and only differ in length due to differences at the 5' end, which lead to different amino-terminal but identical carboxy-terminal regions of the three surface antigens. Therefore, LHBs contain preS1 + preS2 + S (389 or 400 aa residues), MHBs contain preS2 + S (281 aa residues), and SHBs contain the S domain (226 aa residues) alone. For mature/infectious virions, LHBs, MHBs, and SHBs are present in the envelopes at a ratio of approximately 1:1:4. In addition, the major fraction of SHBs forms subviral particles (filaments and spheres) together with the minor parts of LHBs and/or MHBs. HBV: Hepatitis B virus; LHBs: Large surface antigens; MHBs: Middle surface antigens; SHBs: Small surface antigens.

Early reports indicated that MHBs might be dispensable for HBV replication and virion formation; however, our data and those of other groups have shown that MHBs play a role in virion secretion^[33-36]. Recently, MHBs were found to interact with ceruloplasmin and influence the production of extracellular virions^[34]. As the predominant component of viral particles, including infectious virions and noninfectious subviral particles, SHBs are necessary for the production of virions and subviral particles^[35]. For mature/infectious virions, LHBs, MHBs, and SHBs are present in the envelopes at a ratio of approximately 1:1:4^[20]. Disturbance of this proportion impairs the production and release of virions^[33]. For subviral particles, their amount outnumbers virions by 10000- to 1000000-fold, and the particles are detected serologically as HBsAg^[11,37]. The secretion of subviral particles can also be suppressed by LHBs in a dose-dependent manner^[38-41], thus promoting the S protein toward virion formation.

In addition, preS1, preS2, and S domains contain various B- and T-cell epitopes, which play an important role in inducing the host immune response^[42,43]. The major hydrophilic region (MHR) between aa 100-169 of SHBs, especially the a-determinant located at aa

124-147, serves as the most important antigenic determinant in HBV surface proteins and is essential for HBsAg detection and HBV vaccine development^[44,45]. Plasma-derived and recombinant HBsAg have been used for vaccine preparations and have induced strong specific and protective antibody responses in vaccines^[46-48]. The presence of anti-HBs antibodies is considered to confer immunity against HBV infection. In contrast, a high quantity of circulating HBsAg in chronically HBV-infected patients is proposed as a factor leading to immune disturbance. Defective peripheral HBsAg-specific T cell responses in chronically infected patients were found to be correlated with serum HBsAg titers^[49,50], suggesting that HBsAg overproduction influences the host's immune system in a way that is advantageous for the virus. *In vitro*, HBsAg can interfere with Toll-like receptor functions and trigger interleukin (IL)-10 production in Kupffer cells^[51-54]. Recently, published data has suggested that HBsAg may facilitate the induction of myeloid-derived suppressor cells in chronically HBV-infected patients^[55]. HBsAg is also associated with the induction of regulatory T cells, as shown in HBV mouse models^[56,57]. Thus, HBsAg is not only a structural component of virions and subviral

particles, but it also serves as an important immune modulator.

DEFECTIVE SURFACE ANTIGEN MUTATION AND HBV BIOLOGY

HBsAg mutants were first identified in individuals vaccinated against HBV but who were infected despite the presence of protective anti-HBs antibodies^[58]. Those “immune escape” mutants with aa substitutions within a-determinants were found in different clinical settings, including vaccines, transplant patients receiving hyperimmunoglobulins, and immunocompromised patients with HBV reactivation^[59-61]. Such mutant HBsAg commonly showed reduced binding to anti-HBs antibodies and decreased reactivity in established HBsAg detection assays^[59-65]. The most widely known mutation is the sG145R mutation, which has been shown to be replication competent, may persist stably over time, and may be transmitted vertically or horizontally^[66-69]. The sG145R mutation induces a strongly impaired anti-HBs antibody response, which could not efficiently clear HBsAg in an HBV hydrodynamic injection mouse model^[70]. A similar result was also observed for another immune escape mutation, sK122I, indicating that such a defective surface antigen mutation may impair HBsAg neutralization and clearance during HBV infection. In addition, sG145R, sK122I, and other immune escape mutants occurring in the a-determinant of SHBs, such as the sT123N mutation, could affect HBsAg secretion^[70-73].

Recently, chronically HBV-infected patients routinely received antiviral therapy based on nucleotide analogs^[74]. Treatment with first-generation drugs, such as famciclovir and adefovir, resulted in the emergence of drug-resistant HBV mutants, with aa substitutions within the HBV polymerase domain^[75]. Some drug-resistant mutations occurring in the viral polymerase may lead to a stop codon mutation in the overlapping surface gene, cause intracellular retention of surface proteins, and result in secretion defects of viral particles, such as rtA181T/sW172*, rtM204I/sW196*, and rtV191I/sW182*, as shown in previous reports^[76-78] and in our unpublished data. The primary sW182* mutation has also been identified in CHB patients. It was found to induce retention of the truncated S protein in the perinuclear endoplasmic reticulum (ER) and was associated with lower HBV transcript levels owing to decreased stability, but without impact on HBV replication^[79].

Defective surface antigen mutations have been frequently detected in chronic HBV infection^[16,71-73,80,81], in which deletions in the preS domains are the most common mutations^[80,81]. Deletions in the preS domains are often clustered at the 3' end of preS1 and the 5' end of preS2^[11,19,81-83]. Given that the preS2/S promoter is situated within the preS1 domain^[11], deletions at the 3' end of the preS1 may reduce MHBs and SHBs expression at the transcriptional level. Deletions at the

5' end of the preS2 may remove the N-terminal preS2 domain, including the start codon of preS2 in the MHBs protein, leading to an impaired or complete loss of MHBs expression^[84]. These changes may disrupt the proper LHBs, MHBs, and SHBs ratio in the envelopes of virions. In addition, the junction between the preS1 and preS2 domain is required for virion formation^[32]. For these reasons, preS deletions may potentially affect virion assembly, stability, or infectivity.

A large amount of evidence has demonstrated that DHBV envelope proteins can regulate cccDNA formation and amplification^[85,86]. Infection of envelope protein-deficient recombinant DHBV results in more cccDNA accumulation^[85,87,88]. Similarly, deficiencies in HBV envelope proteins can modestly increase the cccDNA level and result in a dramatic accumulation of deproteinized rcDNA^[89-91]. It has been demonstrated that preS/S mutants with surface antigen secretion deficiency isolated from patients can lead to an increased accumulation of cccDNA molecules in the nuclei^[79]. Therefore, defective surface antigen mutation may affect cccDNA synthesis and amplification.

DEFECTIVE SURFACE ANTIGEN MUTATIONS AND THE HOST

Defective surface antigen mutations have been found in acute hepatitis B infection, chronic hepatitis B infection, and occult HBV infection and are associated with advanced liver disease, including liver cirrhosis, fulminant hepatitis B, and HCC^[15,82,92-105]. It has been questioned whether HBV mutants arise due to viral adaptation to inflammation and decreased liver function or, alternatively, causally contribute to liver pathogenesis. The mechanism of defective surface antigen mutations to HCC development has been widely elucidated^[11,23,41,106-111]. Here, we will emphasize in our discussion the relationship between defective surface antigen mutations and fulminant hepatitis B, as well as occult HBV infection.

Defective surface antigen expression and fulminant hepatitis

There is increasing evidence that defective surface antigen expression may play a role in the pathogenesis of fulminant hepatitis (FH). preS deletions, particularly those unable to synthesize the MHBs protein, have been associated with cases of FH^[16,71,112,113], suggesting the potential pathogenic role of preS deletions. A mutation in the CAAT element of the S promoter has been found in the HBV genome isolated from an FH patient. This mutation led to excessive LHBs expression over MHBs and SHBs proteins and resulted in virus retention and misassembly^[114-116]. Obviously, the accumulation of LHBs may be due to hepatocyte injury, as shown in transgenic mice with LHBs expression^[41]. One of our previous studies also identified deletions within the preS

regions from HBV strains isolated from a patient with HBV-associated FH^[84]. In addition, a hepatitis B immune globulin (HBIG)-escape mutant sG145R on the HBsAg, causing 30% inhibition of virion secretion, has been identified from a study on FH strains, suggesting the potential role of defective surface antigen expression in the fulminant clinical course of HBV infection^[71].

Mechanistically, defective surface antigen expression, such as specific mutations in the preS/S gene, may lead to secretion defects of viral proteins and particles, resulting in an accumulation of viral products in the ER of hepatocytes and causing ER stress and hepatocyte injury^[16]. Subsequently, autophagy may be triggered^[117-125] and thus enhance HBV replication^[126,127]. Consistent with this speculation, it has been demonstrated that defective surface antigen expression may increase the replication capability of HBV, albeit the mechanism is still undefined^[71,84]. In addition, the deficiency of hepadnavirus envelope proteins can result in accumulation of cccDNA^[85,87,88] or deproteinized rcDNA^[89-91] and may ultimately cause death of the infected hepatocytes by a direct cytopathic effect^[85,87,88]. Meanwhile, the increase of the cccDNA level may facilitate HBV replication. Both the defect in viral particle secretion and enhanced replication competence may contribute to the severity of fulminant hepatitis^[128].

The adaptive immune response, particularly the cytotoxic T lymphocyte (CTL) response, plays a crucial role in viral clearance and disease pathogenesis of HBV infection^[129-131]. Intracellular retention of HBV surface proteins was found to be associated with FH in a transgenic mouse model showing panlobular necrosis and hepatic failure by inducing the indirect cytotoxic activity of CTLs^[132]. In this setting, intracellular accumulation of viral products due to defective surface antigen expression mutations may cause liver damage through abnormal activation of the CTL response. Consistently, we also observed significantly stronger intrahepatic CTL responses and antibody responses specific to secretion-deficient HBsAg due to preS deletions^[84]. A preS deletion mutant was found in a patient with acute exacerbation of liver diseases, along with wild-type HBV genomes. The co-existence of deletion mutants and wild-type HBV apparently allows the complementation and enhancement of HBV genome replication in hepatocytes. In an HBV mouse model, co-replication of a deletion mutant and wild-type HBV induced higher cellular and humoral immunity. Our findings further suggested the proposed role of HBV variants in the immunopathogenesis of HBV infection. Moreover, the mutations associated with defective surface antigen expression, such as deletion or missense mutation of the preS2 ATG codon, can cause deletions or alterations of B- and T-cell epitopes located in preS1 and preS2 proteins. Considering that M protein-specific T- and B-cell immunities are important early events in the host immune response to HBV infection^[43], these mutations may lead to an immune evasion

and thus likely favor a more severe clinical course of infection^[14,133]. In chronic HBV infection, high HBV replication levels were found to be associated with lower cellular immune responses to HBV; however, massive infiltration of unspecific immune cells occurred within the liver, accompanied by severe liver damage^[134-136]. Thus, the presence of these mutations, including aa substitutions at the immunodominant epitopes for B or T cell recognition, may contribute to the spread of highly replicative escape mutants. It may also facilitate the development of fulminant hepatitis in chronically HBV-infected patients and heavily immunocompromised patients, like those with human immunodeficiency virus (HIV) co-infection^[137] (Figure 2).

Defective surface antigen expression and occult hepatitis B virus infection

Occult HBV infection (OBI) is characterized by the presence of very low levels of HBV DNA in the plasma and/or liver of individuals negative for HBV surface antigen (HBsAg) and positive/negative for antibodies to the hepatitis core antigen (anti-HBc)^[45,138,139]. OBI harbors the potential risk of HBV transmission through blood transfusion, organ transplantation, and hemodialysis as well as from occult infection or HBsAg-positive mothers to newborns^[45]. The persistence of OBI may lead to the development of cirrhosis and HCC^[45,140-145]. The reactivation of OBI can occur in patients following chemotherapy, immunosuppressive therapy, and after transplantation as well as in patients co-infected with HIV or hepatitis C virus (HCV)^[45,146,147], which can result in the development of fulminant hepatitis and death^[139,148-153].

Defective surface antigen expression mutations may be associated with OBI. Point mutations and deletions as well as insertion mutations are commonly encountered in OBI, in which mutations in the *preS/S* gene are the most extensively studied^[45]. High frequencies of MHR mutations, including those mutations within and outside of the a-determinant, have been observed in OBI strains of individuals^[154-158]. *In vitro* and *in vivo* experiments have demonstrated that these MHR mutations can significantly decrease the detection sensitivity of commercial HBsAg immunoassays and impair virion and/or S protein secretion^[156]. *preS/S* mutations with deletions covering the preS1 and preS2/S promoters, preS1 region, and preS2 region have been frequently reported in OBI. This can alter the transcription of 2.4 kb and 2.1 kb HBV RNAs, expression of three envelope proteins, and the ratio of LHbs/MHbs/SHbs proteins^[45]. *preS/S* insertions, such as 2-8 aa insertions between codons 121 and 124 located upstream of the a-determinant, have also been observed in OBI patients^[159].

On one hand, these mutations associated with defective surface antigen expression can directly decrease the levels of surface antigens. On the other hand, these mutations can cause the retention and

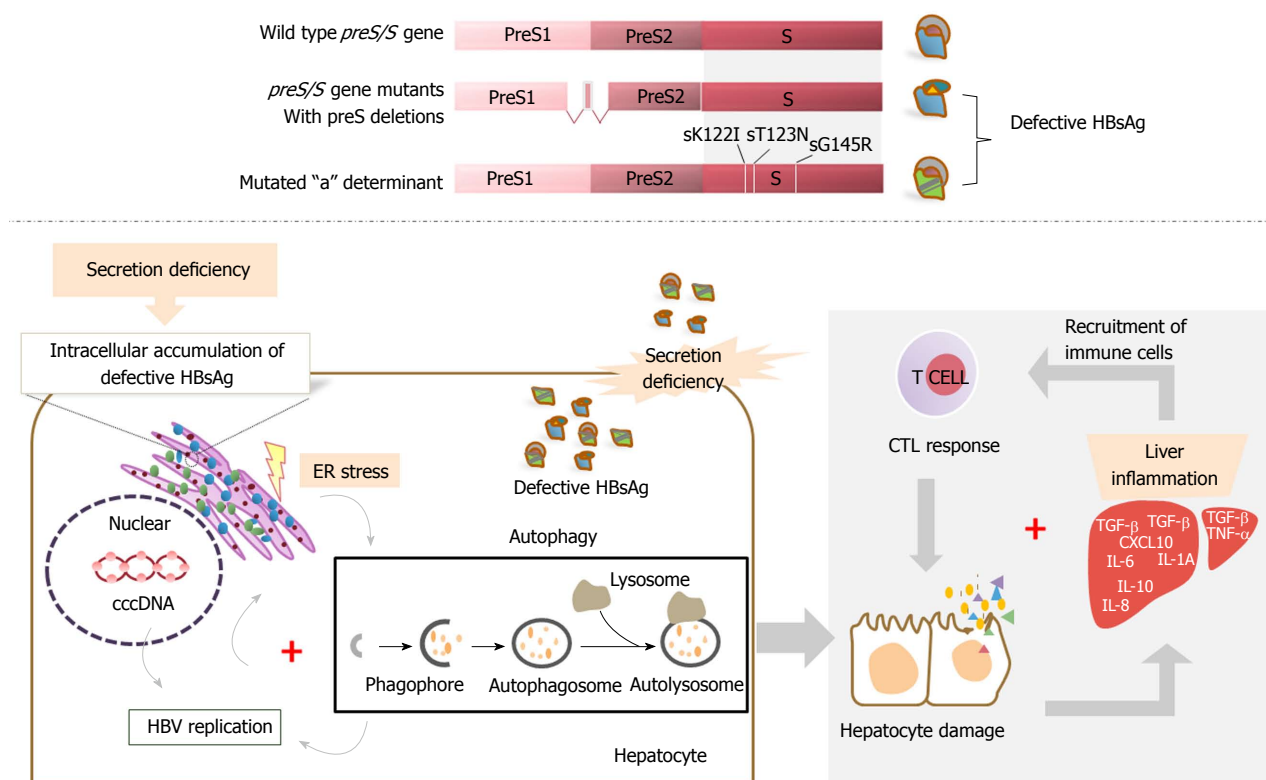


Figure 2 The proposed pathogenic role of mutated secretion-defective hepatitis B surface antigen in fulminant hepatitis. Defective surface antigens, such as preS deletions and mutations within the “a” determinant, may lead to secretion deficiency of HBsAg. Defective HBsAg can promote covalently closed circular DNA (cccDNA) synthesis and amplification, thus facilitating HBV replication. The intracellular accumulation of defective HBsAg can cause endoplasmic reticulum (ER) stress, subsequently trigger autophagy, and may further enhance HBV replication. The enhanced HBV replication, in turn, leads to accumulation of more defective HBsAg, possibly resulting in a positive feedback with unfavorable outcomes and hepatocyte damages. Inflammation may occur in the liver by recruiting immune cells. Cytotoxic T lymphocyte (CTL) response may be abnormally activated and damage infected hepatocytes, contributing to the progression of fulminant hepatitis. HBsAg: Hepatitis B surface antigen.

accumulation of HBsAg within cells and impair the secretion of HBsAg by altering the ratio of LHbS/MHBs/SHBs proteins^[72,73,160,161]. Therefore, circulating HBsAg levels are low in the peripheral blood. Moreover, it is well documented that neutralizing antibodies produced during natural infection, or following active or passive immunization against HBV, are targeted to the conformational epitopes of the a-determinant^[162]. Hence, single or multiple mutations occurring within this region can lead to conformational changes with impaired antigenicity^[72,160]. A recent report has identified novel SHBs mutations outside the MHR from untreated CHB patients. These mutations impaired virion secretion and caused lower binding affinity to antibodies used for HBsAg immunoassays^[163]. For these reasons, the mutations can render HBsAg undetectable or poorly detected by immunoassays based on monoclonal antibodies against wild-type virus^[60,62,65,164], contributing to some cases of OBI^[165-170] (Figure 3).

PERSPECTIVES

Defective surface antigen expression has been well documented to be relevant for the progression of HBV-associated liver diseases, such as HCC. However, the role of defective surface antigen expression in FH still

needs to be clarified in future research, particularly, using *in vivo* models and in patients. The exact molecular mechanisms of how defective HBV surface antigens cause damage to hepatocytes and induce liver injury and subsequent pathogenic processes should be investigated. A deep understanding of the molecular mechanisms of HBV pathogenesis related to defective surface antigens is crucial to designing future therapeutic approaches. A critical question would be whether currently used nucleotide analogues (NAs) and interferon-based therapies can prevent such pathogenic processes. NAs are able to efficiently inhibit HBV DNA synthesis but not gene expression. Thus, HBV proteins, including surface antigens, are continuously produced under NA therapies. Another problem is the production of mutated HBV proteins from integrated HBV DNA, which are not controlled by NA therapies at all. Thus, specific interventions may be required to block the pathogenic potential of HBV proteins, besides efficient inhibition of HBV DNA synthesis. RNA silencing may be a suitable choice to achieve this goal^[5,6,171,172].

An additional issue to be addressed is whether the defective surface antigen-related mutations may represent novel biomarkers of OBI. With improvement of HBV antigen and DNA detection assays, OBI will likely be easier to diagnose in the future. However,

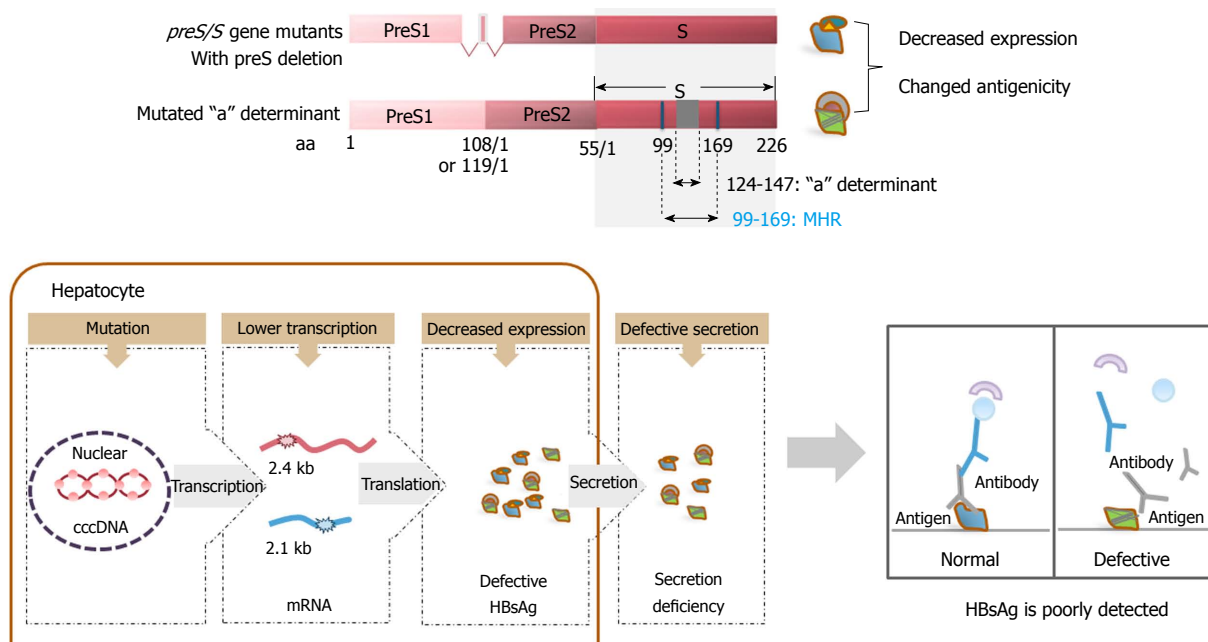


Figure 3 The relationship between the expression of defective surface antigens and occult hepatitis B virus infection. Surface antigen mutations, such as preS deletions, can impair the transcription of 2.4 and 2.1 kb HBV RNAs, leading to decreased levels of three HBV surface proteins. In addition, defective surface antigens with preS deletions and mutations within the “a” determinant are secretion deficient. Single or multiple mutations occurring within the MHR between the aa residues 99-169 of SHBs, especially those within the “a” determinant between aa 124-147, can lead to conformational changes of HBsAg. Mutated HBsAg is poorly detected by immunoassays based on monoclonal antibodies, contributing to some cases of OBI. OBI: Occult hepatitis B virus infection; HBsAg: Hepatitis B surface antigen.

the question remains whether OBI may be related to significant HBV pathogenesis and require therapeutic interventions, such as prophylaxis and antiviral therapy, to prevent HBV reactivation^[173].

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Immunometabolism: A novel perspective of liver cancer microenvironment and its influence on tumor progression

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Abstract

The initiation and progression of liver cancer, including hepatocellular carcinoma and intrahepatic cholangiocarcinoma, are dependent on its tumor microenvironment. Immune cells are key players in the liver cancer microenvironment and show complicated crosstalk with cancer cells. Emerging evidence has shown that the functions of immune cells are closely related to cell metabolism. However, the effects of metabolic changes of immune cells on liver cancer progression are largely undefined. In this review, we summarize the recent findings of immunometabolism and relate these findings to liver cancer progression. We also explore the translation of the understanding of immunometabolism for clinical use.

Key words: Cholangiocarcinoma; Hepatocellular carcinoma; Tumor microenvironment; Local immune status; Metabolite

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Core tip: The liver microenvironment provides a special place for initiation and progression of liver cancer, in which immune cells play a vital role. On the one hand, immunosuppression leads to tumor survival and progression; on the other hand, the instigation of tumor metabolites and signal molecules to immune cells makes the state of immunosuppression further strengthened. Intensive studies of the metabolic state of immune cells in the tumor microenvironment is beneficial to our understanding of the regulation of pro-tumor patterns, and to provide theoretical basis

and guidance for immunometabolic therapies for liver cancer.

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INTRODUCTION

Liver cancer is one of the most common malignancies and has the third leading mortality rate and seventh leading incidence rate worldwide^[1]. To date, with over 42000 cases diagnosed and 30000 deaths in the United States per year, a continuous increase in both morbidity and mortality is observed in liver cancer^[2]. Unfortunately, the prognosis of advanced liver cancer is still poor despite the many treatments that have been developed in the past few decades. Thus, novel approaches to treat liver cancer are urgently needed.

The tumor microenvironment (TME) plays critical roles in tumor development and is characterized by complicated components, including various types of non-tumoral cells and non-cellular materials^[3]. TMEs can be largely distinct among different types of cancers and among different patients with the same type of cancer. Within a patient, the TME can consistently change as the tumor progresses and is influenced by the physiopathological conditions of the patient. Thus, it is theoretically impossible to identify the precise state of the TME. However, under certain conditions, the TME can be specialized to show typical traits, and in particular, this specialized TME may affect tumor progression. Understanding these particular TMEs, if not all of them, can outline the crosstalk between the TME and tumor cells and facilitate the development of novel strategies for tumor treatment^[4].

Pathologically, liver cancer mainly includes hepatocellular carcinoma (HCC) and intrahepatic cholangiocarcinoma (ICC). The two types of liver cancers share a similar hepatic microenvironment, but may have different TMEs due to the various biological characteristics of the tumor cells. For instance, in a considerable proportion of cases, ICC harbors isocitrate dehydrogenase (IDH) 1 and IDH2 mutations^[5], which are rare in HCC^[6]. IDH1 and IDH2 are important enzymes involved in cellular metabolism. Therefore, IDH1/2 mutations can substantially influence the metabolite profiles in cells and TMEs. In this case, the roles of the TME in liver cancer progression may be greatly altered. However, knowledge in this field is poor and scattered.

Immune cells are key players in liver cancer progression, and their recruitment and functions are

profoundly affected by the TME^[7]. Other molecules in the TME, such as fatty acids and glucose, are able to regulate the metabolism, phenotype and function of immune cells^[8,9]. The term "immunometabolism" has recently been proposed and indicates the functional intracellular metabolic alterations that occur within immune cells^[10]. These affected immune cells, in turn, could have significant effects on adjacent tumor cells. In this minireview, we collected evidence of TME heterogeneity resulting from the different biological features of cancer cells and functional changes of immune cells resulting from an altered TME and how the TME affects tumor progression *via* metabolically regulated immune cells.

CHARACTERISTICS OF IMMUNE CELLS IN LIVER CANCER MICROENVIRONMENT

With genetic and epigenetic changes, hepatoma cells express specific tumor-associated antigens, such as α -fetoprotein (AFP), glypican-3 (GPC3) and melanoma-associated gene-A1 (MAGE-A1), which can be taken up by antigen-presenting cells and presented to T cells, resulting in a cytotoxic reaction to eliminate cancerous cells^[11,12]. However, immunosuppressive factors and immune-inhibitory checkpoint molecules inhibit anti-tumor reactions and create a special microenvironment to facilitate tumor progression^[12]. Almost all types of immune cells are deeply involved in the TME of liver cancer (Figure 1), including macrophages, Kupffer cells, neutrophils, T cells, B cells, innate lymphoid cells (ILCs), dendritic cells (DCs), natural killer (NK) cells, natural killer T (NKT) cells, and myeloid-derived suppressor cells (MDSCs)^[13-18].

Macrophages and neutrophils

Macrophages display remarkable heterogeneity in liver cancer for various reasons, such as the cell origin (resident Kupffer cells and recruited monocyte-derived macrophages), stimulating signals (*i.e.*, microbes, cell debris) and functional phenotype (*i.e.*, inflammatory, anti-inflammatory). Notably, macrophages can play two or more contradictory roles in a particular TME. As guardians, macrophages are normally activated by inflammatory signals and together with CD4⁺ T cells eliminate precancerous senescent cells^[19]. Kupffer cells directly show cytotoxicity against tumor cells^[20-22]. In addition, macrophage-derived interleukin (IL)-12 hampers tumor progression by activating NK and NKT cells^[23,24]. As an accomplice, however, tumor-associated macrophages (TAMs, most of which are M2-polarized macrophages), induced by IL-4 and tumor growth factor (TGF)- β , accumulate in liver cancer and are correlated with the poor prognosis of patients^[25,26]. Importantly, these macrophages express the immune checkpoint protein programmed cell death-ligand 1 (PD-L1, also known as B7-H1), which inactivates CD8⁺ T cells^[13,27,28]. *Via* other immunosuppressive signals,

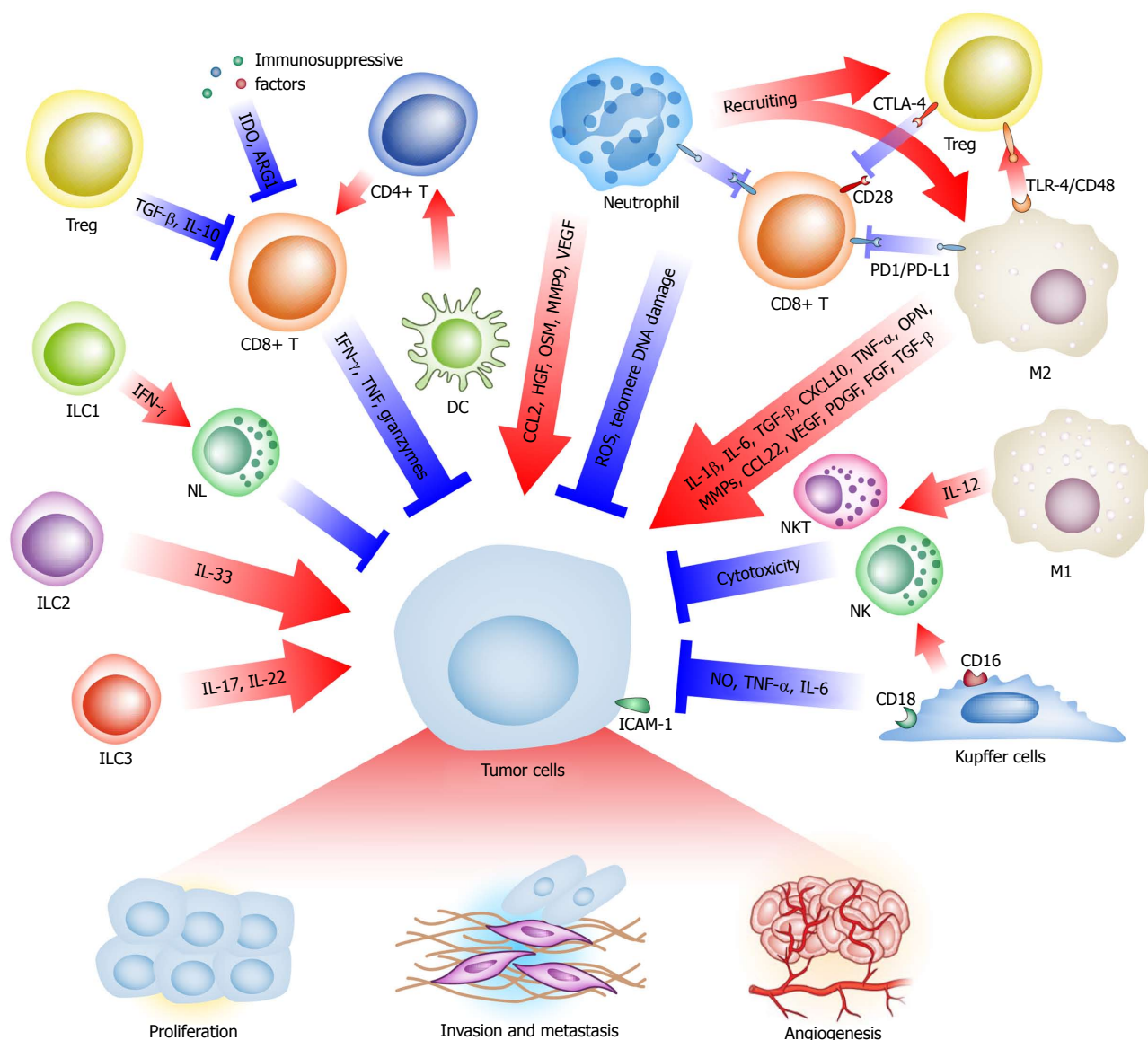


Figure 1 The immune cells in the tumor microenvironment regulate liver cancer progression. Many types of immune cells in the TME show pro- or anti-tumoral effects on the liver cancer cells by cell-specific mechanisms. Complicated crosstalk between immune cells is also common. TME: Tumor microenvironment; ILC: Innate lymphoid cell; NKT: Natural killer T.

such as Toll-like receptor (TLR) 4 and CD48/2B4, M2-polarized macrophages promote the recruitment of regulatory T cells (Tregs) and suppress the activity of NK cells^[29-31]. Moreover, these macrophages can secrete various tumor proliferation-promoting cytokines, such as IL-1 β , IL-6, TGF- β , C-X-C motif chemokine (CXCL) 10, invasion and metastasis-promoting factors like tumor necrosis factor (TNF)- α , osteopontin (OPN), matrix metalloproteinases (MMPs), C-C Motif chemokine ligand (CCL) 22, and proangiogenic growth factors, like vascular endothelial growth factor (VEGF), platelet derived growth factor (PDGF), fibroblast growth factor (FGF), and TGF- β , to build a tumor-prone inflammatory microenvironment^[3,26,32-35].

Similar to macrophages, neutrophils also have diverse functions at different stages of liver cancer progression. In the case of a hepatic infection or injury, neutrophils

gather at the wound site together with macrophages to eliminate pathogens and necrotic materials. Additionally, neutrophils stimulate reactive oxygen species (ROS) and telomere DNA damage in hepatocytes, mediating neoplasia and progression^[36]. Mirroring macrophage plasticity, a pro-tumoral phenotype of tumor-associated neutrophils (TANs) is proposed^[37,38]. Despite biomarkers of this subtype, immunosuppression is the most central function of TANs. The immunosuppressive molecule PD-L1 is regularly displayed in TANs^[39] and recruits macrophages and Treg cells to the liver cancer TME and induces impaired anti-tumoral immunity^[14]. The infiltrating TAN density and neutrophil-lymphocyte ratio is reported to be a predictor of outcome, chemotherapy resistance, and recurrence risk^[40-42]. Furthermore, neutrophils promote tumor progression by secreting cytokines and other functional molecules, such as CCL2

for tumor growth, hepatocyte growth factor (HGF) and oncostatin M (OSM) for metastasis, and MMP9 and VEGF for angiogenesis^[38,43-47].

T cells

CD8⁺ T cells are the most important executors of adaptive immunity against neoplasms, including liver cancer. Unfortunately, the TME transforms these 'warriors' into 'servants'. Compared with the normal liver, tumor tissue has a lower density of CD8⁺ T cells and a higher density of Tregs. The ratio of CD8⁺ T cells to Tregs typically indicates a poor prognosis^[48-50]. Recent studies suggest that interferon (IFN)- γ , TNF and granzyme secretion by CD8⁺ cytotoxic T lymphocytes (CTLs) represent a common cytotoxic reaction against tumors^[51,52]. Tregs, characterized by CD4, CD25, cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) and forkhead box P3 (FoxP3) expression, can eliminate IL-2 *via* its receptor subunit CD25, downregulate CD80 and CD86 and conjugate to the co-stimulatory molecule CD28 competitively with CTLA-4 to suppress immune responses. In addition, Tregs secrete TGF- β and IL-10 into the TME to suppress T effector cells^[52]. *Via* a complicated regulatory network, several subtypes of T cells contribute to the immunosuppressive TME.

ILCs

ILCs are recently identified innate immune cells that lack a specific antigen receptor. These cells originate from mucosal-associated lymphoid tissues and act as a sentry of the rapid immune response and regulator of immune homeostasis and inflammation^[53]. Mirroring the classification of helper T cells (Th), ILCs are divided into three classes. ILC1s produce Th1-associated cytokines, ILC2s are associated with Th2-associated cytokine release, and ILC3s secrete Th17-associated cytokines^[54]. As these three components simultaneously exist in the liver, they are likely to be involved in hepatocarcinogenesis and progression. ILC1s produce IFN- γ to activate NK cells and indirectly participate in cancer immunosurveillance, while ILC3s release IL-17 and IL-22, which may promote tumor growth and angiogenesis^[16,55,56]. Moreover, we observed an increasing number of ILC2 in HCC tissue (unpublished data) and an elevated level of IL-33 in both serum and tumor tissue samples from HCC patients^[57]. IL-33 can stimulate rapid growth and metastatic progression in breast cancer and cholangiocarcinoma^[58,59]. Therefore, the initiation and growth of liver cancer promoted by the ILC2-related IL-33/ST2 axis might be theoretically tenable^[60].

the survival of tumor cells seems to be in question. However, the tumor is able to reprogram the cellular metabolism for neoplastic proliferation. The abnormal metabolism induced by cancer provides energy and metabolites for cell activity and additionally modifies many related pathways that influence various biological processes^[61].

General alterations

The liver is a metabolic organ, and metabolic disruption of the liver can lead to spontaneous hepatocarcinogenesis^[62]. The principal metabolic alterations in the liver cancer were profiled by metabolomics analysis, which showed elevated glycolysis, gluconeogenesis and β -oxidation, with reduced tricarboxylic acid cycle (TCA cycle) activity^[63,64]. Aerobic glycolysis, also known as the "Warburg effect", is frequently observed in various tumors. This theory indicates that tumor cells predominantly use glycolysis, even in the presence of sufficient oxygen^[65]. For liver cancer, glycolysis also plays a dominating role in glucose metabolism^[63]. Accumulating studies have revealed that glycolysis is associated with genetic and epigenetic changes. Activated oncogenes and mutant tumor suppressors are associated with glycolysis. Glucose transporters (GLUTs), glycolysis-related enzyme hexokinase2 (HK2), pyruvate kinase M2 (PKM2), and lactate dehydrogenase (LDH) A are also overexpressed in liver cancer tissue, suggesting an increased glycolysis activity^[66]. Moreover, the hypoxic TME and overexpression of β -catenin in liver cancer stabilize hypoxia inducible factor (HIF)-1 α to activate glycolytic enzymes^[67-70].

Fatty acid β -oxidation is enhanced in liver cancer to overcome the energy shortage and reduce tumor dependence on glucose. Metabolic alteration increases FA biosynthesis and glycerolipid metabolism, leading to fatty acid and lipid accumulation^[71,72]. However, the alterations of various types of fatty acids are complicated. Additionally, almost all amino acids are increased in liver cancer due to the reduction of amino acid catabolism^[63]. Although these general changes were identified, many other factors may influence the levels of metabolites in TME.

Involvement of specific mutations

Some specific mutations profoundly change the metabolism of liver cancer. The Tumor Cell Genomic Atlas (TCGA) project of HCC demonstrated that IDH and fibroblast growth factor receptor (FGFR) are meaningful mutations in HCC. IDHs are critical enzymes for cell metabolism, particularly the TCA cycle. IDH1/2 mutations convert α -ketoglutarate (α -KG) into 2-hydroglutarate (2-HG)^[73]. The unusually decreased ratio of α -KG/2-HG can significantly influence tumor cell biology by competing with α -KG and regulating epigenetic expression^[74]. However, overproduced 2-HG by tumor cells can also be released into the TME since elevated serum and urinary levels of 2-HG can

ALTERED METABOLISM OF LIVER CANCER AND ITS INFLUENCE ON THE TUMOR MICROENVIRONMENT

With their rapid growth and limited nutrition supply,

be detected in patients with IDH1/2-mutated solid tumors^[75,76]. Although 2-HG seems to be impermeable, this enzyme acts on stromal cells within the bone marrow microenvironment through an ROS/extracellular signal-regulated kinase (ERK) signaling pathway^[77], suggesting that 2-HG may influence immune cells in the TME of liver cancer. This finding is important since IDH-like HCCs (particularly those containing IDH1/2 mutations and those with IDH-like gene expression) are indicative of worse clinical outcomes for undefined reasons^[6]. In addition to 2-HG, IDH-like HCCs and IDH1/2 mutated ICCs have other significant metabolic alterations, such as gliomas due to pseudohypoxia, an interrupted Krebs cycle, and epigenetic changes^[78]. In addition, IDH gain-of-function mutations also induce the reprogramming of pyruvate and lipid metabolism to maintain cell proliferation and clonogenicity^[79,80]. Therefore, the TMEs of these tumors likely have distinct features, and the immune cells within such TMEs may be reprogrammed to have different functions.

FGFR genetic aberrations include mutations, amplifications, and gene fusions, which have been observed in over 10% of liver cancer^[81-83]. FGFR2 fusions are active kinases with the highest incidence^[84]. These genetic aberrations indirectly affect glucose and lipid metabolism by activating the kinase network^[85]. Additionally, the oncogenic FGFR3-transforming acidic coiled-coil containing protein (TACC) 3 fusion activates oxidative phosphorylation and mitochondrial biogenesis, causing a mitochondrial respiration-dependent subtype of tumor cell^[86].

Influence of hepatic viruses

Hepatitis viruses, particularly HBV in eastern countries and HCV in western countries, cause specific metabolic alterations during hepatocarcinogenesis and tumor progression. Hepatic virus infections activate many abnormal signaling pathways, which cause aberrant functions and expression of metabolism related enzymes^[87]. As a consequence, HBV infection in patients is associated with increased free fatty acids (FFAs) and acyl-carnitines and decreased triglycerides, phospholipids, and sphingomyelins^[88]. Thus, in the TME of HBV-related liver cancer, the increased FFAs and decreased glucose may result from increased β -oxidation and glycolysis, respectively. HBV-related inflammation can stimulate the expression of HIF-1 α through the PI3K/AKT and mitogen-activated protein kinase (MAPK)-Ras-Raf pathways. The latter up-regulates GLUT1 and glycolytic enzymes, increases the glycolytic flow, and induces ROS accumulation. These alterations eventually cause DNA oxidative damage and malignant transformation^[89-92]. HBx activates the adenosine 5'-monophosphate-activated protein kinase (AMPK) and fatty acid oxidation (FAO) pathways as well as the HBx-LXR α -SREBP1/FAS pathway, which allows HCC cells to survive under metabolic stress^[93-95]. HCV establishes an insulin-resistant TME in the liver through several

mechanisms^[96,97]. For instance, HCV protein can induce the overexpression of protein phosphatase 2A (PP2A), which dysregulates hepatic glucose homeostasis by inhibiting AKT and the dephosphorylation of FoxO1^[98]. However, the molecular mechanism of viral hepatitis-related metabolic alternations is not well understood. HBV integration into the tumor suppressor gene region causes metabolic alterations. Signaling molecules, such as TGF- β , mammalian target of rapamycin (mTOR), Smad3, and c-Myc, are activated by HBV and HCV, which is closely correlated with tumor progression^[87,96].

Participation of other concomitant diseases

Liver cancer has a higher incidence in people with chronic non-infectious liver diseases. Therefore, the metabolic changes of liver cancer are related to cirrhosis and nonalcoholic fatty liver disease (NAFLD), which typically includes lipid anomalies, particularly dysregulated *de novo* lipogenesis^[99]. For instance, peripheral insulin resistance together with enhanced mitochondrial β -oxidation and oxidative stress are the most prominent features of NAFLD and nonalcoholic steatohepatitis (NASH)^[100]. Thus, NAFLD-related liver cancer is associated with elevated oxidative metabolism and amplified anaplerosis/cataplerosis^[101]. With the increasing content of hepatic FFAs, liver cells may endure a mild respiratory dysfunction. The increasing import of FFAs into the mitochondria is accompanied by an elevated rate of β -oxidation. The overloaded fatty acid β -oxidation triggers the subsequent accumulation of ROS, which further leads to lipid peroxidation and severe mitochondrial oxidative damage^[102,103]. These strong oxidizing products promote inflammation, fibrosis, and even carcinogenesis. Lipid metabolism shows an alteration from β -oxidation to ω -oxidation during liver cirrhosis^[104]. Intriguingly, a metabolic switch from oxidative phosphorylation to glycolysis in hepatocytes in early-stage cirrhosis may satisfy the extreme energy requirements under such conditions^[105]. This evidence demonstrates that concomitant liver diseases or even systemic metabolic diseases, such as diabetes mellitus, can influence the function of immune cells and their functions in promoting tumor progression.

Metabolic reprogramming of local immune cells in liver cancer

The role of metabolism in regulating immune cells has recently aroused general concerns. Evidence collected in several types of solid tumors indicated the importance of tumor immunometabolic reprogramming and suggested a novel and crucial area for future research of liver cancer^[106]. The complicated crosstalk between metabolically reprogrammed immune cells and liver cancer cells has been suggested, but the molecular mechanisms need further exploration (Figure 2).

Because they exist at a considerable quantity, macrophages play a leading role in the crosstalk between liver cancer cells and immune cells. The

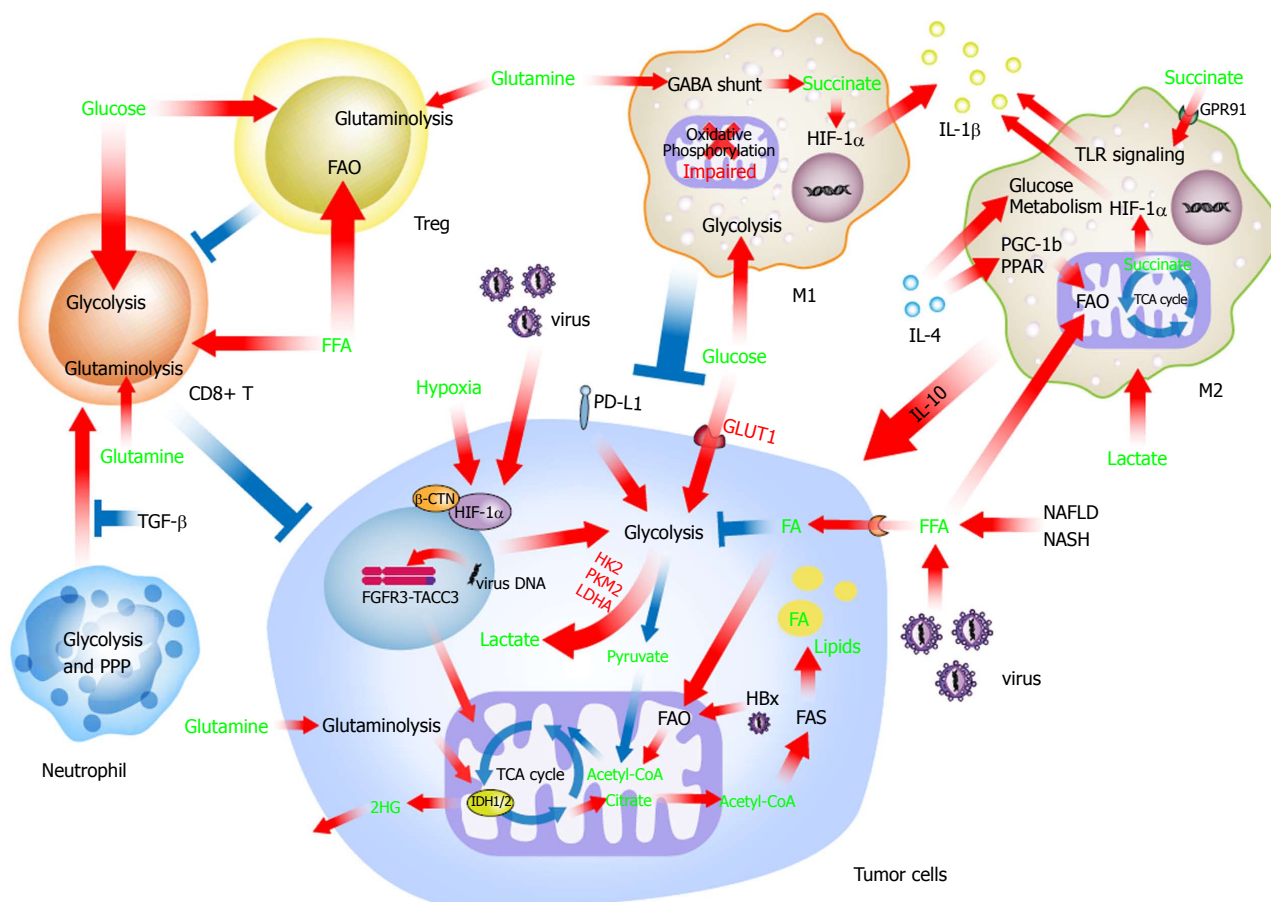


Figure 2 Metabolites in the tumor microenvironment affect the anti/pro-tumoral functions of immune cells. Energy resources including glucose, glutamine, free fatty acids, and other metabolites such as succinate largely alter the functions of macrophages, neutrophils, and T cells. These metabolically reprogrammed immune cells then have a differed influence on the liver cancer cells compared to the original immune cells. FAO: Fatty acid oxidation.

phenotypes and functions of macrophages are hot topics in the field of immunometabolism. Professor O' Neill's group and other investigations have conducted several pioneering and important studies to decipher macrophage immunometabolism. Recent evidence has suggested that the energy source (*e.g.*, glucose and fatty acids) participates in the determination of macrophage polarization^[107,108]. However, the role of FAO in the alternative activation of macrophages is still under debate. Huang *et al.*^[108] initially demonstrated an essential role for FAO in the alternative activation of mouse macrophages, while two groups in Germany and the United States subsequently provided convincing evidence that FAO was indispensable for the M2 polarization of human and mouse macrophages, respectively^[109,110]. This discrepancy may partially reflect differences between mouse and human macrophages and the potential off-target effects of etomoxir (a carnitine palmitoyltransferase I A, CPT1A inhibitor used to inhibit FAO by some researchers). Although the role of FAO in macrophage activation has not yet been determined, FAO enhances the functions of M2 polarized macrophages^[111].

Generally, M2 polarized macrophages use oxidative phosphorylation, FAO in particular, to obtain the

required energy and exert pro-tumor function in various scenarios, including liver cancer^[108,112,113]. Mechanistically, IL-4 induces the expression of peroxisome proliferator-activated receptors (PPAR) and PPAR gamma coactivator 1-beta (PGC-1b), which orchestrate alteration of FAO as well as mitochondrial respiration^[114]. Similar to liver cancer cells in a background of chronic fatty liver disease, FFA accumulation attenuates mitochondrial respiration and increases FFA uptake *via* CD36, resulting in a predominant FAO mode in macrophages^[115,116]. In addition, IL-4 signaling also increases glucose metabolism by the AKT/mTOR pathway^[117-119]. Lactic acid produced by liver cancer cells through glycolysis is another non-negligible issue when considering the metabolic reprogramming of liver cancer-associated macrophages. The polarization of macrophages to an immunosuppressive and pro-tumoral phenotype is mediated by lactic acid *via* a different, as yet unidentified pathway^[119-121] in liver cancer. M2 polarized macrophages also take up insulin growth factor 1 for a self-immunometabolic reprogramming, leading to reduced phagocytosis and lower energy expenditure^[122], which may consequently regulate liver cancer progression.

However, M1 polarized macrophages have enhanced glycolytic metabolism and impaired oxidative phosph-

orylation through the AKT/mTOR/HIF-1 α pathway^[123]. This association is consistent with the fact that many glycolytic enzymes facilitate inflammatory cytokine production. For example, PKM2, which is critical for glycolysis, activates HIF-1 α and induces IL-1 β production^[124]. Although under some conditions, FAO was also found to support inflammasome activation in M1 polarized macrophages by regulating CPT1A activity^[125,126].

Other metabolites in the TME can also influence the phenotype and function of macrophages. Succinate is a known inflammation inducer of macrophages. Succinate enhances IL-1 β secretion *via* succinate receptor 1 (SUCNR1, also known as GPR91)-mediated amplification of TLR signaling^[127]. In addition, intracellular succinate, derived from the γ -aminobutyric acid (GABA) shunt and anaplerosis of α -KG upon stimulation of TLR4, enhances IL-1 β production through the repurposing of mitochondrial function from ATP production to ROS generation^[128,129].

Neutrophils are metabolically similar to M1 polarized macrophages and rely on aerobic glycolysis and the pentose phosphate pathway (PPP) as their principal mode of energy metabolism, by which the formation of neutrophil extracellular traps produces biological effects^[130].

During differentiation, a switch from FAO to glycolysis and glutaminolysis triggers the maturation of T effector cells^[131]. The rapid supply of ATP helps CTLs to meet their increasing bioenergetic and biosynthetic requirements^[132]. Nevertheless, glucose shortage and lactic acid abundance limit the function of CTLs, and the enhancement of FAO preserves the cytotoxicity of CTLs in tumors^[133]. By contrast, Treg cells favor FAO rather than glycolysis, by which these cells survive in the persistent low-glucose and hypoxic tumor microenvironment and suppress the tumor-killing function of CTLs^[131,134]. Moreover, Treg cells rely on oxidative phosphorylation for energy supply, on FAO for cell differentiation, and on glutaminolysis for cell proliferation^[134,135]. Taken together, these observations demonstrate that environment-related metabolism regulates the anti- and pro-tumor functions of tumor-infiltrating lymphocytes.

INFLUENCE OF REPROGRAMMED IMMUNE CELLS ON LIVER CANCER PROGRESSION

Immunometabolic reprogramming has a dual-function in tumor progression. Typically, M1 polarized macrophages facilitate inflammation and the antitumor response *via* elevated glycolysis, while M2 polarized macrophages play an FAO predominant role, secreting IL-10 to suppress the immune reaction. The switch in the metabolism of TAMs leads to an ample signaling transition by which these cells suppress immune reactions (by presenting PD-1, *etc.*), accelerate tumor proliferation (by releasing TNF, Wnt signals, *etc.*), promote angiogenesis (by secreting VEGF,

FGF2, *etc.*), and enhance tumor invasion and metastasis (by MMP9, TGF- β , *etc.*)^[26,136]. We further revealed that IL-1 β facilitated epithelial-to-mesenchymal transition and subsequent metastasis in liver cancer, and this effect was mediated by a group of pro-inflammatory M2-like TAMs with an up-regulated level of glycolysis^[137]. Interestingly, the function of TANs is opposite that of TAMs under different circumstances. For instance, the absence of TGF- β leads to a TANs-induced anti-tumor response by CTLs, whereas this situation is completely different in the presence of TGF- β ^[37].

The influence of metabolic reprogramming on lymphocytes differs in the presence of high functional heterogeneity. CTLs enhance glycolysis, glutaminolysis, and even FAO to exert anti-tumoral cytotoxicity, while CD4⁺ T cells develop into two phenotypes with contrary functions. With a similar switch characterized by up-regulated glycolysis as well as increased glutaminolysis and PPP, Th1 cells induce macrophage- and NK cell-related anti-tumoral responses, whereas Th2 cells induce immunosuppressive reactions^[113].

PERSPECTIVES OF LIVER CANCER THERAPY FROM IMMUNOMETABOLISM

Theoretically, it is feasible to target metabolic enzymes or metabolites in immune cells for therapeutic purposes. Indeed, several cancer-related immunometabolic molecules are suitable as potential targets for drug development (Table 1).

Considering carbohydrate metabolism, glycolysis is important to activated immune cells. Inhibition of HIF-1 α can attenuate TAM/TAN-mediated IL-1 β secretion, reduce hypoxic adaptation of tumor cells, and regulate the differentiation and function of lymphocytes^[137,138]. The regulation of PI3K signaling by PTEN in immune cells may also show some effects on macrophage activation and Treg cell function with a concurrent influence on glycolysis^[139,140].

The mTOR pathway may be a suitable target to regulate immune cells by manipulating cellular lipid metabolism. Inhibition of mTOR by rapamycin can block the development of macrophages and CD4⁺ T cells in several scenarios, including liver cancer^[141,142]. Moreover, FAO plays a predominant role in the metabolism of M2 polarized macrophages. Hence, inhibition of FAO by etomoxir or other methods (*e.g.*, targeted delivery of CPT1A siRNA/shRNA) may limit the immunosuppressive function of M2 macrophages. However, in a resource-deficient microenvironment, CTLs also take up FFA and exert cytotoxicity; thus, the selective increase of FFA import to CTLs enhances the anti-tumoral capacity of these cells^[133]. It is also feasible to target proteins that play central roles in metabolic pathways (*i.e.*, iNOS, PKM2, Foxp3, *etc.*). The difficulty of this strategy is that targeting should be cell specific because the same metabolic pathway can have diverse effects on different

Table 1 Immunometabolic therapies for cancers

Targets	Agents	Mechanisms	Developments
PKM2	DASA, TEPP46	Inhibition of HIF1 α	Preclinical
HIF1 α	PX-478, RO7070179, EZN-2968	Inhibition of HIF1 α	Phase 1
PTEN	VO-Ohpic, SF1670	Inhibition of PI3K	Preclinical
PDK	Dichloroacetate	Inhibition of glycolysis	Phase 2
GLUT1	Ritonavir	Inhibition of glycolysis	FDA-Approved
LDH	Gossypol (AT-101), FX11, Galloflavin	Inhibition of glycolysis	Phase 3
CPT1A	Etomoxir	Inhibition of FAO	Preclinical
CTLA-4	Ipilimumab	Checkpoint blockade; Inhibition of FAO	FDA-Approved
PD-1/PD-L1	Nivolumab, Pembrolizumab, Atezolizumab	Checkpoint blockade; Inhibition of FAO	FDA-Approved
AMPK	Metformin	Increased FAO; Inhibition of Complex I; Decreased mitochondrial ROS	FDA-Approved
mTOR	Temsirolimus, Everolimus	Inhibition of HIF-1 α translation	FDA-Approved
IDO	Epacadostat	Regulation of tryptophan metabolism; Inhibition of mTORC1	FDA-Approved
IDH1/2 mutations	Ivosidenib (AG-120), IDH305, AG-881, DS-1001b	Inhibition of 2-HG production	Phase 3
FGFR	Regorafenib, Sunitinib, TAS120	Inhibition multi-targeted kinase	Phase 2
iNOS	L-NMMA, 1400W	Inhibition of NO production	Phase 2
FOXP3	P60	suppress NF- κ B and NFAT	Preclinical

PKM2: Pyruvate kinase M2; HIF: Hypoxia inducible factor; LDH: Lactate dehydrogenase; FAO: Fatty acid oxidation; CTLA-4: Cytotoxic T-lymphocyte-associated protein 4; mTOR: Mammalian target of rapamycin; FGFR: Fibroblast growth factor receptor; FoxP3: Forkhead box P3; ROS: Reactive oxygen species.

immune cells.

Furthermore, drugs targeting tumor specific metabolic changes can also regulate the function of immune cells by altering the metabolites of the tumor. For instance, IDH1/2 inhibitors specifically reduce 2-HG production leading to destabilization of HIF-1 α in immune cells, which can cause reduction of IL-1 β secretion by macrophages.

CONCLUSION

Immunometabolism has increasingly become a component of immunology in the past decade. The current understanding suggests that a complicated metabolic network regulates the various functions of immune cells. This network can either be functionally oriented or environmentally adapted, but together, these complex interactions lead to immune microenvironment homeostasis, which affects the progression of liver cancer. However, numerous findings indicate that almost all types of immune cells present a self-contradictory function under different conditions, although the mechanisms are still unknown. In the future, more subtypes among immune cells will be defined as single cell detection systems are further developed, which may provide a key for functional heterogeneity. Therefore, liver cancer therapy that targets immunometabolism is a promising approach. Further work is urgently needed to explore the utility of targeting specific immunometabolic events in the liver cancer microenvironment for therapeutic gain.

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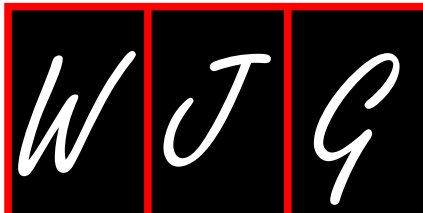
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Osteoporosis in primary biliary cholangitis

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Abstract

Primary biliary cholangitis (PBC) is an autoimmune cholestatic liver disease with multiple debilitating complications. Osteoporosis is a common complication of PBC resulting in frequent fractures and leading to significant morbidity in this population, yet evidence for effective therapy is lacking. We sought to summarize our current understanding of the pathophysiology of osteoporosis in PBC, as well as current and emerging therapies in order to guide future research directions. A complete search with a comprehensive literature review was performed with studies from PubMed, EMBASE, Web of Science, Cochrane database, and the Countway Library. Osteoporosis in PBC is driven primarily by decreased bone formation, which differs from the increased bone resorption seen in postmenopausal osteoporosis. Despite this fundamental difference, current treatment recommendations are based primarily on experience with postmenopausal osteoporosis. Trials specific to PBC-related osteoporosis are small and have not consistently demonstrated a benefit in this population. As it stands, prevention of osteoporosis in PBC relies on the mitigation of risk factors such as smoking and alcohol use, as well as encouraging a healthy diet and weight-bearing exercise. The primary medical intervention for the treatment of osteoporosis in PBC remains bisphosphonates though a benefit in terms of fracture reduction has never been shown. This review outlines what is known regarding the pathogenesis of bone disease in PBC and summarizes current and emerging therapies.

Key words: Biliary cirrhosis; Cholestatic liver disease; Osteopenia; Hepatic osteodystrophy; Bisphosphonates; Hormone replacement therapy

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Core tip: This article reviews the available literature on the pathophysiology and management of osteoporosis in primary biliary cholangitis (PBC). PBC-related osteoporosis is driven mainly by decreased bone formation as opposed to the increased bone resorption seen in postmenopausal osteoporosis. Despite this and a lack of evidence of efficacy, bisphosphonates remain the cornerstone of treatment. Future attention should be given to the use of anabolic bone agents in the treatment of PBC-related osteoporosis.

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INTRODUCTION

Primary biliary cholangitis (PBC) is a chronic, progressive cholestatic liver disease associated with numerous extrahepatic complications. Osteoporosis, a disease of decreased bone density and strength, is a common complication of PBC^[1-3]. The prevalence of osteoporosis in patients with PBC is roughly 30%^[1-3] and higher in advanced stages of liver disease, up to 44% in those awaiting liver transplantation^[4]. Osteoporosis is a major risk factor for fractures^[3,5,6]. The incidence of fractures in PBC ranges from 0-14% over a two-year period^[6-9]. The prevalence of fractures is reported to be 10%-20%^[3,5,6], increasing to 22% in transplant waitlisted patients^[4]. Serious injuries such as fractures are more difficult to manage in patients with advanced liver disease with perioperative morbidity and mortality approaching 80% and 60% respectively in cirrhotics undergoing emergent total hip arthroplasty^[10]. Patients would therefore benefit from a timely diagnosis, effective risk factor modification, and treatment of PBC-related osteoporosis.

While effective treatments exist for postmenopausal osteoporosis, management of osteoporosis in PBC is limited by an incomplete understanding of pathophysiology specific to this disease process and a paucity of studies evaluating potential treatment. The current American Association for the Study of Liver Diseases guidelines recommend vitamin D and calcium supplementation based on experience in postmenopausal women as well as alendronate based on a single RCT in PBC^[11]. An overreliance on postmenopausal osteoporosis data may lead to relatively ineffective treatment of PBC-related osteoporosis. To this end, we aim to summarize our current understanding of the

pathophysiology behind bone disease in PBC as well as the evidence behind current and emerging therapies for osteoporosis in PBC.

The term hepatic osteodystrophy is sometimes used to refer to all metabolic bone disease seen in chronic liver disease. It refers to both osteomalacia, or decreased bone mineralization, and osteoporosis, or decreased bone mass, which can both be seen in advanced liver disease. Osteomalacia was once thought to be common in cholestatic liver disease; theoretically due dietary vitamin D malabsorption in the setting of severe cholestasis and impaired hepatic 25-hydroxylation^[12,13]. However, it appears osteomalacia is actually quite rare in PBC and cholestatic liver disease and early studies were plagued by selection bias and a loose definition of osteomalacia^[14]. It is now widely accepted that osteoporosis is the primary metabolic bone disease in PBC^[15] and this review will focus on the management of osteoporosis in PBC.

Pathogenesis

The pathogenesis of osteoporosis in PBC appears to be largely driven by decreased bone formation, though increased bone resorption may play a role in certain scenarios. Several studies evaluating bone histomorphometry have shown decreased tetracycline double-labeling, decreased bone formation rates, decreased osteoblast numbers, and decreased serum osteocalcin, a marker of bone formation, all pointing towards osteoblast dysfunction and deficient bone formation as central to the pathogenesis of PBC-related osteoporosis^[5,16-18].

Osteoblast dysfunction is a multifactorial process caused both by decreased osteoblast stimulation and increased osteoblast inhibition. Serum levels of insulin-like growth factor-1 (IGF-1), an osteoblast trophic factor, are lower in cirrhotics compared to controls^[19]. Supplementation of IGF-1 in cirrhotic rats results in improvement in bone mass and bone density^[20]. Vitamin K is also involved in bone metabolism through carboxylation of the non-collagenous bone protein, osteocalcin, and has been shown to stimulate osteoblastogenesis and inhibit osteoclastogenesis^[21,22]. Vitamin K levels may be decreased in patients with severe cholestasis and impaired fatty-soluble vitamin absorption resulting in impaired osteoblast function. Indeed a meta-analysis does indicate some reduction in bone loss with vitamin K supplementation, but was not performed exclusively in patients with chronic liver disease^[23].

Elevated levels of bilirubin, bile salts, and altered fibronectin production may also play a role in decreased bone formation through osteoblast inhibition in PBC. In one study, plasma mitogenic activity of osteoblasts was significantly lower in patients with cholestatic liver disease compared to healthy controls^[24]. In addition, removal of bilirubin by plasma photobleaching resulted in improved plasma mitogenic activity^[24]. Similarly, elevated lithocolic acid concentrations have been shown to decrease osteoblast survival through impaired

vitamin D stimulation of osteoblast gene transcription^[25]. Patients with chronic liver disease also exhibit altered hepatic fibronectin production, resulting in increased production of a fibronectin isoform containing the oncofetal domain, which inhibits osteoblast-mediated mineralization in humans and mice^[26].

Increased bone resorption may also play a role in osteoporosis in PBC in certain populations such as postmenopausal women and men with hypogonadism^[5,14,16]. One study showed increased osteoblast numbers and increased eroded surface area indicative of increased resorption, but only in female patients with cholestatic liver disease^[16]. Estrogen promotes apoptosis of osteoclasts and its absence results in a sharp decline in bone mineral density (BMD) after menopause^[27,28]. Men with cholestatic liver disease show no signs of increased bone resorption despite similar degrees of osteopenia^[16].

Theoretically, calcium and vitamin D deficiencies may develop in those with cholestatic liver disease leading to secondary hyperparathyroidism and increased bone resorption. Data is conflicting, however. Some studies have found decreased calcium absorption and serum vitamin D levels in PBC patients compared to controls^[5,29], but others have found normal vitamin D, calcium, and PTH levels even among osteoporotic patients with PBC^[16,17,26]. In addition, vitamin D supplementation to normal levels has not been shown to improve BMD in PBC^[30,31]. While vitamin D absorption may be impaired in those taking cholestyramine, this is overcome by increasing the oral dose of vitamin D^[32].

Diagnosis and monitoring

No data exists as to the optimal timing of screening and monitoring for osteoporosis in PBC, however, expert opinion recommends bone densitometry be performed in all PBC patients at diagnosis^[11]. The World Health Organization defines osteoporosis as BMD at the spine or proximal femur less than 2.5 standard deviations (SDs) below the mean of a young adult population (expressed as a T score)^[33]. Osteopenia refers to those with a T score between -1.0 and -2.5 SDs below the mean. Patients who initially have normal bone densitometry should be reassessed every 2-3 years with repeat bone densitometry, while those with additional risk factors for low bone density and fractures (*i.e.*, severe cholestasis, long-term corticosteroid use, postmenopausal women, BMI < 19, menopause before age 45, alcohol abuse, smoking) should be reassessed annually. Serum calcium, phosphorus, 25-vitamin D, and parathyroid hormone levels should also be checked at diagnosis of PBC and yearly thereafter^[14,34,35]. Patients in whom treatment has been initiated should have repeat BMD measured every 1-2 years^[36].

MANAGEMENT

Prevention

General measures to prevent bone loss in PBC are

extrapolated from osteoporosis risk factors in the general population. Epidemiologic data suggests lifestyle factors such as tobacco and alcohol use, low dietary calcium intake, and low levels of exercise are associated with decreased bone density and fracture risk^[33]. Based on this, tobacco and alcohol cessation are recommended in all PBC patients to reduce risk of bone loss. A balanced diet with adequate levels of calcium and vitamin D should also be encouraged. General recommendations for daily dietary calcium and vitamin D intake in at-risk populations (women older than 50) are 1200 mg and 800 IU daily, respectively^[33].

Evidence for routine weight-bearing exercise comes from menopausal women. In a 16-year prospective study of early-postmenopausal women with mild osteopenia, those who exercised regularly had significant improvement in BMD compared to controls. This finding was sustained and even greater at 16 years compared to 4^[37].

Treatment

Timing of treatment is based on recommendations from the postmenopausal osteoporosis literature^[36]. Treatment should be initiated in all PBC patients with osteoporosis (T score < -2.5). The ideal time to start treatment in those with osteopenia (T score < -1 to -2.5) is less well established. The National Osteoporosis Foundation recommends treatment in individuals with a prior hip or vertebral fracture or 10-year hip fracture risk \geq 3% or osteoporosis-related fracture risk \geq 20% based on the World Health Organization Fracture Risk Assessment Tool in those with osteopenia^[36]. In PBC, patients with a T score < 1.5 appear to be at increased risk of fracture^[3] and initiation of specific treatment could be considered at this point (Figure 1). A number of different therapeutic approaches have been evaluated, however, most are limited by small sample size and short follow-up (Tables 1 and 2). The duration of treatment is unclear even in the postmenopausal population, though the National Osteoporosis Foundation emphasizes that treatment should not be indefinite and generally is continued for anywhere from 2 to 5 years based on individual risk assessment^[36].

THERAPEUTIC OPTIONS

Vitamin D and calcium supplementation

In PBC patients with osteopenia or osteoporosis, vitamin D and calcium supplementation has not been shown to improve BMD or reduce fracture risk, though given few side effects and potential for deficiency, supplementation is generally recommended^[14,34,35]. The only randomized controlled trial (RCT) looking at calcitriol supplementation did not find a significant improvement in BMD from baseline at one year, though BMD did significantly worsen in those who received no treatment^[38]. Most studies use some combination of calcium and vitamin D supplementation as standard of care in both the intervention and control groups, though

Table 1 Summary of results in randomized-controlled trials of active agent vs placebo or no treatment

Agent	Treatment	No. of patients (n)	BMD changes at 1 yr (%)	BMD changes at 2 yr (%)	Fractures (n)
Etidronate	400 mg/d (3 mo cycles)	6 (etidronate)	+1.0 (L), +0.2 (F)	N/A	0
		6 (no treatment) ³	-1.7 (L), +0.4 (F)		0
Lindor <i>et al</i> ^[6] , 2000	400 mg/d (3 mo cycles)	29 (etidronate)	+0.7 (L), +1.3 (F)	+1.0 (L), +0.5 (F)	4 (V)
		31 (placebo)	-0.6 (L), +0.9 (F)	+2.6 (L), +0.8 (F)	4 (V)
Alendronate	70 mg/wk	15 (alendronate)	+10.4 (L) ^{1,2} , +1.4 (F) ¹	N/A	1 (V), 0 (P)
		13 (placebo)	-0.1 (L) ¹ , -2.1 (F) ¹		0 (V), 1 (P)
HRT	50 mcg twice weekly TD	8 (HRT)	+3.1 (L) ² , +1.7 (F) ^{1,2}	N/A	0
		9 (no treatment) ³	+1.0 (L), -0.6 (F) ¹		0
Boone <i>et al</i> ^[9] , 2006	0.05 mg/d TD estradiol + 0.25 mg/d TD progesterin	8 (HRT)	N/A	-0.6 (L), +0.2 (F)	0 (V)
		14 (placebo)		-0.8 (L), -3.7 (F) ²	2 (V)
Sodium fluoride	50 mg/d sodium fluoride	8 (fluoride)	N/A	+2.9 (L) ¹	0
		8 (placebo)		-6.6 (L) ^{1,2}	0
Calcitriol	0.5 mcg/d BID calcitriol	17 (calcitriol)	+0.1 (L) ¹	N/A	N/A
		17 (no treatment) ³	-3.1 (L) ¹		
Vitamin K	45 mg/d vitamin K ₂	15 (vitamin K)	+0.3 (L) ¹	-0.8 (L) ¹	N/A
		15 (no treatment) ³	-3.5 (L) ¹	-6.9 (L) ¹	

¹Statistical significance ($P < 0.05$) between groups; ²Statistical difference ($P < 0.05$) from baseline; ³Patients in no treatment groups received vitamin D and calcium supplementation. L: Lumbar; F: Femoral; V: Vertebral; P: Peripheral; BMD: Bone mineral density.

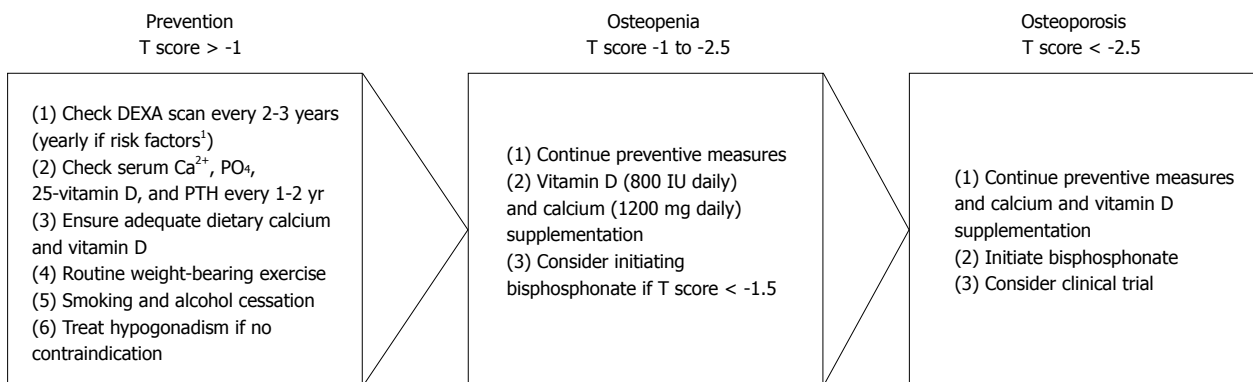


Figure 1 Summary of prevention and treatment strategies for osteoporosis in Primary biliary cholangitis. ¹Prolonged steroid use (> 3 mo), BMI < 19 kg/m², heavy alcohol or tobacco use.

notably, BMD continues to worsen in the control group despite supplementation^[9,39,40].

Bisphosphonates

Bisphosphonates reduce bone resorption and are effective in increasing BMD while reducing fractures in postmenopausal osteoporosis^[41]. Their effectiveness in PBC is not as clear due to the small number of studies with small study size and short follow-up. A 2011 Cochrane review of bisphosphonates in PBC concluded there was insufficient data supporting improved BMD and fracture risk^[42]. It appears etidronate is not effective in improving BMD and preventing fractures in PBC. In two RCTs comparing etidronate to calcium alone or placebo, neither demonstrated an improvement in BMD from baseline with etidronate^[6,43], though one did show significantly less bone loss compared to calcium alone^[43]. Neither showed a difference in fracture risk over 1-2 years of follow-up^[6,43].

Alendronate, a nitrogen-containing bisphosphonate as opposed to etidronate, has had more promising results in PBC. Only one RCT has been performed

comparing alendronate to placebo in PBC^[44]. In this study, 34 patients were randomized to receive oral alendronate or placebo. After 1 year, patients in the alendronate arm experienced a 10.4% increase in lumbar spine BMD compared to -0.12% for placebo^[44]. However, there was no difference in fracture incidence over a year and the study included only one male and two post-menopausal females^[44].

Several studies have also compared bisphosphonates to one another. Alendronate was found to be superior to etidronate in terms of BMD improvement in a small trial of 32 women with PBC and osteopenia in which patients were randomized to receive cyclical etidronate or weekly alendronate^[45]. The alendronate group had significantly higher lumbar BMD (5.8%) at the end of 2 years compared to the etidronate group (1.9%). There was no significant improvement in either lumbar or femoral BMD in the etidronate group from baseline. However, 2 patients in the alendronate group experienced new non-vertebral fractures during the study period compared to 1 in the etidronate group^[45].

Ibandronate was also compared to alendronate in

Table 2 Summary of results in comparative randomized controlled trials of different agents for treatment of osteoporosis in primary biliary cholangitis

Agent	Treatment	No. of patients (n)	BMD changes at 1 yr (%)	BMD changes at 2 yr (%)	Fractures (n)
Guañabens <i>et al</i> ^[39] , 1997					
Etidronate	400 mg/d (3 mo cycles)	13 (etidronate)	-0.1 (L), -0.4 (F)	+0.5 (L) ² , -0.2 (F)	0 (V), 3 (P)
Sodium fluoride	50 mg/d sodium fluoride	10 (fluoride)	-1.7 (L), -0.6 (F)	-2.1 (L), -1.5 (F)	2 (V), 2 (P)
Guañabens <i>et al</i> ^[45] , 2003					
Alendronate	10 mg/d	13 (alendronate)		+5.8 (L) ^{1,2} , +3.9 (F) ^{1,2}	0 (V), 2 (P)
Etidronate	400 mg/d (3 mo cycles)	13 (etidronate)		+1.9 (L) ¹ , +0.4 (F) ¹	0 (V), 1 (P)
Guañabens <i>et al</i> ^[2] , 2005					
Alendronate	10 mg/d	16 (alendronate)	+3.3 (L) ² , +1.2 (F) ²		
Alendronate	70 mg/wk	10 (alendronate)	+1.2 (L), -0.3 (F)		
Guañabens <i>et al</i> ^[46] , 2013					
Ibandronate	150 mg/mo	14 (ibandronate)	+3.8 (L), +1.0 (F)	+5.7 (L) ² , +1.1 (F)	0 (V), 0 (P)
Alendronate	70 mg/wk	19 (alendronate)	+4.6 (L), +1.4 (F)	+4.5 (L) ² , +2.5 (F)	1 (V), 0 (P)

¹Statistical significance ($P < 0.05$) between groups; ²Statistical difference ($P < 0.05$) from baseline. L: Lumbar; F: Femoral; V: Vertebral; P: Peripheral; BMD: Bone mineral density.

a more recent study of 42 post-menopausal women with PBC and osteoporosis^[46]. In this study, women were randomized to receive IV ibandronate monthly or weekly oral alendronate. There was no significant difference in BMD between the 2 groups at the end of 2 years, however, compliance was significantly better in the ibandronate group^[46]. One patient in the alendronate group developed a new vertebral fracture. Another advantage of IV administration is the avoidance of the theoretical concern of esophagitis and variceal bleeding with oral bisphosphonates in cirrhotics. However, none of the studies with alendronate and etidronate noted any esophagitis or variceal bleeds^[6,40,43-46].

Evidence for the use of bisphosphonates in PBC is limited with only one small trial of alendronate showing improvement in BMD compared to placebo, though this occurred almost exclusively in postmenopausal women, and none demonstrating fracture risk reduction^[6,43,44]. Similarly powered trials in postmenopausal osteoporosis have shown improvement benefit in terms of both fracture reduction and BMD improvement^[47], and the PBC-specific benefit of bisphosphonates remains unclear.

Hormone replacement

Estrogens also have strong anti-resorptive effect on bones and for a period of time were widely used in postmenopausal osteoporosis^[48]. Concerns over worsening of cholestasis initially limited their use in PBC. However, several observational studies did not show any significant worsening in liver disease with hormone replacement therapy (HRT)^[49,50] and subsequently two RCTs similarly found no worsening in liver disease^[9,51]. In these RCTs, those randomized to transdermal estrogen and progesterone had femoral and vertebral BMD compared to controls after 1-2 years of treatment^[9,51], though only one showed an improvement in BMD from baseline^[51] and neither showed a reduction in fracture risk^[9,51]. In addition, both studies noted an increase in noncholestatic adverse events, such as vaginal bleeding and headaches, in the HRT arm leading to increased

dropout^[9,51]. Hormone replacement is also associated with increased risk of venous thromboembolism, stroke, ischemic heart disease, and breast cancer and is not recommended in women older than age 60 or greater than 10 years after menopause^[52]. Hormone replacement may be effective in improving BMD in PBC, though no improvement in fracture risk has been shown and side effects limit their use.

Calcitonin

Calcitonin has been shown to have some effect in postmenopausal osteoporosis, however, data in PBC is lacking. A crossover study of IV calcitonin for 6 mo compared to oral calcium supplementation did not find a significant difference between the two and BMD ultimately fell in both groups^[53]. A 3-year study of vitamin D, calcium, and IM calcitonin found significantly less BMD loss in treatment patients compared to controls who received no treatment^[54,55]. However, there was no significant improvement in the calcitonin group and, since the control group received no therapy, the stabilization of BMD may have been from calcium and vitamin D supplementation^[55].

Selective estrogen receptor modulators

Raloxifene is a selective estrogen receptor modulator that maintains the antiresorptive effects of estrogen in bone with anti-estrogen effects in the uterus and breast. A single pilot study has examined the efficacy of raloxifene in PBC. In this study, 9 women with PBC treated with raloxifene were compared to 3 age-matched controls^[56]. After 1 year, there was a small (0.02 g/cm² vs 0.00 g/cm²) but significant improvement in lumbar BMD compared to controls, though there was no difference in femoral BMD and no data on fracture risk^[56].

Sodium fluoride

Sodium fluoride increases bone formation and has been shown to be effective in postmenopausal osteoporosis,

but is not as effective as anti-resorptive agents. One randomized, controlled trial examined sodium fluoride in PBC and found a significant increase in BMD (+2.9%) compared to placebo (-6.6%) in 22 women with PBC followed for 2 years^[7]. No fractures occurred in either group^[7]. A subsequent trial comparing sodium fluoride to etidronate, however, found etidronate to be superior and actually observed a decrease in femoral BMD in the sodium fluoride group after 2 years^[39]. In addition, 2 patients in the sodium fluoride group experienced new vertebral fractures compared to none in the etidronate group^[39].

Vitamin K

Patients with severe cholestasis may have decreased absorption of fat-soluble vitamins, such as vitamin K. Vitamin K is involved in bone formation through stimulation of osteoblastogenesis^[21,22]. One meta-analysis did indicate some reduction in bone loss with vitamin K supplementation, but did not focus on patients with cholestatic liver disease^[23]. One small RCT in PBC found significantly less bone loss in vitamin K patients compared to controls, but was ultimately not effective in improving BMD^[57].

Parathyroid hormone

Human parathyroid hormone (PTH) improves BMD and reduces fractures in postmenopausal osteoporosis through stimulating bone formation, the major driver of osteoporosis in PBC^[58,59]. The recombinant form consisting of the bioactive portion of the hormone (teriparatide) is approved for treatment of postmenopausal osteoporosis, but has not been studied in PBC. Recombinant human PTH 1-34 (rhPTH 1-34) has been studied in rats that have undergone biliary ductal ligation^[60]. In this study, rats that underwent biliary ductal ligation had significant worsening in BMD compared to rats that underwent a sham operation. Biliary ductal ligation rats were then administered rhPTH 1-34 at 40 and 80 µg/kg/d. Those rats who received 40 µg/kg/d experienced significant improvement in femoral and tibial BMD compared to untreated rats and those who received 80 µg/kg/d (who did not experience significant improvement compared to untreated rats)^[60]. No trials have been undertaken in humans with PBC.

PBC-specific therapies

Therapies directed at PBC itself have not been shown to improve bone disease. Patients enrolled in a randomized, controlled trial of ursodeoxycholic acid (UDCA) were followed over a 3-year period with dual-photon densitometry annually. After 3 years, there was no significant difference in lumbar BMD between UDCA and placebo^[61].

In the initial phase 3 trial of obeticholic acid, BMD was measured at baseline and 12 mo^[62]. BMD continued to decline in the obeticholic acid groups (both 5-10 mg and 10 mg groups), however, this decline was significantly less at the femoral neck compared to placebo. BMD

decreased in both groups at the lumbar spine as well and, while there was a trend toward less decline in the obeticholic acid groups, there was no significant difference^[62]. There was no difference in fracture rates^[62].

No data currently exists evaluating the effects of fibrates on BMD when used to treat PBC.

Future therapies

Concerns over long-term efficacy and safety of bisphosphonate use in postmenopausal osteoporosis have led to ongoing development of new medications. Abaloparatide, a parathyroid hormone-related peptide analog, was recently approved by the Food and Drug Administration for treatment of postmenopausal osteoporosis and may avoid the pro-resorptive and hypercalcemic effects of teriparatide^[63]. Along with teriparatide, these recombinant human PTH agents differ in that they promote bone formation, the primary deficit in PBC, as opposed to decrease resorption, the driving issue in postmenopausal osteoporosis and the current target of most treatments. Based on our understanding of the pathogenesis of osteoporosis in PBC, future studies should include therapies that promote bone formation and ample male and premenopausal female PBC patients to decrease the likelihood that results reflect only treatment of postmenopausal osteoporosis.

CONCLUSION

Osteoporosis is a common complication of PBC resulting in a significantly increased risk of fractures especially in those with a T score < -1.5. Severity of bone disease is related to the severity and duration of the underlying liver disease as well as increasing age. The mechanism of decreased bone density primarily involves decreased bone formation resulting from decreased osteoblast function. Increased bone resorption may also play a role in postmenopausal women.

For prevention of osteoporosis, mitigation of risk factors is recommended through smoking and alcohol cessation as well as a balanced diet and regular weight-bearing exercise. Treatment is recommended in patients who have experienced fractures or have osteoporosis (T score < -2.5), though may also be considered in those with a T score < -1.5 in PBC. No treatment has been adequately shown to reduce fractures in PBC, though the bisphosphonates ibandronate and alendronate may be effective in increasing BMD. HRT may also be effective in improving BMD in PBC, though with more side effects. Treatment of the underlying liver disease with UDCA or OCA does not appear to effectively treat the bone disease. Ultimately further research is required, with special attention to anabolic bone agents, to identify effective treatment in PBC-related osteoporosis.

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Ubiquitin-proteasome system and oxidative stress in liver transplantation

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Abstract

A major issue in organ transplantation is the development of a protocol that can preserve organs under optimal conditions. Damage to organs is commonly a consequence of flow deprivation and oxygen starvation following the restoration of blood flow and reoxygenation. This is known as ischemia-reperfusion injury (IRI): a complex multifactorial process that causes cell damage. While the oxygen deprivation due to ischemia depletes cell energy, subsequent tissue oxygenation due to reperfusion induces many cascades, from reactive oxygen species production to apoptosis initiation. Autophagy has also been identified in the pathogenesis of IRI, although such alterations and their subsequent functional significance are controversial. Moreover, proteasome activation may be a relevant pathophysiological mechanism. Different strategies have been adopted to limit IRI damage, including the supplementation of commercial preservation media with pharmacological agents or additives. In this review, we focus on novel strategies related to the ubiquitin proteasome system and oxidative stress inhibition, which have been used to minimize damage in liver transplantation.

Key words: Liver transplant; Ischemia-reperfusion injury; Oxidative stress; Proteasome; Redox regulation; Ubiquitin

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Core tip: Ischemia-reperfusion injury is a complex multifactorial process that causes cell damage during liver transplantation. The role of the ubiquitin proteasome system during liver transplantation remains unclear. The

use of proteasome inhibitors is a new strategy aimed at improving organ preservation.

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INTRODUCTION

The definitive treatment option for many liver diseases is liver transplantation; and in these cases, one important issue is the optimization of organ preservation.

During liver transplantation, damage is initiated by vascular occlusion during hepatic resections. This is aggravated by cold storage of the liver graft (usually at 4 °C) in the preservation solution; and finally by warm reperfusion and subsequent implantation into the recipient. During ischemia, a long period of tissue hypoxia can result in tissue injury and organ dysfunction; as the organ is deprived of oxygen, ATP and energy becomes depleted. Paradoxically, the reintroduction of oxygen during reperfusion aggravates the damage. The whole process has a plethora of consequences that are collectively known as ischemia-reperfusion injury (IRI)^[1-3]. While oxygen deprivation due to ischemia depletes cell energy, subsequent reoxygenation due to reperfusion induces many cascades, from induction of reactive oxygen species (ROS)^[4] to initiation of apoptosis (Figure 1). Such events are, in part, responsible for organ failure. Variables related to the donor (age, steatosis) and surgery (prolonged ischemia times)^[5] are the most commonly reported risk factors for graft dysfunction^[6]. Other factors such as shear stress and small graft size^[7] have been recognized as important factors associated with oxidative stress, lack of primary function, early dysfunction allograft and biliary complications after liver transplantation^[8]. Together with the immunological mechanisms of graft rejection, IRI remains as one of the main clinical problems following organ transplantation.

Current strategies to prevent and modulate IRI include: ischemic pre-^[9-15] or post-conditioning^[16] protocols; static cold storage^[17] or machine perfusion^[18-20] and the use of pharmacological agents^[21-23]. The most common methods applied in liver surgery have recently been reviewed^[5,24]. Conventional hypothermic cold storage continues to be the main method for liver preservation, largely because of its cost-effectiveness, simplicity and logistics. However, hypothermia can have multiple side effects, including the induction of oxidative stress^[25].

Because of the wide range of mechanisms that can contribute to cell damage in IRI (involving ROS, oxidized

products, inflammatory mediators and cytokines), adoption of a specific therapeutic strategy often results in only limited improvements in organ transplantation. Given these circumstances, it is worthwhile to focus on the assessment of agents that can counteract the damage induced by oxidative stress. As oxidative stress is the result of an imbalance between the rate of ROS generation and the capacity to detoxify these reactive species^[26-28], interventions that could result in ROS scavenging or the detoxifying of ROS products could protect against IRI. Three lines of defence against oxidative stress have been reported^[29]. Antioxidant molecules (such as glutathione) represent the first line of antioxidant defence; the second line incorporates enzymatic antioxidants; and the third consists of repair system proteins, including the proteolytic pathways. In this third line, the ubiquitin-proteasome system (UPS) is widely recognized as the main system for degradation of cytosolic proteins^[30,31]

The purpose of this review is to present an update of effects of oxidative stress while summarizing recent findings on the role of the UPS in organ preservation and liver transplantation. In this review we outline the current data of the literature, previous search in databases - PubMed, Web of Science and Scopus - that support the hypothesis on the potential involvement of UPS and oxidative stress in IRI. We will focus on the new strategies used to minimize damage in liver transplantation.

STATIC COLD STORAGE, MACHINE PERFUSION AND STORAGE SOLUTIONS

The strategy most commonly adopted to reduce ischemic injury is the cooling of organs and the use of a preservation solution to minimize enzymatic activity and depletion of the energy substrate. Cold storage slows down cellular metabolism^[32,33], but this can be responsible for further ATP and energy depletion^[34]. In addition, cold has adverse side effects due to the induction of cellular inflammation, alterations of the cytoskeleton^[35], and oxidative stress.

Protective strategies to reduce hepatic IRI include the use of the machine perfusion, which represents a new line of research opposed to static cold storage.

Perfusion machine involves a pulsatile perfusion of the liver with a cold (subnormothermic, hypothermic) perfusate^[18,36-40]; with normothermic perfusate^[41,42]; or with a gradual increase in of the perfusate temperature^[43]. These references confirm that machine perfusion protects against IRI damage in animal models. Livers preserved by subnormothermic machine perfusion at 20 °C showed significantly less liver damage at the end of reperfusion compared to cold storage. The release of LDH was reduced while the production of bile, ATP levels, glycogen and glutathione content increased in preserved livers by subnormothermic machine perfusion

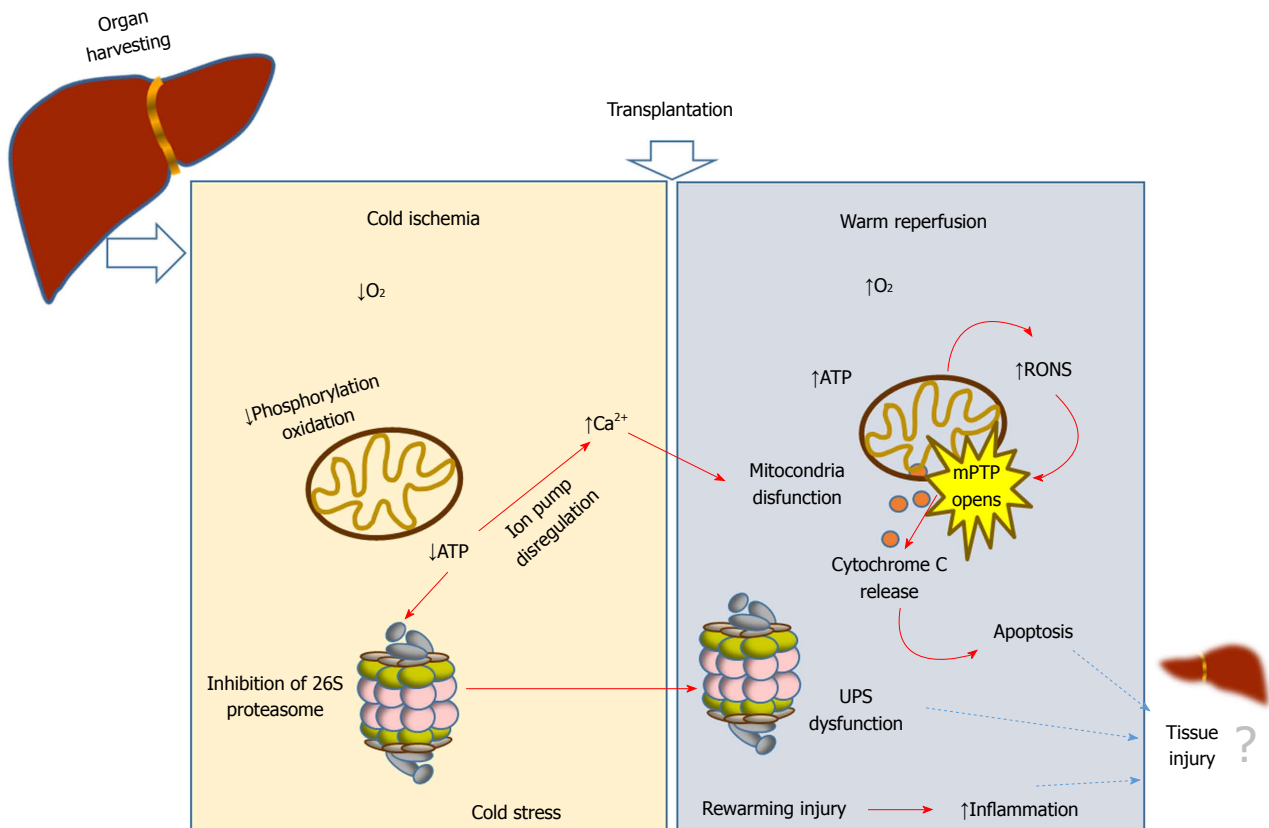


Figure 1 Ischemia-reperfusion injury: A complex multifactorial process that causes cell damage during liver transplantation. While the oxygen deprivation due to ischemia depletes cell energy, subsequent reoxygenation due to reperfusion induces many cascades, from production of reactive oxygen species to initiation of apoptosis. UPS: Ubiquitin-proteasome system; mPTP: mitochondrial permeability transition pore.

than livers submitted to cold storage^[44]. Normothermic machine perfusion has also been assessed in discarded human liver grafts^[45]. The reported data demonstrate the viability of normothermic perfusion, which results in the continuous production of bile, the fall of lactate levels and the preservation of hepatic morphology. However, the safety and efficacy of machine perfusion is yet to be assessed by randomized controlled clinical trials.

Due to its cost-effectiveness and simplicity, cold storage with conventional hypothermia remains the main method for liver conservation. In fact, major advances in the field of organ preservation have included the development of new improved preservation solutions capable of reducing cold-induced cellular damage^[46]. Euro-Collins solution was first developed in the 1970s; while more recently, University of Wisconsin (UW)^[47] Celsior^[48], Histidine-Ketoglutarate (HTK)^[49] and Institute Georges Lopez (IGL-1)^[50] solutions tend to be extensively used for liver transplantation. Commercial preservation solutions include oncotic agents, like hydroxy-ethyl starch (HES) in UW and polyethyleneglycol-35 (PEG-35) in IGL-1, which confer high viscosity to the media. They also contain metabolic precursors (adenosine and ketoglutarate) and antioxidants (glutathione, allopurinol). Although the use of commercial preservation solutions has improved

conditions for liver graft preservation, with the urgent need to expand the donor pool and the subsequent use of suboptimal grafts, new additives have been proposed to combat oxidant and apoptotic damage with the aim of prolonging graft quality during cold storage.

THE ROLE OF OXIDATIVE STRESS IN IRI

ROS are highly reactive and capable of oxidizing lipids, proteins and DNA^[51], thereby leading to structural and cellular changes that may cause oxidative stress and cellular apoptosis. Abundant information has been published demonstrating that increased ROS production is involved in IRI pathology^[28,50,52,53]. The involvement of ROS was initially observed based on the detection of enhanced production of chemical products generated by the reaction of ROS with cellular components. Lipid peroxidation products, such as malondialdehyde and hydroxynonenal^[13,36,54-56] have been widely used as a biomarkers of oxidative stress in IRI. The accelerated ROS production in post-ischemic tissues has been attributed to enzymes capable of reducing molecular oxygen and forming superoxide: xanthine oxidase^[57-59], NADPH oxidase^[60] and nitric oxide synthase^[11]. The contribution of each of these enzymes in IRI is assessed in the excellent review by Granger and Kvietys^[28]. All this indicates that radicals can be formed from different

sources, and consequently several protective strategies to decrease liver IRI have targeted different sources of ROS: xanthine oxidase (using allopurinol^[59,61]) or NADPH oxidase^[62], for example. Other strategies have included pharmacological interventions with antioxidants resulting in the neutralization of ROS effects^[63-66].

As mentioned above, Jung *et al.*^[29] describe three main lines of defence against oxidative stress. Thus, to those molecules widely recognized as antioxidants, such as glutathione, and enzymatic antioxidants, they add a third line of defence: repair system proteins. This system includes the proteolytic pathways, such as the UPS^[30,31]. The activity of the UPS is necessary so that the cells can cope with oxidative stress, but in turn, the activity of the UPS are also modulated by the redox state^[67].

THE UBIQUITIN-PROTEASOME SYSTEM

In order to eliminate damaged proteins, cells have highly regulated mechanisms, such as the autophagy-lysosome pathway and the UPS, which is recognized as the principal system for degrading oxidized cytosolic proteins. Proteasomes are protein complexes that, via proteolysis, degrade unnecessary or damaged proteins. It has always appeared that autophagy within lysosomes is involved in the pathogenesis of hepatic IRI, although the specific alterations it causes and their subsequent functional significance are highly controversial^[68]. The use of proteasome inhibitors has been demonstrated to enhance myocardial viability^[69,70] and protect liver against IRI^[4,71-73], which suggests this may be a promising strategy to reduce the damage inherent to transplantation protocols.

Ubiquitin

Ubiquitin is a highly conserved and small 76-amino-acid protein that acts as a post-translational protein modifier and regulates protein lifespan. Ubiquitin was isolated in the 1970s by Goldstein *et al.*^[74] and since then has been identified in many cellular processes, including proteasomal proteolysis and also DNA damage repair. Ubiquitin can be attached covalently to a target protein in a process known as ubiquitination. Ubiquitin is conjugated to other proteins through a peptide bond between its C-terminal glycine and a primary amine on the substrate, most typically a lysine residue. Conjugation is dependent on the successive activities of enzymes named E1 (ubiquitin activating enzyme), E2 (ubiquitin conjugating enzyme), and E3 (ubiquitin ligase)^[75]. In the 1980s, biochemical studies elucidated the chemical reactions catalysed by these enzymes^[76,77]. E1 activates ubiquitin as a thioester of the active site cysteine residue at expenses of ATP^[78]. The activated ubiquitin molecule is then transferred to an E2 enzyme via the formation of a new thioester with the catalytic cysteine residue of the E2 enzyme. E2 transfers the

activated ubiquitin moieties to the protein substrate that is specifically bound to a unique ubiquitin ligase: E3. Finally, an isopeptide bond is formed between the C-terminal glycine residue of the ubiquitin (Gly76) and the e-NH₂ group of an internal lysine (Lys119) of the protein substrate. Several protein families have been discovered that are evolutionarily related to ubiquitin, as they share the characteristics of the ubiquitin-fold proteins and the capacity to become conjugated to substrates through the action of related E1, E2, and E3 enzymes^[79].

Target proteins can be modified by mono- or poly-ubiquitination. The seven lysines in ubiquitin contribute to the assembly of various poly-ubiquitin chains that may be involved in different cellular processes^[80]. The K48-linked (Lys 48) poly-ubiquitin chain targets proteins for proteasomal degradation, while the K11-linked poly-ubiquitin chain is involved in endoplasmic reticulum-associated degradation^[81] and the K63-linked poly-ubiquitin chain can act in non-proteolytic events, including protein trafficking, DNA repair, and inflammation^[82]. Furthermore, ubiquitination can be reversed by the removal of ubiquitin from target proteins by de-ubiquitinating enzymes (DUBs).

Degradation of damaged proteins

The proteasome is a multicatalytic protease involved in the degradation of intracellular proteins. The processing of damaged proteins is mainly mediated by the 20S and 26S proteasomes^[76,77].

The 20S proteasome is a large complex, formed of four stacked rings: two alpha and two beta rings, each containing seven different subunits (from α 1 to α 7 or from β 1 to β 7). Three of the beta subunits are responsible for the proteolytic activity. β 1 exhibits caspase-like activity, while β 2 exhibits trypsin-like activity, and β 5, chymotrypsin-like activity. Whereas the beta rings are responsible for proteolytic degradation, the alpha rings perform substrate recognition and regulate substrate access to the proteolytic active centre.

The 26S proteasome is formed by the addition of one or two regulatory 19S subunits to an alpha ring in the 20S core proteasome in an ATP-dependent manner. The binding to this regulator increases the proteasomal activity and allows the proteasome to degrade the substrate proteins that have been tagged through the binding of a chain of ubiquitin, as explained above. The ubiquitin chain acts as a labelled sequence to direct proteins to the 26S proteasome where they are degraded. The 19S subunits first remove the poly-ubiquitin "tags" of the targeted proteins and unfold those proteins. Then, the unfolded proteins are degraded by the 20S core of the 26S proteasome. In this way, while the 20S core proteasome can degrade unfolded proteins in an ATP-independent manner, the 26S proteasome is only capable of degrading natively folded and functional proteins in an ATP- and ubiquitin-

dependent manner^[83].

ACTIVATION OF THE PROTEASOME UBIQUITIN SYSTEM (UPS) AND PROTEOLYSIS IN IRI

It has been well established that proteolysis is an important regulatory mechanism that helps maintain homeostasis^[77]. The proteasome and the UPS are necessary for the control of protein concentrations, to prevent abnormal accumulations and to modulate regulatory proteins involved in cell metabolism. However, proteolysis can have detrimental effects on organs and tissues after transplantation^[84]. Free amino acids in the effluent from human livers was used as a marker to predict postoperative graft function. In fact, the prevention of liver graft proteolysis and proteasome activation can be modulated by the use of additives to organ preservation solutions^[85,86]. In this way, it has been demonstrated that lactobionate, a component of UW solution, prevents the release of metalloproteinases during cold preservation^[85]. Moreover, the UPS is an energy-dependent system and ATP levels affects 26S proteasome assembly, stability, and function^[87]. The following processes are dependent on ATP: The first step in ubiquitin conjugation by E1, which is required for the poly-ubiquitination of proteins; the assembly of alpha and beta rings and ATP-dependent proteases; and the degradation of poly-ubiquitinated proteins by the 26S proteasome^[79,87]. In addition, it is well known that oxygen deprivation leads to a significant decrease in ATP in liver grafts^[34], which could affect liver outcomes.

Therefore, during cold storage of organs, and because of the ATP decrease, the formation of 26S proteasomes and poly-ubiquitin-dependent protein degradation are expected to be impaired. However, it has been well established that a subset of 26S proteasomes appears to be activated as ATP levels decline^[70]. In that study, Geng *et al.*^[70] demonstrated that the activation of the 26S proteasome is a pathophysiologically relevant mechanism in cold ischemic myocardial injury. Such observations imply that a subset of 26S is acting as a harmful protease that is activated when the cellular energy supply decreases. The finding that ATP negatively regulates proteasome activity is consistent with previous results concerning increased proteolysis during cold preservation of human liver grafts^[84]. Moreover, hypothermia also affects proteasome activity in isolated perfused rat liver, increasing chymotrypsin-like activity^[36].

Degradation of protein substrates by 26S proteasomes requires the 19S regulatory cap to recognize ubiquitin protein conjugates and to regulate the entry of the substrate into the proteolytic cavity of the 20S core. Covalent regulation via phosphorylation of a subunit in the 19S regulatory cap of the proteasome allows for a fast increase in the 26S proteasome activity, which becomes an important regulatory mechanism for

proteasome control^[88-90]. In fact, we have previously reported that phosphorylation of the 19S subunit Rpt6 increases in cold perfused rat livers^[36].

The combination of proteasome and oxidative stress in IRI

ROS are capable of oxidatively modifying cell structures. Due to the abundance of proteins, the presence of oxidatively modified proteins and aggregates of oxidized proteins has been reported in the cytosol. There is a certain degree of consensus that proteasomal activity degrades oxidized proteins, although the attribution to 20S or 26S is yet to be elucidated. The 26S proteasome was found to be less active in the degradation of oxidatively damaged proteins^[91]. A growing body of evidence suggests that the degradation of oxidatively damaged proteins does not require ATP and polyubiquitination of the substrate^[92]. Alternatively, oxidative proteins are removed independently of ubiquitin by the ATP-independent 20S proteasome^[93].

The proteasome is responsible for the selective degradation of oxidatively damaged proteins. In this sense it has been shown that certain oxidized proteins degrade faster than their native counterparts^[94], and, furthermore, it has been shown that inhibition of the proteasome stabilizes the oxidized proteins^[95]. During oxidative stress, the ratio of oxidized to reduced glutathione increases^[36], and this redox status of the cells can also modulate protein ubiquitination by reversible S-thiolation^[96,67]. This is concurrent with a decrease in the ubiquitin-activating enzyme, E-1 and ubiquitin conjugates. According to some models, glutathiolation of the E1 or E2 components of a ubiquitinated protein protects it from unnecessary degradation. Thus, S-glutathiolation can be regarded as a general mechanism of a redox signal controlling gene expression. In addition, direct oxidative modifications of the proteasome may also occur, including carbonylation, glycoxidation and modification with lipid peroxidation products. Although it is not clear to what extent these modifications affect the proteasome, they could modulate proteasomal activity. It should be noted that an inefficient proteasomal system would result in an accumulation of protein aggregates in the cytoplasm, as has been reported in brain due to aging or Alzheimer's disease^[97], while excessive protein depletion activity may have deleterious effects by affecting detoxifying systems, membranes, or RNA stability^[69,84].

PROTEASOME INHIBITION IN LIVER IRI

The use of proteasome inhibitors has been shown to offer protection and maintain the physiological ubiquitin-protein conjugate pool during cold organ preservation^[98]. Table 1 summarizes the protective effects of different proteasome inhibitors against IRI during organ preservation. The potential pharmacological role of proteasome inhibitors was first reported by Campbell *et al.*^[99]. Those

Table 1 Effect of different proteasome inhibitors on organ preservation

Inhibitor	Organ and condition	Manifestations	Ref.
PS-519	Heart after IRI (rat)	Improved cardiac contractility Improved coronary flow	Campbell <i>et al</i> ^[99]
Epoxomicin	Heart after cold ischemia (rat)	Reduced PMN infiltration Reduced edema formation Preserved ultrastructural integrity	Geng <i>et al</i> ^[70]
MG132	Liver, warm IRI (rat)	Decreased LDH and ALT Increased protein oxidation	Alexandrova <i>et al</i> ^[4]
MG132	Liver, cold IRI (rat)	Decreased antioxidant activities Decreased AST and ALT	Zaouali <i>et al</i> ^[71]
Bortezomid	Liver, cold IRI (rat)	Reduced inflammation (IL1 β and TNF α) Decreased AST, ALT and mitochondrial damage Increased bile production Decreased lipid peroxidation Decreased apoptosis (Cyt C and Caspase 3)	Zaouali <i>et al</i> ^[71] Bejaoui <i>et al</i> ^[72]

IRI: Ischemia-reperfusion injury.

authors demonstrated that proteasome inhibition can prevent loss of cardiac contractile function in isolated perfused rat heart. The adherence of polymorphonuclear leukocytes to the endothelium was also reduced. However, controversy regarding whether inhibiting the proteasome is beneficial or detrimental to cardiac function continues^[95]. Few studies have examined the role of UPS inhibitors as a strategy to reduce damage in liver IRI. In rat liver subjected to warm IRI, the administration of the proteasome inhibitor MG132 decreased LDH and AST levels during ischemia and reperfusion^[4]. In addition, the same authors studied whether MG132 can modulate the prooxidant and antioxidant status of rat liver. The results showed that MG132 did not significantly affect liver lipid peroxidation. However, MG132 increased protein carbonyls and decreased the main antioxidant enzyme activities (catalase and superoxide dismutase).

In contrast to that modulation of oxidative stress, the proteasome inhibitor Bortezomib, used at a non-toxic low dose, up-regulates liver antioxidant enzymes in chronic ethanol-fed rats^[86]. Exposure to the proteasome inhibitor increased antioxidant defences by enhancing the levels of mRNA and protein expression transcripts of glutathione reductase, glutathione synthetase and glutathione peroxidase, as well as superoxide dismutase in rat liver. The increase in antioxidant defences was concomitant with enhanced 26S proteasome activity. As mentioned by those authors, the beneficial effects of the proteasome inhibitor Bortezomib could be due to the low dose used and to the reversibility of the drug.

In accordance with the previous research, we have recently demonstrated that the addition of the reversible UPS inhibitors Bortezomib and MG132 to UW solution improved steatotic and non-steatotic rat liver preservation in the face of cold IRI^[71]. Both inhibitors prevented liver injury, decreasing AST and ALT, and prevented the release of the inflammatory cytokines IL-1 beta and TNF-alpha. The protective effect of Bortezomib was superior to that of MG132. Bortezomib increased bile production, decreased vascular resistance in fatty rat liver through

an increase in nitric oxide generation, prevented lipid peroxidation and mitochondrial damage, and increased AMP-activated protein kinase (AMPK) phosphorylation. It is well known that AMPK phosphorylation is a key process in fatty liver graft preservation, as it can reduce inflammation^[9,44].

The supplementation of IGL-1 preservation solution with Bortezomib has also been shown to have protective effects^[72], reducing steatotic liver injury and decreasing liver apoptosis (cytochrome c and caspase 3 release) in the face of cold IRI. These effects were partially mediated through the activation of the Akt/mTOR signalling pathway, a key regulator in cell growth and proliferation, and through the phosphorylation of AMPK.

Besides its role in preventing inflammation, AMPK activation also keeps the liver in an energy-conserving state during cold storage. AMPK triggers ATP-producing pathways, balancing the metabolic process towards increasing energy homeostasis in the cell. We have recently found a correlation between AMPK activation, ATP levels, lower proteasome activity and decreased damage in fatty liver grafts preserved in different solutions^[73]. As AMPK is regulated and degraded by the UPS, the use of proteasome inhibitors in the preservation solution could avoid AMPK depletion and may contribute to maintaining the beneficial effects of proteasome inhibition after IRI.

CONCLUSION

Remarkable progress has been made over the past few decades regarding the role of the UPS in many cellular processes. However, the function and regulation of the proteasome in organ transplantation still remains unclear. We have proposed that UPS inhibitors reduce IRI in liver grafts *via* up-regulation of AMPK phosphorylation and the consequent preservation of the energy state. As some proteasome inhibitors have been approved for the treatment of different diseases, we propose to explore their use in liver. Well-designed

randomized controlled trials will be needed to evaluate the use of proteasome inhibitors in liver transplantation. The supplementation of low and non-toxic doses of proteasome inhibitors offers a new opportunity for the improvement of organ preservation solutions.

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Basic Study

Stomach wall structure and vessels imaging by acoustic resolution photoacoustic microscopy

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Abstract**AIM**

To image stomach wall blood vessels and tissue, layer-by-layer.

METHODS

We built up the acoustic resolution photoacoustic microscopy (AR-PAM) system for imaging layered tissues, such as the stomach wall. A tunable dye laser system was coupled to a fiber bundle. The fibers of the bundle were placed in nine directions with an incident angle of 45° around a high-frequency ultrasound transducer attached to the acoustic lens. This structure formed a dark field on the tissue surface under the acoustic lens and the nine light beams from the fibers to be combined near the focal point of the acoustic lens. The sample piece was cut from a part of the porcine stomach into a petri dish. In order to realize photoacoustic depth imaging of tumor, we designed a tumor model based on indocyanine green (ICG) dye. The ICG solution (concentration of 129 μM/mL)

was mixed into molten gel, and then a gel mixture of ICG (concentration of 12.9 $\mu\text{M}/\text{mL}$) was injected into the stomach submucosa. The injection quantity was controlled by 0.1 mL to make a small tumor model.

RESULTS

An acoustic resolution photoacoustic microscopy based on fiber illumination was established and an axial resolution of 25 μm and a lateral resolution of 50 μm in its focal zone range of 500 μm has been accomplished. We tuned the laser wavelength to 600 nm. The photoacoustic probe was driven to do B-scan imaging in tissue thickness of 200 μm . The photoacoustic micro-image of mucosa and submucosa of the tissue have been obtained and compared with a pathological photograph of the tissue stained by hematoxylin-eosin staining. We have observed more detailed internal structure of the tissue. We also utilized this photoacoustic microscopy to image blood vessels inside the submucosa. High contrast imaging of the submucosa tumor model was obtained using ICG dye.

CONCLUSION

This AR-PAM is able to image layer-by-layer construction and some blood vessels under mucosa in the stomach wall without any contrast agents.

Key words: Photoacoustic imaging; Stomach; Layered tissue; Acoustic resolution; Fiber

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Core tip: In order to image layered tissue and blood vessels, acoustic resolution photoacoustic microscopy based on fiber illumination was established and an axial resolution of 25 μm and a lateral resolution of 50 μm in its focal zone range of 500 μm was accomplished. Layer-by-layer imaging of the stomach tissue and stomach mucosa blood vessels were obtained. High contrast imaging of the submucosa tumor model was obtained using ICG dye.

Wang C, Lu YF, Cai CM, Xiang HZ, Zheng G. Stomach wall structure and vessels imaging by acoustic resolution photoacoustic microscopy. *World J Gastroenterol* 2018; 24(31): 3531-3537 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v24/i31/3531.htm> DOI: <http://dx.doi.org/10.3748/wjg.v24.i31.3531>

INTRODUCTION

Stomach submucosal tumors (SMT) are any intramural growth underneath the mucosa of the gastrointestinal tract^[1]. These tumors are very hard to find because they are usually asymptomatic and therefore most often discovered as accidental findings during surgery, autopsy, and so on. When examining submucosal

tumors, standard optical stomach endoscopy, capsule optical endoscopy and push-and-pull enteroscopy together with barium contrast X-ray do not alone provide sufficient information. Endoscopic ultrasound (EUS), computed tomography (CT) and magnetic resonance imaging (MRI) are recommended as supplementary tools^[2] because CT and MRI often lack either sufficient spatial resolution or satisfactory contrast (or both) to be effective for early-stage tumor imaging^[3]. Optimal EUS imaging of an SMT needs submersion of the tumor under water. However, benign SMTs, for example the submucosal inflammation, cannot be distinguished endosonographically^[4]. Therefore, early-phase tumor detection or in situ characterization of diseased tissue is challenging for EUS. Because the mechanism of EUS imaging is ultrasound imaging, this is based on tissue bulk mechanical properties. Tumor tissue boundaries and blood vessel structures are clinically relevant and provide necessary information for assessing disease stage and planning treatment therapies.

Recently, optical endoscopic imaging modalities, like narrow band imaging endoscopy^[5], endoscopic optical coherent tomography^[6] and confocal laser endomicroscopy^[7] have been developed. They can detect tissue or tissue changes with high sensitivity and high spatial resolution. Because of the strong optical scattering properties of tissue, these techniques are unable to image targets beyond a 1-2 mm depth. Photoacoustic imaging has a lot of advantages, such as, endogenous optical chromophore contrast enables label-free imaging of the microvasculature with a high resolution^[8], and *in vivo* blood vessel photoacoustic imaging can cover the length scale from a superficial capillary^[9] to an abdominal aorta^[10], demonstrating the potential of photoacoustic imaging to bridge the resolution and penetration gaps between microvascular microscopy, clinical angiography and so on^[11,12]. This paper's aim is to demonstrate that photoacoustic imaging is able to image the layered tissue and blood vessels under the surface of the tissue. In the future, we can design and develop an photoacoustic endoscopic imaging system to image deeper tissue with higher resolution for diagnosis and treatment.

MATERIALS AND METHODS

AR-PAM system

The acoustic resolution photoacoustic microscopy (AR-PAM) system for stomach wall imaging was shown in Figure 1A. A tunable dye laser system pumped by a Q-switch Nd:YAG laser (ND6000, continuum) was used to provide laser pulse with a pulse repetition of 10 Hz and a pulse width of 5.5 ns. The tunable range of the laser light was 415 nm to 940 nm. A pair of concave and convex lenses expanded and collimated the light beam to approximately 5 mm in diameter. Then coupling to a fiber bundle that was composed by nine optical fibers (FT400UMT, Thorlabs) which have a 400 μm core

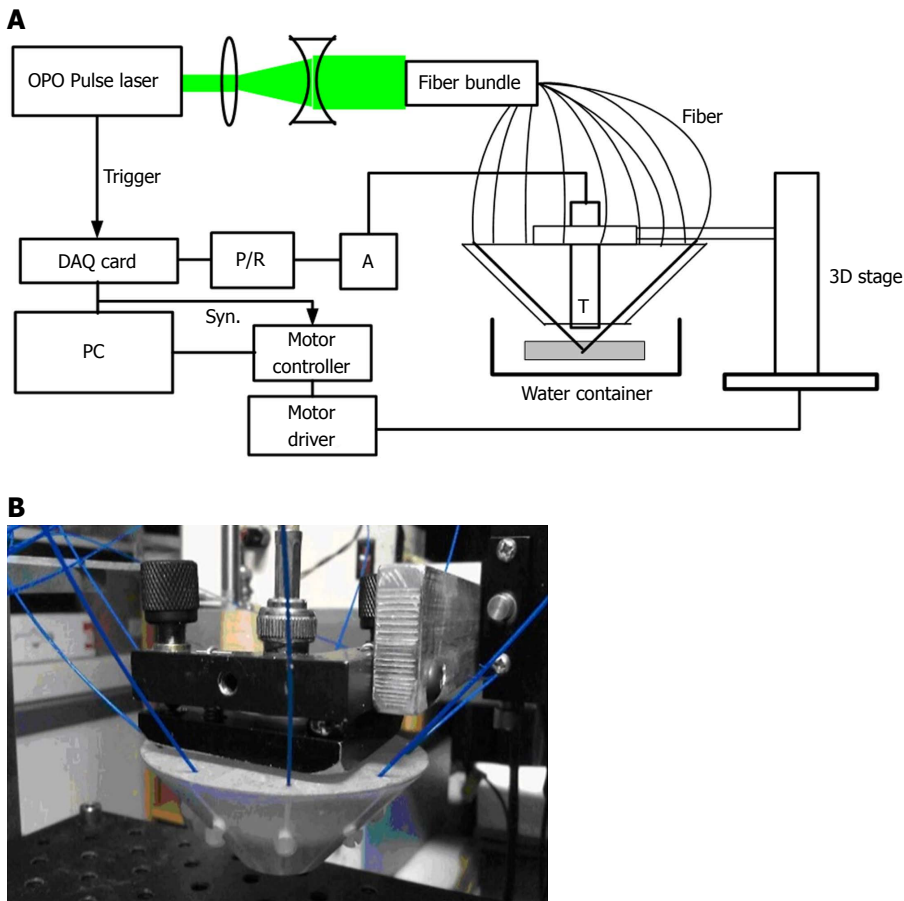


Figure 1 Schematic of the acoustic resolution photoacoustic microscopy system (A) and photograph of the photoacoustic probe (B). P/R: Pulser/receiver; A: Preamplifier; T: Transducer, PC: Personal computer.

diameter and numerical aperture of 0.39 were placed in nine directions (40° intervals in 360°) around a high-frequency (50-MHz, bandwidth of 30 MHz) ultrasound transducer attached with the acoustic lens (the $f/\#$ is 1.3 and focal length is 4 mm). The cross angle between the fibers with the transducer axis direction were set to 45° , so that it formed a dark field on the tissue surface under the acoustic lens and the nine light beams from the fibers were combined near the focal point of the acoustic lens, *i.e.* it is then weakly focused into the tissue with the focal region coaxially overlapping the ultrasonic focus inside the tissue. In an optically transparent medium, the optical focus is about 2 mm in diameter, which is much wider than the ultrasonic focus. The focal acoustic transducer and output end of the fibers were fastened with a holder made by a 3D printer. We can refer to it as a photoacoustic probe (Figure 1B). According to the parameters of the ultrasonic transducer, an axial resolution of $25\ \mu\text{m}$ and a lateral resolution of $50\ \mu\text{m}$ in its focal zone range of $500\ \mu\text{m}$ can be accomplished. The photoacoustic probe is translated in a water bath. A window at the bottom of the water container is sealed with an optically and ultrasonically transparent disposable polyethylene membrane (thickness: 0.04 mm). After commercial ultrasound gel is applied to the region of interest on the sample for acoustic coupling, the sample is placed between the sample supporter and

the water container for imaging. The photoacoustic wave is recorded at each location of the ultrasonic transducer and subsequently converted into a one-dimensional (1D) depth-resolved image (A-scan) based on the sound velocity in soft tissue ($1.54\ \text{mm}/\text{us}$). Images were generated by one dimension (B-Scan) in the X or Y direction or two-dimensional (C-Scan) raster scanning of the photoacoustic probe in the X-Y plane with a step size of $30\ \mu\text{m}$. In addition to, we can also scan in the Z direction with a step of $200\ \mu\text{m}$ for producing an image of the deeper tissue by utilizing deeply penetrable diffused light to excite photoacoustic signals. At each scanning position, signals were recorded by an 8 bits digitizer card (DP1400, Agilent Tech, United States) after it was amplified by a preamplifier (AU-2A-0150-BNC, MTEQ, United States) and then amplified and filtered (high pass 1 MHz) by a pulser/receiver (5073PR, Olympus, Japan). No signal averaging is performed. As shown in Figure 2, photoacoustic imaging of a hair with a diameter of $80\ \mu\text{m}$ were obtained with this photoacoustic system for verifying the imaging ability. Figure 2A was a B-scan image and Figure 2B was a C-scan image of the hair.

Preparing a porcine stomach wall sample

A porcine stomach was received the day after the animal was sacrificed for an unrelated study. The sample piece was cut from a part of the porcine stomach into a petri

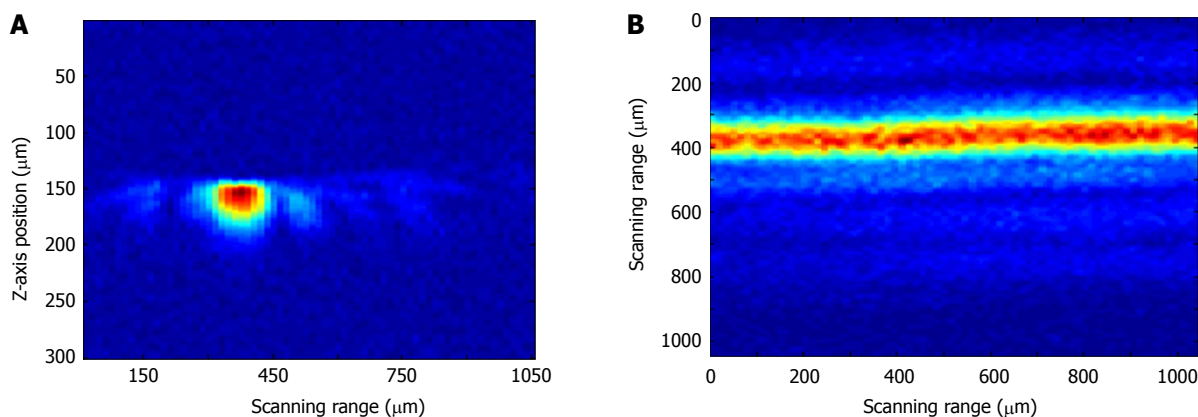


Figure 2 Photoacoustic image of a hair with a diameter of 80 μm . A: B-scan imaging. B: C-scan imaging.

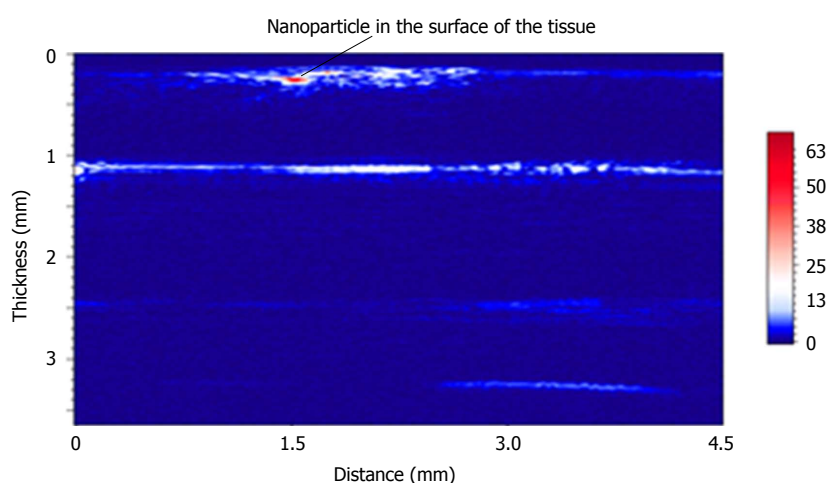


Figure 3 Imaging of layer-by-layer structure of stomach wall.

dish with a diameter of 140 mm and a thickness of 22 mm. In order to obtain a photoacoustic depth image of the tumor, we designed a tumor model based on indocyanine green (ICG) dye, wherein the ICG solution at a concentration of 129 $\mu\text{M}/\text{mL}$ was mixed into molten gel, and then the gel mixture of ICG at a concentration of 12.9 $\mu\text{M}/\text{mL}$ was injected into the stomach submucosa at a 2–3 mm position. The injection quantity was controlled to 0.1 mL to make a small tumor model.

RESULTS

In order to verify photoacoustic imaging can also be used to implement stratified imaging of the stomach wall, we tuned the laser wavelength to 600 nm. The photoacoustic probe obtained many B-scan images at tissue thickness direction with a lateral scanning step of 200 μm . Then, all of the B-scan images were combined to complete an image of the layered structure of the stomach wall (Figure 3). A particle with the diameter of 300 μm was placed on the surface of stomach tissue, in order to indicate the surface position of the tissue. As shown in Figure 4, the photoacoustic microimage of the mucosa and submucosa of the tissue have been obtained

and compared with a pathological photograph of the tissue stained by hematoxylin-eosin staining. We have observed more detailed internal structure of the tissue by the photoacoustic imaging.

In addition, we also utilized this photoacoustic microscopy to image blood vessels inside the submucosa. The dissected stomach wall after imaging by photoacoustic microscopy is shown in Figure 5A. The vessels under submucosa after imaging by photoacoustic microscopy is shown in Figure 5B. We very clearly saw the artery vessels and vein vessels.

In order to realize the photoacoustic depth imaging of the tumor, we designed a labeled tumor model based on ICG dye, wherein 0.1 mL ICG gelatin solution with a concentration of 129 $\mu\text{M}/\text{mL}$ was injected into the stomach submucosa at 2–3 mm deep. After the ICG-gel mixture was injected into the tissue and coagulated for 20 minutes, the C-scan imaging at different depths was completed. When doing the scanning, the output wavelength of the laser was tuned to 700 nm because is the absorption peak of the ICG dye with molar extinction coefficient of $1.1 \times 10^5 \text{ cm}^{-1}/\text{M}$ in water. This will improve the signal: noise ratio of the image.

Some diffusion phenomena of the ICG resolution

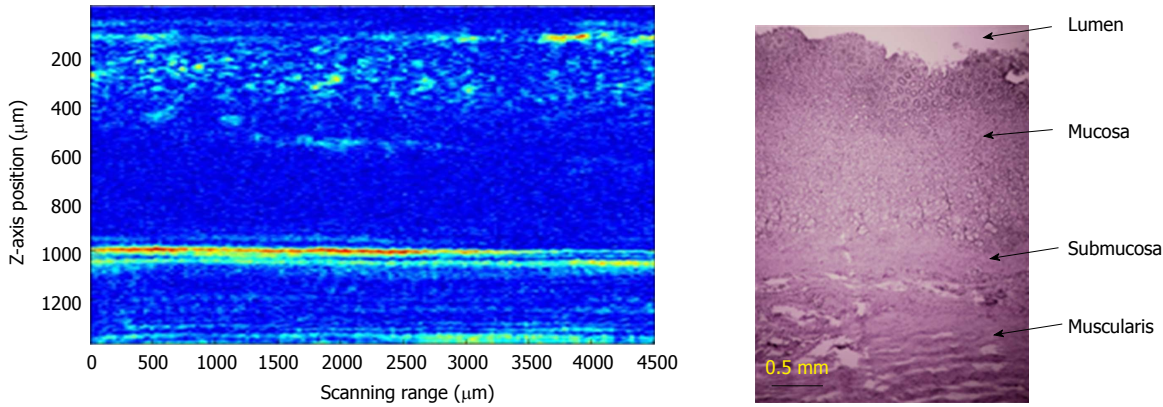


Figure 4 Compared photoacoustic image with pathological photograph stained by hematoxylin-eosin staining for mucosa and submucosa of the tissue.

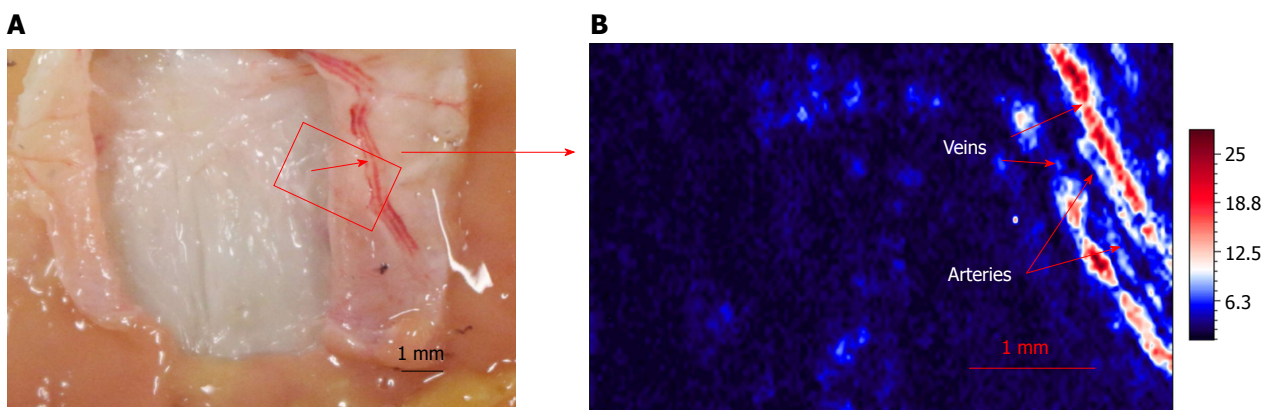


Figure 5 Photograph of the dissected stomach wall after imaging by photoacoustic microscopy (A) and photoacoustic imaging under surface of the tissue of 500 μm (red arrow indicate vessels) (B).

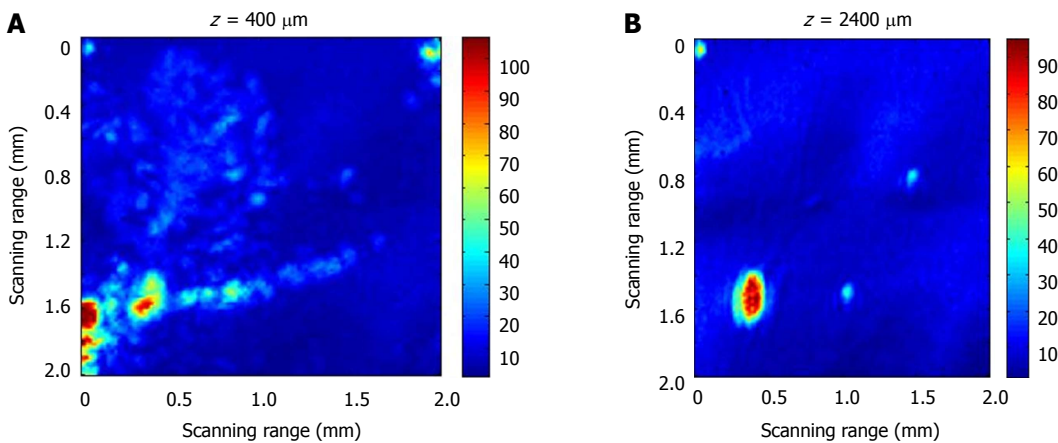


Figure 6 Photoacoustic imaging with laser wavelength of 700 nm for contrast agent with concentration of 12.9 $\mu\text{M}/\text{mL}$ in depth of 400 μm (A) and 2400 μm (B).

at the mucosal site of 400 μm was observed (Figure 6A). The ICG dye may have combined with blood in the vessels, so some tubular structures were observed. At a depth of 2400 μm , the ICG labeled tumor model was still visible (Figure 6B). This indicated that we can achieve deeper detection.

DISCUSSION

Ultrasound uses high-frequency sound waves to produce

images of the organs and structures inside the body such as ovaries, uterus, liver, gallbladder, pancreas, or aorta. EUS combines endoscopy and ultrasound in order to obtain images and information about the digestive tract and the surrounding tissue and organs. EUS can obtain information about the layers of the intestinal wall as well as adjacent areas such as lymph nodes and the blood vessels. EUS provides doctors with more information than other imaging tests by providing detailed images of the digestive tract. Although contrast-enhanced

ultrasonic techniques^[13,14] such as Doppler ultrasound^[15] are able to image blood vessels, the resolution of these imaging techniques are much lower than that of PAM, which has recently achieved lateral resolution up to 15 mm^[16]. Additionally, photoacoustic imaging provides functional information with endogenous contrast and with the aid of an exogenous contrast agent. Therefore, photoacoustic endoscopy based on photoacoustic tomography and EUS, which has achieved spatially coincident photoacoustic and ultrasonic imaging, provides unprecedented information and promotes morphologic and functional understanding of the gastrointestinal tract imaging^[17]. But the research on tissue structure based on photoacoustic imaging technique has not been published yet. This paper reported that utilizing AR-PAM to image layered tissue in the stomach wall and blood vessels under the mucosa in s without any contrasting agents. In the next step, this acoustic resolution photoacoustic microscopy will combine with endoscopy and minimize the photoacoustic probe to make a micro-photoacoustic endoscopy for obtaining morphologic and functional information with higher resolution and depth *in vivo*.

In conclusion, we have presented a fiber illumination based acoustic resolution photoacoustic microscopy method. We have realized an axial resolution of 25 μm and a lateral resolution of 50 μm in its focal zone range of 500 μm . This system was utilized to image layered stomach wall tissue and blood vessels under the mucosa without any contrasting agents. Using ICG dye enhance a tumor model, the tumor model was imaged to depths of 2400 μm with very high contrast. The photoacoustic microscopy has the ability to image layered tissue with high resolution and high contrast.

ARTICLE HIGHLIGHTS

Research background

When checking submucosal tumors, traditional methods (such as standard optical stomach endoscopy, capsule optical endoscopy and push-and-pull enteroscopy together with barium contrast X-ray) can't provide accurate information. Computed tomography and magnetic resonance imaging are often lower in resolution and contrast. Optimal endoscopic ultrasound (EUS) imaging of stomach submucosal tumors (SMT) needs submersion of the tumor under water. However, benign SMTs, for example the submucosal inflammation, cannot be distinguished endosonographically. Therefore, it is still a challenge for EUS to detect early-phase tumor *in situ*. Our team aimed to demonstrate that photoacoustic imaging is able to image layered tissue and blood vessels under the surface of the tissue. In the future, we can design and develop a photoacoustic endoscopic imaging system to image deeper tissues with higher resolution for diagnosis and treatment.

Research motivation

To image layered tissue and blood vessels in layered tissue.

Research objectives

Our aim is to demonstrate that photoacoustic imaging can detect the structure of layered tissue and blood vessels beneath the surface of the tissue.

Research methods

Our team established the acoustic resolution photoacoustic microscopy (AR-PAM) system for stomach wall structure imaging. Photoacoustic microimaging

of the stomach wall structure was compared to an HE pathology image to verify the structure, vessels, and vessel direction.

Research results

As a result, we have established a fiber illumination based acoustic resolution photoacoustic microscopy method. The imaging ability has an axial resolution of 25 μm and a lateral resolution of 50 μm in its focal zone range of 500 μm . We have observed more detailed internal structure of the tissue from AR-PAM imaging. We also utilized this photoacoustic microscopy to image blood vessels inside the submucosa. By using ICG dye enhance a tumor model in the submucosa, the images obtained at a depth of 2400 μm depth had very high contrast.

Research conclusions

In this study, we have established a fiber illumination based acoustic resolution photoacoustic microscopy. Layer-by-layer imaging of the stomach tissue and blood vessels under stomach mucosa were obtained. By using ICG dye to enhance the tumor model, high contrast images at a depth of 2400 μm tissue were obtained. This proved that photoacoustic microscopy has the ability to image layered tissue and deep tissue targets with high resolution and high contrast. In the near future, this technique combined with endoscopy will supply a simple tool for physicians to see differences in layered tissues and imaging of tumor angiogenesis in submucosa.

Research perspectives

This technique combined with endoscopy will supply a simple tool to visualize layered tissues and tumor angiogenesis in submucosa. Scientific research should aim at solving practical problems in clinical practice. Innovative scientific research is demonstrated in the ability to effectively solve the difficult problems doctors encounter in clinical practice.

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E- Editor: Huang Y



Basic Study

Clinical correlation of B7-H3 and B3GALT4 with the prognosis of colorectal cancer

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Author contributions: Zhang T, Ge XS, Qi XW, Mao Y and Hua D designed the research; Zhang T, Wu JY, Qiu ZC, Wang Y and Liu F performed the research; Zhang T and Wang F analyzed the data; Zhang T, Wang F and Wu JY wrote the paper; Ge XS, Qi XW, Mao Y and Hua D revised the paper.

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Conflict-of-interest statement: To the best of our knowledge, no conflict of interest exists.

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Abstract**AIM**

To investigate the expression and clinical significance of B7 homolog 3 (B7-H3) and β -1,3-galactosyltransferase-4 (B3GALT4) in colorectal cancer (CRC) patients.

METHODS

Using tissue microarray, we identified the expression of B7-H3 and B3GALT4 in 223 CRC patient samples by immunohistochemistry and evaluated the possible correlation between B7-H3 and B3GALT4 and clinical

outcomes. Further, the mRNA and protein expression were identified to establish the regulatory relationship of B7-H3 with B3GALT4 *in vitro*.

RESULTS

A significant positive correlation between B7-H3 and B3GALT4 was observed in CRC specimens ($r = 0.219$, $P = 0.001$). High expression of B7-H3 was identified as a significant independent predictor of poor overall survival (OS) [hazard ratio (HR) = 1.781; 95%CI: 1.027-3.089; $P = 0.040$]. Moreover, high expression of B3GALT4 was also recognized as an independent predictor of inferior OS (HR = 1.597; 95%CI: 1.007-2.533; $P = 0.047$). Additionally, CRC patients expressing both high B7-H3 and high B3GALT4 contributed to a significant decrease in OS (HR = 2.283; 95%CI: 1.289-4.042; $P = 0.005$). In CRC cell lines with stable expression of high B7-H3, the mRNA and protein expressions of B3GALT4 were significantly upregulated. Similarly, the expression of B3GALT4 was significantly reduced when expression of B7-H3 was knocked down.

CONCLUSION

The expression of B3GALT4 in CRC is positively correlated with B7-H3 expression *in vitro*. B7-H3/B3GALT4 may be used as dual prognostic biomarkers for CRC.

Key words: B7 homolog 3; β -1,3-galactosyltransferase-4; Colorectal cancer; Prognosis; Correlation

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Core tip: The present study for the first time revealed the expression of β -1,3-galactosyltransferase-4 (B3GALT4) in colorectal cancer (CRC) and its correlation with B7 homolog 3 (B7-H3) *in vitro*. Overall, the findings of the present study suggest that B7-H3 and B3GALT4 are novel prognostic biomarkers for CRC and highlight the significance of both B7-H3 and B3GALT4 as promising therapeutic targets for CRC. Thus, here we present our preliminary work on the relationship of the immune function and glycosylation of tumor-associated protein in CRC.

Zhang T, Wang F, Wu JY, Qiu ZC, Wang Y, Liu F, Ge XS, Qi XW, Mao Y, Hua D. Clinical correlation of B7-H3 and B3GALT4 with the prognosis of colorectal cancer. *World J Gastroenterol* 2018; 24(31): 3538-3546 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v24/i31/3538.htm> DOI: <http://dx.doi.org/10.3748/wjg.v24.i31.3538>

INTRODUCTION

Colorectal cancer (CRC) is the most prevalent gastrointestinal tract malignancy worldwide among both men and women. Overall CRC incidence and mortality rates

have been declining over the recent decades, yet CRC ranks third overall among other malignancies in men and women^[1]. In China, there were approximately 376300 new cases and 191000 potential deaths for CRC in 2015^[2]. Despite several therapeutic advancements including surgical resection, neoadjuvant chemoradiotherapy, and targeted therapy, the prognosis of CRC patients remains relatively poor. With unprecedented survival benefits in selected patients, immunotherapy has become a promising treatment strategy and continuous progress has been made with immunomodulatory agents that target immune system checkpoints such as anti-programmed death 1 (PD-1) and cytotoxic T-lymphocyte antigen 4 (CTLA-4)^[3].

B7 homolog 3 (B7-H3), also known as CD276, is a type I transmembrane glycoprotein that belongs to the B7/CD28 immunoglobulin superfamily. B7-H3 mRNA is widely expressed on many tissues and cell types. However, B7-H3 protein is not constitutively expressed on T-cells, natural killer cells and antigen-presenting cells, and its expression can be induced on immune cells. While limited expression has been noticed on normal tissues, overexpression is observed in a majority of human malignancies including CRC^[4] and has been correlated with the poor prognosis of patients^[5]. Moreover, B7-H3 has been suggested to promote tumor growth, migration, invasion, and metastasis. Thus, it may be a potential therapeutic target for active immunotherapy.

The β -1,3-galactosyltransferase-4 (B3GALT4) gene belongs to the β -1,3-galactosyltransferase (β 3GalT) gene family, which encodes type II membrane-bound glycoproteins and is located in the centromeric segment of the human MHC class II region^[6]. This gene is abundantly expressed in human organs and tissues, predominantly in the brain and involved in GM1/GD1 ganglioside synthesis^[7]. The β 3GalT family plays an essential role in the O-glycosylation process. The surface of cancer cells express glycoproteins, which are rich in O-glycosylation domains^[8]. Thus, the family may be closely related to the tumor. Besides, Seko *et al.*^[9] had confirmed that B3GALT4 could be used as a novel biomarker for the diagnosis of gynecological cancers. However, there are insufficient reports about the correlation between B3GALT4 and CRC.

Therefore, the present study aimed to investigate the clinical correlation of B7-H3 and B3GALT4 with CRC. Further, correlation between the expression of B7-H3 and B3GALT4 was evaluated to determine their prognostic significance in CRC.

MATERIALS AND METHODS

Patients and tissue samples

The medical records of patients who received a histopathological diagnosis and underwent surgery for CRC at Affiliated Hospital of Jiangnan University between June 2008 and December 2011 were retrieved. A total

of 223 formalin-fixed paraffin-embedded CRC tissue samples were included in the study. These patients did not receive radiotherapy or chemotherapy before the surgery. Only histologically confirmed cases were included in the study. However, patients who received chemo- or radiotherapy before surgery and cases with incomplete clinical data were excluded from the study. The study was approved by the Medical Ethics Committee of Affiliated Hospital of Jiangnan University, and written informed consent was obtained from all patients. All the patients were followed up by telephone up to October 31, 2017, to obtain the survival data. The median follow-up was 79 mo (range, 6-114 mo).

Tissue microarray preparation

Two experienced pathologists examined the section stained with hematoxylin and eosin and marked the carcinoma sites in the corresponding paraffin block. Using a manual tissue microarrayer (Quick-Ray, UNITMA, Seoul, Korea), tissue cylinders with a 1.0 mm diameter were punched from representative tissue areas of each donor tissue block and implanted into the hole of the premade recipient paraffin block (UNITMA, Seoul, Korea). The tissue microarray paraffin block was then constructed and cut into 4 μm thick continuous sections, which were attached to anti-dewaxing slides and stored at room temperature.

Immunohistochemistry

The tissue paraffin blocks were serially sectioned into a 4 μm thickness, dewaxed in xylene, and hydrated in an ethanol gradient. Antigen retrieval was performed by heating the tissue sections at 100 $^{\circ}\text{C}$ for 30 min in citrate buffer. Moreover, endogenous peroxidase activity was blocked by incubation in 3% hydrogen peroxide for 10 min. Subsequently, the sections were incubated in 5% bovine serum albumin at room temperature for 30 min. Primary antibodies, mouse anti-human B7-H3 monoclonal antibody (1:200, Santa Cruz, Dallas, TX, United States) and rabbit anti-human B3GALT4 monoclonal antibody (1:50, Abcam, Cambridge, MA, United States) respectively were added drop-wise followed by overnight incubation at 4 $^{\circ}\text{C}$. The slides were washed and incubated with a horseradish peroxidase-conjugated secondary antibody for 30 min. The immunostaining was carried out by staining with 3,3'-diaminobenzidine tetrahydrochloride solution (GTVisionII Immunohistochemistry Detection Kit for Rabbit/Mouse, Gene Tech, Shanghai, China), counter-stained with hematoxylin, dehydrated, and mounted. Sections were examined under a microscope.

Evaluation of immunohistochemistry staining

Two independent pathologists performed a blinded manner review of the sections. Both the intensity and extent of immunological staining were analyzed semi-quantitatively. According to the percentage of positively stained cells, the sections were graded by five levels: 0 ($\leq 5\%$), 1 (6%-25%), 2 (26%-50%), 3 (51%-75%) and 4 ($> 76\%$). The staining intensity was scored

similarly, with 0 used for negative staining, 1 for weakly positive, 2 for moderately positive and 3 for strongly positive. The scores for the percentage of positive cells and the staining intensity were multiplied to generate an immune-reactive score for each specimen (0-12). Based on the total score, scores of 0-3 were considered as the low expression group, and scores of 4-12 were defined as the high expression group.

Cell lines and culture

The two human CRC cell lines, SW480 and Caco-2, which exhibited different expression levels of B7-H3 were maintained in our lab. We constructed SW480 cells that expressed a high level of B7-H3 (SW480-B7-H3) by transfection with an overexpression plasmid, and Caco-2 cells were stably transfected with a B7-H3 shRNA (Caco-2-shB7-H3). Cells transfected with a mock vector were used as negative controls (SW480-NC and Caco-2-shNC). SW480-NC and SW480-B7-H3 were cultured in L-15 medium (HyClone GE Healthcare Life Sciences, South Logan, UT, United States). Caco-2-NC and Caco-2-shB7-H3 were maintained in RPMI-1640 medium (the same as above). All the media were supplemented with 10% fetal bovine serum (Clark Bioscience, Houston, TX, United States). The cells were incubated at 37 $^{\circ}\text{C}$ in a humidified atmosphere with 5% CO_2 .

RNA extraction and cDNA synthesis

Total RNA was extracted from 1×10^6 cells using TRIzol (Invitrogen, Carlsbad, CA, United States), according to the manufacturer's protocol. A NanoDrop 2000 Spectrophotometer (Thermo Scientific, Waltham, MA, United States) was used to estimate the purity and concentration of total RNA by measuring the optical density. The first strand cDNA was generated from 1 μg RNA using the HiScript II 1st Strand cDNA Synthesis Kit (Vazyme, Nanjing, China) following the manufacturer's instructions.

Real-time quantitative polymerase chain reaction

The expression levels of B7-H3 and B3GALT4 were detected using the QuantiNovaTM SYBR Green PCR Kit (QIAGEN, Hilden, Germany) on ViiATM 7 Real-Time PCR System (Applied Biosystems, Foster City, CA, United States). β -actin was used as an internal control for normalization of the expression data. The first strand cDNA was amplified in a total 20 μL PCR reaction mixture: 10 μL 2 x QuantiNova SYBR Green PCR Master Mix, 0.1 μL QN ROX Reference Dye, 0.4 μL of each specific primer set, 2 μL cDNA and ddH₂O added to 20 μL . The sequences of primers were as follows: β -actin 5'-CATGTACGTTGCTATCCAGGC-3' (sense), 5'-CTCCTTAATGTCACGCACGAT-3' (antisense); B7-H3 5'-AGCACTGTGGTTCTGCCTCACA-3' (sense), 5'-CACCAGCTGTTTGGTATCTGTGTCAG-3' (antisense); B3GALT4 5'-ACTCCTACCGCAACCTCA-3' (sense), 5'-CACATCATCGTCCGTCTT-3' (antisense). Each sample and internal control gene were run in triplicate, using an amplification condition of denaturation at 95 $^{\circ}\text{C}$ for

2 min, followed by 40 cycles of 95 °C for 5 s and 60 °C for 10 s. The $2^{-\Delta\Delta Ct}$ method was used to calculate the relative expression level of the target genes.

Western blotting

Total proteins were extracted from 1×10^6 cells by using ice-cold RIPA lysis buffer containing a cocktail of protease inhibitors (KeyGEN BioTECH, China) for 30 min. The concentrations of whole cell proteins were determined using a BCA Protein Assay Kit (CWBio, Beijing, China) and adjusted to the same concentration. For western blotting assay, the proteins of equal quantity were separated by 10% SDS-PAGE and then transferred onto a PVDF membrane (Merck Millipore, Germany). After blocking with 5% nonfat dry milk for 1 h at room temperature, the membranes were incubated with the primary antibodies at a concentration of 1:1000 at 4 °C overnight. The antibodies included rabbit anti-human B7-H3 monoclonal antibody (Abcam, Cambridge, MA, United States), rabbit anti-human B3GALT4 monoclonal antibody (Abcam, Cambridge, MA, United States) and mouse anti-human β -actin monoclonal antibody (Beyotime, Nantong, China). After washing with TBST (TBS with 0.1% Tween), the membranes were incubated with a corresponding goat-anti-mouse or goat-anti-rabbit IgG-horseradish peroxidase secondary antibody (1:1000, Beyotime, Nantong, China) for 1 h at room temperature. The membranes were finally treated with enhanced chemiluminescence (ECL) assay reagents (absin, Shanghai, China) and the immunoreactive bands were visualized using the ChemiDoc™ XRS+ system with Image Lab™ Software (Bio-Rad, Hercules, CA, United States). Quantitative analysis was carried out with Quantity One (Bio-Rad, Hercules, CA, United States).

Statistical analysis

Statistical analysis of clinical data was performed using the software package SPSS 19.0 software (IBM, Chicago, IL, United States). Chi-square test analyzed the association between B7-H3 or B3GALT4 and the clinicopathological data. The non-parametric Spearman test evaluated the correlation of B7-H3 and B3GALT4 expression. Overall survival (OS) was plotted using the Kaplan-Meier method and was compared using the log-rank test. Multivariate survival analysis was performed using the Cox proportional hazard model. All the *in vitro* experiments were performed in triplicate. A non-paired *t*-test analyzed differences in mean values between groups. All data were analyzed using GraphPad Prism 6.0 (GraphPad Software Inc., La Jolla, CA, United States). A *P*-value less than 0.05 indicated a statistically significant difference.

RESULTS

Expression of B7-H3 and B3GALT4 and their relationship with clinicopathological features of CRC

The expression of B7-H3 and B3GALT4 was analyzed

using immunohistochemistry in CRC tissue. Positive staining of B7-H3 was predominantly detected in the membrane and cytoplasm (Figure 1C), and the location of B3GALT4 expression was identified in the cytoplasm (Figure 1D). The positive rates of the B7-H3 and B3GALT4 expressions were 70.4% (157/223) and 54.7% (122/223), respectively. Further, a highly significant correlation between the positive expression of B7-H3 with the depth of tumor invasion ($P = 0.049$), distant metastasis ($P = 0.034$) and differentiation ($P = 0.017$) was observed. However, the expression of B3GALT4 had no significant correlation with clinicopathological parameters (Table 1).

Correlation between B7-H3 and B3GALT4 expression in CRC

Of the 223 CRC cases, 97 (43.5%) patients exhibited higher expression of both B7-H3 and B3GALT4, and 41 (18.4%) showed lower expression of both. Also, there were 85 (38.1%) cases with either B7-H3 low or B3GALT4 low. Spearman's Correlation was used to examine the association of B7-H3 expression with B3GALT4 expression in CRC. The result showed that there was a highly significant positive correlation between B7-H3 and B3GALT4 expression ($r = 0.219$, $P = 0.001$, Table 2).

High expression of B7-H3 and B3GALT4 in patients with CRC is associated with poor OS

Notably, patients with high expression of B7-H3 had a significantly worse OS as compared to patients with low expression ($P = 0.037$) (Figure 2A). Similarly, the OS in the high B3GALT4 expression group was significantly inferior to that in the low expression group ($P = 0.044$) (Figure 2B). Moreover, a subgroup of patients with high expression of B7-H3 and high B3GALT4 exhibited a significantly worse prognosis as compared to patients with a low expression of B3GALT4 ($P = 0.016$) (Figure 2C). However, in a subgroup of patients with low expression of both B7-H3 and B3GALT4 prognosis of patients with CRC was unaffected ($P = 0.061$) (Figure 2D).

Furthermore, the univariate Cox proportional hazard model analysis was performed to evaluate the risk factors related to the prognosis of patients with CRC. As shown in Table 3, high expression of B7-H3, high expression of B3GALT4, high expression of both B7-H3 and B3GALT4, depth of tumor invasion (T3/4), lymph node metastasis (N1/2), distant metastasis, TNM stage (III/IV), neural invasion, and vascular invasion were correlated with the OS of patients with CRC. However, there was no correlation of OS with gender, age, tumor location, colon cancer site, mucinous adenocarcinoma, differentiation, and B7-H3 low expression group (Table 3). Besides, the multivariate analysis revealed that distant metastasis, TNM stage (III/IV), and vascular invasion were significant independent prognostic factors for OS of patients with CRC (Table 3).

Table 1 Expression of B7 homolog 3 and β -1,3-galactosyltransferase-4 in colorectal cancer patients and their correlation with clinicopathological parameters

Clinicopathological parameter	Case (n)	B7-H3 expression		P value	B3GALT4 expression		P value
		Low	High		Low	High	
Gender				0.616			0.213
Male	124	35	89		63	61	
Female	99	31	68		42	57	
Age (yr)				0.259			0.791
< 60	87	22	65		40	47	
\geq 60	136	44	92		65	71	
Tumor location				0.361			0.905
Colon	88	23	65		41	47	
Rectum	135	43	92		64	71	
Colon cancer site				0.119			0.352
Right-sided	37	7	30		20	17	
Left-sided	186	59	127		85	101	
Depth of tumor invasion				0.049			0.527
T1/2	64	25	39		28	36	
T3/4	159	41	118		77	82	
Lymph node metastasis				0.433			0.145
N0	116	37	79		60	56	
N1/2	107	29	78		45	62	
Distant metastasis				0.034			0.425
Yes	16	1	15		6	10	
No	207	65	142		99	108	
TNM stage				0.297			0.068
I / II	113	37	76		60	53	
III / IV	110	29	81		45	65	
Neural invasion				0.146			0.683
Yes	32	6	26		14	18	
No	191	60	131		91	100	
Vascular invasion				0.079			0.585
Yes	35	6	29		15	20	
No	188	60	128		90	98	
Mucinous adenocarcinoma				0.579			0.506
Yes	20	7	13		8	12	
No	203	59	144		97	106	
Differentiation				0.017			0.186
Poor	73	14	59		39	34	
Moderate/well	150	52	98		66	84	

B7-H3: B7 homolog 3; B3GALT4: β -1,3-galactosyltransferase-4.**Table 2 Correlation between B7 homolog 3 and β -1,3-galactosyltransferase-4 expression in colorectal cancer**

B3GALT4 expression	B7-H3 expression		r	P value
	Low	High		
Low	41	60	0.219	0.001
High	25	97		

B7-H3: B7 homolog 3; B3GALT4: β -1,3-galactosyltransferase-4.**Correlation between B7-H3 and B3GALT4 in CRC cell lines**

We further investigated the relationship between expression of B7-H3 and B3GALT4 *in vitro*. The mRNA and protein expression was detected in the CRC cell lines with different B7-H3 expression levels, which were maintained in our lab. Both the mRNA and protein expression of B7-H3 and B3GALT4 were significantly upregulated in SW480-B7-H3 cell line expressing a high level of B7-H3 as compared to SW480-NC cell line. Similarly, as compared to Caco-2-shNC cell line,

Caco-2-shB7-H3 cell line with low expression of B7-H3 significantly downregulated the expression of B3GALT4. Therefore, B7-H3 and B3GALT4 had a positive correlation both in mRNA and protein expression *in vitro* (Figure 3).

DISCUSSION

CRC continues to be a major cause of cancer-related morbidity and mortality with over 1200000 cases diagnosed every year, and more than 600000 patients

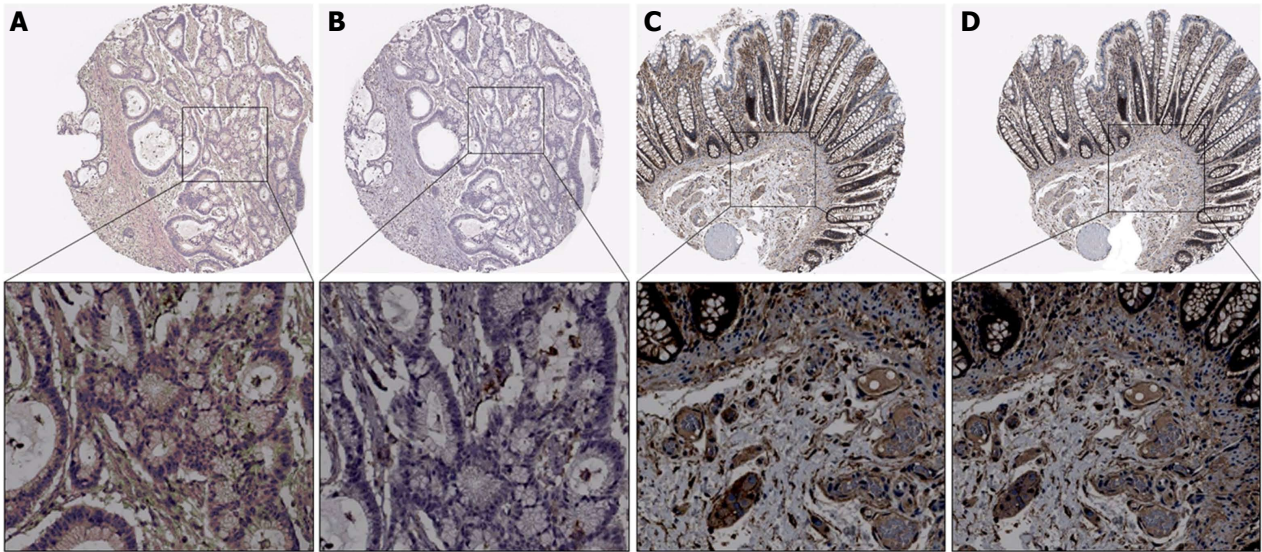


Figure 1 The representative immunohistochemical images of B7 homolog 3 and β -1,3-galactosyltransferase-4 expression in colorectal cancer tissues. A: Low expression of B7 homolog 3 (B7-H3); B: Low expression of β -1,3-galactosyltransferase-4 (B3GALT4); C: High expression of B7-H3; D: High expression of B3GALT4 (100 \times). The images below show the magnification of each zone (400 \times). A and B are from one patient; C and D are from another patient.

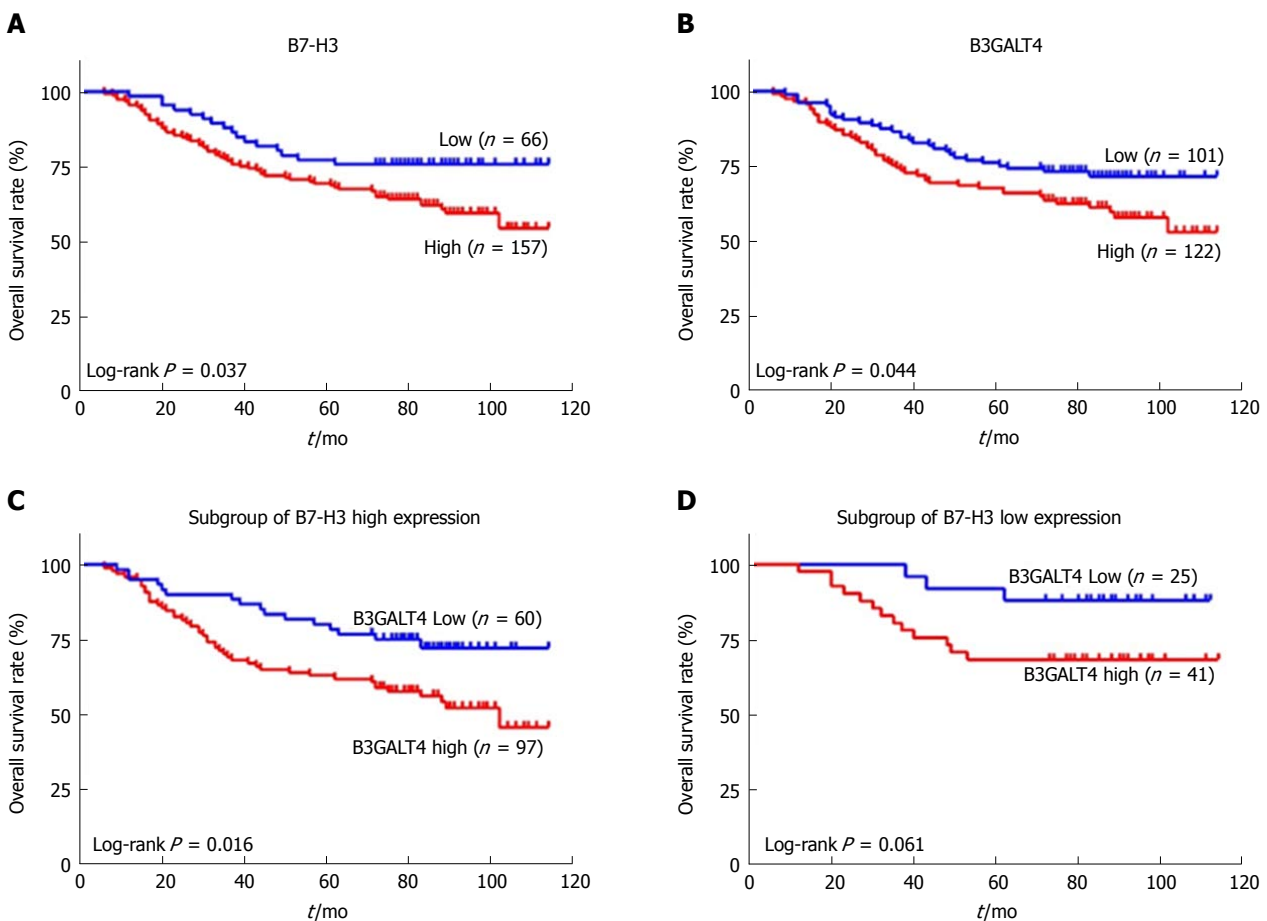


Figure 2 Kaplan-Meier survival curves of the 223 patients with colorectal cancer expressing B7 homolog 3 and β -1,3-galactosyltransferase-4. A: Patients with low expression of B7 homolog 3 (B7-H3) vs high expression of B7-H3; B: Patients with low expression of β -1,3-galactosyltransferase-4 (B3GALT4) vs high expression of B3GALT4; C: Subgroup of patients with high expression of B7-H3 and low expression of B3GALT4 vs high expression of B3GALT4; D: Subgroup of patients with low expression of B7-H3 and high expression of B3GALT4 vs low expression of B3GALT4.

succumb to the disease worldwide. Moreover, five-year survival rates for stage I CRC was more than 90%

where as for stage IV was 10%^[10]. Given the poor prognosis of CRC, the search for novel diagnostic and

Table 3 Univariate and multivariate Cox proportional hazards analyses of overall survival in patients with colorectal cancer

Clinical parameter	Univariate analysis		Multivariate analysis	
	HR (95%CI)	P value	HR (95%CI)	P value
Gender (male <i>vs</i> female)	0.999 (0.637-1.566)	0.995		
Age (≥ 60 <i>vs</i> < 60) (yr)	0.951 (0.603-1.500)	0.829		
Tumor location (rectum <i>vs</i> colon)	1.351 (0.863-2.117)	0.188		
Colon cancer site (left-sided <i>vs</i> right-sided)	0.970 (0.534-1.760)	0.919		
Depth of tumor invasion (T3/4 <i>vs</i> T1/2)	2.522 (1.362-4.670)	0.003	1.807 (0.949-3.443)	0.072
Lymph node metastasis (N1/2 <i>vs</i> N0)	2.922 (1.801-4.739)	0.000	0.322 (0.077-1.341)	0.119
Distant metastasis (yes <i>vs</i> no)	9.353 (5.206-16.804)	0.000	4.635 (2.224-9.660)	0.000
TNM stage (III/IV <i>vs</i> I/II)	3.497 (2.114-5.783)	0.000	7.490 (1.636-34.280)	0.009
Neural invasion (yes <i>vs</i> no)	2.240 (1.320-3.802)	0.003	0.800 (0.410-1.561)	0.514
Vascular invasion (yes <i>vs</i> no)	2.531 (1.529-4.188)	0.000	1.962 (1.082-3.558)	0.026
Mucinous adenocarcinoma (yes <i>vs</i> no)	1.063 (0.488-2.314)	0.877		
Differentiation (poor <i>vs</i> moderate/well)	0.799 (0.504-1.267)	0.340		
B7-H3 (high <i>vs</i> low)	1.781 (1.027-3.089)	0.040	1.289 (0.721-2.307)	0.392
B3GALT4 (high <i>vs</i> low)	1.597 (1.007-2.533)	0.047	1.209 (0.721-2.307)	0.392
B7-H3 and B3GALT4 (high <i>vs</i> low)	0.737 (0.552-0.983)	0.038	1.153 (0.845-1.572)	0.369
B7-H3 high (B3GALT4 high <i>vs</i> low)	2.283 (1.289-4.042)	0.005		
B7-H3 low (B3GALT4 high <i>vs</i> low)	0.321 (0.091-1.127)	0.076		

B7-H3: B7 homolog 3; B3GALT4: β -1,3-galactosyltransferase-4.

prognostic biomarkers is highly desirable to prevent CRC-related deaths.

Immune checkpoint signaling pathways are most frequently modulated in cancer to inhibit the nascent anti-tumor immune response. Checkpoint antibody inhibitors, such as CTLA-4 and PD-1/PD-L1 are the most extensively studied novel class of inhibitors. Currently, drugs inhibiting these pathways are employed for a wide variety of malignancies and have demonstrated durable anti-tumor activities in a subset of cancer patients^[11,12]. Furthermore, investigations on new inhibitory pathways are also undergoing, and drugs are being investigated including those targeting B7-H3^[13]. As an immune checkpoint protein, B7-H3 has been recognized as an immunoregulatory molecule for T cell activation, proliferation, and cytokine production^[14]. Thus far, overexpression of B7-H3 has been reported in several different cancer types and the expression level of B7-H3 correlated with tumor growth, invasion, metastasis, malignant stage, and recurrence rate^[15]. Furthermore, several groups have generated anti-B7-H3 antibodies and reported overall suppression of tumor growth *in vitro* and *in vivo*^[16]. Therefore, it is expected that B7-H3 plays a crucial role in cancer diagnosis and treatment. The present study revealed that B7-H3 was highly expressed in CRC tissue (70.4%) and significantly associated with the depth of tumor invasion ($P = 0.049$), distant metastasis ($P = 0.034$) and differentiation ($P = 0.017$). These results were consistent with previous findings^[17,18].

Furthermore, B7-H3 is a type I transmembrane glycoprotein and plays a role in immunosuppression. Chen *et al*^[19] demonstrated that glycoprotein B7-H3 was involved in the pathological process and tumor growth of oral squamous cell carcinoma, and the glycans of B7-H3 from oral cancer cells comprised of terminal α -galactoses and more diverse N-glycan structures with

higher fucosylation than that of healthy cells. In addition, the presence of a carbohydrate-lectin receptor interaction between the tumor-associated B7-H3 from oral cancer cells and immune cells was detected^[19]. B3GALT4, encoding a UDP-galactose: β -N-acetylgalactosamine β -1,3-galactosyltransferase activity, belongs to the human β -3-galactosyltransferase gene family^[7]. Galactosyltransferase (GT) of the glycosyltransferase family, is the most common Golgi "marker" enzyme, catalyzes the transfer of galactose to glycoprotein-bound acetylglucosamine. The enzyme is provided with one N-linked oligosaccharide and palmitate residues and plays a vital role in the process of O-glycosylation. Moreover, in patients suffering from ovarian and breast cancer, increased expression of GT enzyme activity has been reported^[20]. Enzymatic activity of B3GALT4 and T5 in ovarian cancer tissues, and significant overexpression of B3GALT4/T5 mainly in stage I uterine corpus cancers, indicated that B3GALT4/T5 is a novel tumor marker for uterine corpus cancer and other gynecological cancers^[9]. Consequently, B7-H3 and B3GALT4 were both correlated with glycosylation and tumor progression. However, there was a paucity of literature on the expression and association of B7-H3 and B3GALT4 in CRC. Therefore, the association of B7-H3 and B3GALT4 expression in CRC tissues and cell lines was investigated.

The present study revealed that high expression of B7-H3 or B3GALT4 reduced the OS rate of CRC patients independently ($P = 0.037$, $P = 0.044$, respectively). Furthermore, overexpression of both B7-H3 and B3GALT4 in CRC resulted in poorer prognosis ($P = 0.016$). Besides, there was a significant positive correlation between B7-H3 and B3GALT4 ($r = 0.219$, $P = 0.001$). Taken together, B7-H3 and B3GALT4 could serve as a novel, reliable prognostic marker for CRC. Furthermore, we detected that the expression of B3GALT4 was positively altered following B7-H3 expression *in vitro*.

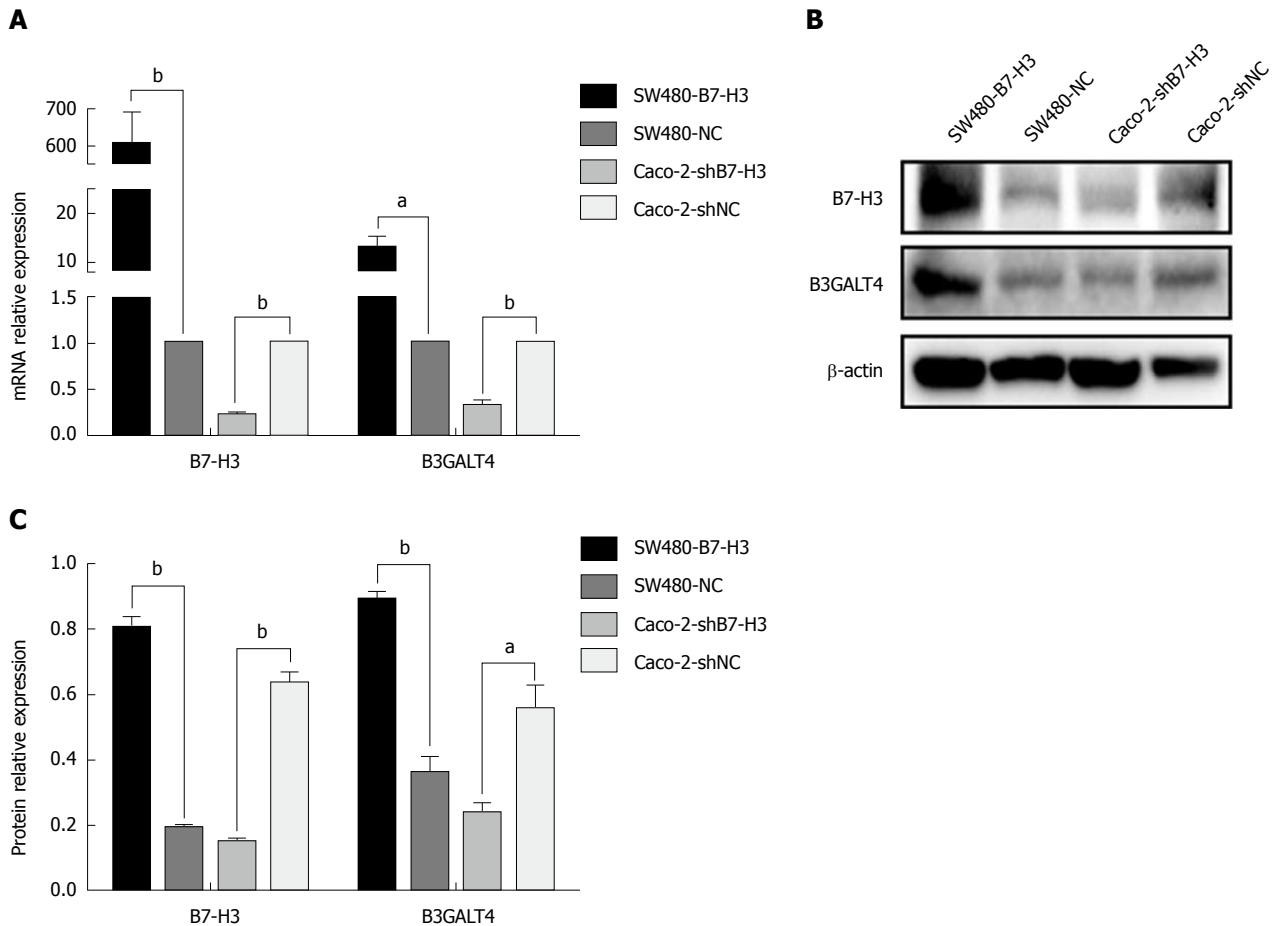


Figure 3 The expression of B7 homolog 3 and β -1,3-galactosyltransferase-4 in colorectal cancer cell lines. A: Real-time quantitative polymerase chain reaction results of relative mRNA expression; B: Western blotting results for protein expression; C: Statistical analysis of protein expression ($^aP < 0.05$, $^bP < 0.01$).

Combined with the results of clinical samples, this study indicated that B7-H3 could positively regulate B3GALT4 at the mRNA as well as the protein level. However, the underlying mechanism of regulation of B7-H3 and B3GALT4 in CRC warrants further investigation.

In summary, the present study for the first time revealed the expression of B3GALT4 in CRC and its correlation with B7-H3 *in vitro*. Overall, the findings of the present study suggested that B7-H3 and B3GALT4 are novel prognostic biomarkers for CRC and highlight the significance of both B7-H3 and B3GALT4 as promising therapeutic targets for CRC. Thus, here we present our preliminary work on the relationship of the immune function and glycosylation of tumor-associated protein in CRC.

ARTICLE HIGHLIGHTS

Research background

Colorectal cancer (CRC) is the most prevalent gastrointestinal tract malignancy worldwide. The prognosis of CRC patients remains relatively poor. B7 homolog 3 (B7-H3) mRNA is widely expressed on many tissues and cell types. However, B7-H3 protein is not constitutively expressed on T-cells, natural killer cells and antigen-presenting cells. The β -1,3-galactosyltransferase-4 (B3GALT4), which belongs to β -1,3-galactosyltransferase (β 3GalT) gene family is abundantly expressed in human organs and tissues, predominantly in brain and involved in

GM1/GD1 ganglioside synthesis. The β 3GalT family may be closely related to the tumor.

Research motivation

There are insufficient reports about the correlation between B3GALT4 and CRC.

Research objectives

The aim of the present study is to investigate the clinical correlation of B7-H3 and B3GALT4 with CRC, and the correlation between the expression of B7-H3 and B3GALT4 was evaluated to determine their prognostic significance in CRC.

Research methods

The authors identified the expression of B7-H3 and B3GALT4 in 223 CRC patient samples by immunohistochemistry and evaluated the possible correlation between B7-H3 and B3GALT4 and clinical outcomes. The mRNA and protein expression were also identified to establish the regulatory relationship of B7-H3 with B3GALT4 *in vitro*.

Research results

A significant positive correlation between B7-H3 and B3GALT4 was observed in CRC specimens. High expression of B7-H3 was identified as a significant independent predictor of poor overall survival (OS). High expression of B3GALT4 was also recognized as an independent predictor of inferior OS. In CRC cell lines with the stable expression of high B7-H3, the mRNA and protein expressions of B3GALT4 were significantly upregulated. The expression of B3GALT4 was significantly reduced when expression of B7-H3 was knocked down.

Research conclusions

The expression of B3GALT4 in CRC and its positive correlation with B7-H3 *in vitro* was revealed, as well as B7-H3/B3GLAT4 as dual prognostic biomarkers for CRC.

Research perspectives

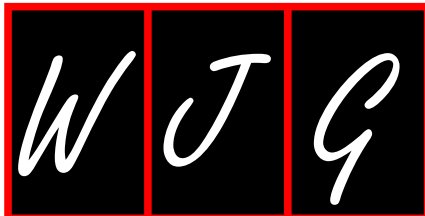
The present study suggested that B7-H3 and B3GALT4 are novel prognostic biomarkers for CRC, and the significance of both B7-H3 and B3GALT4 as promising therapeutic targets for CRC are highlighted.

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Retrospective Cohort Study

Favorable clinical outcome of nonalcoholic liver cirrhosis patients with coronary artery disease: A population-based study

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statistical analysis; Lin CC obtained funding; Tseng MH and Lin CC contributed to study supervision.

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Abstract

AIM

To elucidate the prevalence and risk of mortality of nonalcoholic liver cirrhosis (LC) patients with coronary artery disease (CAD).

METHODS

The study cohort included newly diagnosed nonalcoholic LC patients age ≥ 40 years old without a diagnosis of CAD from 2006 until 2011 from a longitudinal health insurance database. The mean follow-up period for the study cohort was 1152 ± 633 d. The control cohort was matched by sex, age, residence, and index date. Hazard ratios (HRs) were calculated using the Cox proportional hazard model and the Kaplan-Meier method.

RESULTS

After exclusion, a total of 3409 newly diagnosed nonalcoholic cirrhotic patients were identified from one million samples from the health insurance database. We found that CAD (5.1% *vs* 17.4%) and hyperlipidemia (20.6% *vs* 24.1%) were less prevalent in nonalcoholic LC patients than in normal subjects (all $P < 0.001$), whereas other comorbidities exhibited an increased prevalence. Among the comorbidities, chronic kidney disease exhibited the highest risk for mortality (adjusted HR (AHR) = 1.76; 95%CI: 1.55-2.00, $P < 0.001$). Ascites or peritonitis exhibited the highest risk of mortality among nonalcoholic cirrhotic patients (AHR = 2.34; 95%CI: 2.06-2.65, $P < 0.001$). Finally, a total of 170 patients developed CAD after a diagnosis of nonalcoholic LC. The AHR of CAD in nonalcoholic LC patients was 0.56 (95%CI: 0.43-0.74, $P < 0.001$). The six-year survival rates for nonalcoholic LC patients with and without CAD were 52% and 50%, respectively ($P = 0.012$).

CONCLUSION

We conclude that CAD was less prevalent and associated with a reduced risk of mortality in nonalcoholic cirrhotic patients.

Key words: Nonalcoholic liver cirrhosis; Coronary artery disease; Population-based study

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Core tip: Coronary artery disease (CAD) is less prevalent and associated with a reduced risk of mortality in nonalcoholic liver cirrhosis (LC) patients. Nonalcoholic LC patients with CAD exhibit an increased six-year survival rate compared to cirrhotic patients without CAD. The LC complication rates did not differ between nonalcoholic LC patients with and without CAD. Of note, nonalcoholic LC patients with ascites or peritonitis exhibited the highest risk of mortality among LC complications.

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INTRODUCTION

Liver cirrhosis (LC) is the 14th leading cause of death in adults and accounted for one million deaths in 2010 worldwide^[1]. In Taiwan, LC and chronic liver disease constituted the 8th most common cause of death in 2011^[2]. These conditions contribute to numerous lethal complications and comorbidities that result in poor clinical outcomes. Variceal bleeding, systemic infection, hepatic encephalopathy, and hepatocellular carcinoma (HCC) are the primary complications of LC and causes of mortality^[3,4]. In addition, LC is associated with systemic comorbidities, such as hemorrhagic stroke and digestive tract malignancies^[5-7].

Controversy has emerged regarding the association between LC and coronary artery disease (CAD) in recent decades^[7-17]. Several comorbidities of cirrhotic patients have been regarded as cardioprotective factors (*e.g.*, low blood pressure, coagulopathy, thrombocytopenia, malnutrition, and lower serum cholesterol levels)^[8,18-20]. However, case-controlled studies have revealed conflicting results and an increased prevalence of CAD in LC patients compared to the normal population^[7,9,17,21,22]. A different etiology with an increased proportion of alcoholic and nonalcoholic steatohepatitis (NASH)-related LC in Western populations may have contributed to this result. Furthermore, the application of interferon and nucleot(s)ide analogues for viral hepatitis aided in prolonging survival in recent decades^[23,24]. Age-related risks associated with CAD also may have led to an increased prevalence of CAD.

There is a paucity of available data regarding the association between nonalcoholic LC and CAD. Taiwan is an endemic area of viral hepatitis where the majority of LC in patients is caused by hepatitis B (HBV) and hepatitis C (HCV) viral infections^[25]. Hence, the nonalcoholic LC population in Taiwan is an ideal cohort in which the confounding effect of alcohol consumption

is minimized.

The aim of our study was to elucidate the association between nonalcoholic LC and CAD using a national population-based database in Taiwan. Additionally, we analyzed the prevalence, hazard ratio (HR), and survival for concomitant comorbidities and complications.

MATERIALS AND METHODS

Study population and design

This study was a nationwide retrospective longitudinal population-based cohort study based on the Taiwanese National Health Insurance research database (NHIRD). The National Health Insurance program has provided compulsory medical insurance for greater than 99% of the Taiwanese population since March 1, 1995. We identified all LC patients with a first-time diagnosis of LC using International Classification of Disease, 9th Revision, Clinical Modification (ICD-9-CM) codes (ICD-9-CM code: 571.5) for the period from 2004 to 2011. The following patients were excluded from the study: patients who had LC or CAD before the end of 2005, had LC after diagnosis of CAD from 2006 to 2011, were younger than 40 years old, had a diagnosis of alcoholic LC (ICD-9-CM code: 571.2) or biliary LC (ICD-9-CM code: 571.6), and were outpatients with less than two follow-up visits after the first visit. The control subjects were matched with the patients in the study cohort at a ratio of five to one (5 control subjects *per case patient*) in terms of sex, age (40-49, 50-59, 60-69, and > 69 years), residence, and entry year.

Other comorbidity data and the ICD-9-CM codes are summarized in Table Appendix 1. The diagnosis of comorbidities was defined as having three outpatient visits or one admission. Hyperlipidemia was defined as having a lipid profile with any one of the following factors: total cholesterol (TC) \geq 2000 mg/L, low-density lipoprotein cholesterol (LDL-C) \geq 1600 mg/L, or a triglyceride (TG) level \geq 1500 mg/L. Complications of LC that occurred after enrollment included esophageal varices (EV) (ICD-9-CM codes: 456-456.21), EV with bleeding (ICD-9-CM codes: 456.0, 456.20) concomitant with ICD-9 procedure codes for ligation of EV or sclerotherapy, ascites (ICD-9-CM codes: 789.5 and 568.82) or peritonitis (ICD-9-CM codes: 567.xx), and hepatic encephalopathy (ICD-9-CM code: 572.2).

End point measurement

We followed up all the subjects enrolled from the index date to the end of 2011. The mean follow-up period for the newly diagnosed nonalcoholic LC cohort (3409 patients) was 1152 ± 633 d with a median of 1169 d, maximum of 2920 d, and minimum of 7 d. Patients with newly diagnosed CAD (one inpatient or three outpatient codes) were categorized based on the first incidence of CAD. The first-time diagnosis of CAD was identified as the primary end point, and the death of the subject served as the secondary end point. All-cause mortality was analyzed in both the study and control cohorts.

Statistical analysis

Microsoft SQL Server 2008 R2 (Microsoft Corporation, Redmond, WA, United States) was used to perform data processing. Statistical analyses were conducted using SPSS software 19.0 (SPSS, Inc., Chicago, IL, United States). Chi-square tests and analysis of variance (ANOVA) were used to analyze the demographic data, concomitant comorbidities, and complications of cirrhosis. A Cox proportional hazards model was developed to calculate the overall mortality HRs of all comorbidities and complications in cirrhotic patients. The results are expressed in unadjusted and adjusted HRs (AHRs) with 95% confidence intervals (CI). The six-year cumulative survival and survival curve were calculated using the Cox regression method and Kaplan-Meier method. A two-tailed *P* value less than or equal to 0.05 was considered statistically significant.

RESULTS

Primary outcome: CAD was less prevalent in patients with nonalcoholic LC

A total of 10142 cases of LC were retrieved from one million random samples in the NHIRD from 2004 to 2011. To ensure that only newly diagnosed LC cases were included, we excluded patients who met the following criteria: LC diagnosed before the end of 2005, CAD occurred before LC, alcoholic or biliary LC, and age younger than 40 years old. Finally, a total of 3409 newly diagnosed nonalcoholic LC patients between 2006 and 2011 were identified and included in the study (Figure 1). To select age-, sex-, residence-, and entry year-matched controls, we further excluded 173 cirrhotic patients to achieve 100% randomization. A total of 3236 patients with nonalcoholic LC and 16180 matched controls were analyzed for all demographic characteristics (Table 1). Patients with nonalcoholic LC were more likely to have comorbidities including hemorrhagic stroke, hypertension, heart failure (HF), diabetes mellitus (DM), chronic kidney disease (CKD), chronic obstructive pulmonary disease (COPD) (all *P* < 0.001), and ischemic stroke (*P* = 0.005). In contrast, hyperlipidemia was less prevalent in nonalcoholic LC patients (*P* < 0.001). During six years of follow-up, 165 (5.1%) patients in the nonalcoholic LC cohort and 2814 (17.4%) subjects in the control cohort developed CAD (*P* < 0.001).

Nonalcoholic LC patients with and without CAD

As shown in Table 2, we stratified nonalcoholic LC patients (*n* = 3409) into two groups according to the presence of CAD. Nonalcoholic LC patients with CAD were older (\geq 60 years old), more likely female, and exhibited increased concomitant comorbidities of ischemic stroke, hypertension, HF, DM, CKD, hyperlipidemia, and COPD (all *P* < 0.001). When we compared the complications of liver cirrhosis between the two groups, nonalcoholic LC patients with CAD had fewer LC-related complications, including EV with bleeding, ascites or peritonitis, and hepatic encephalo-

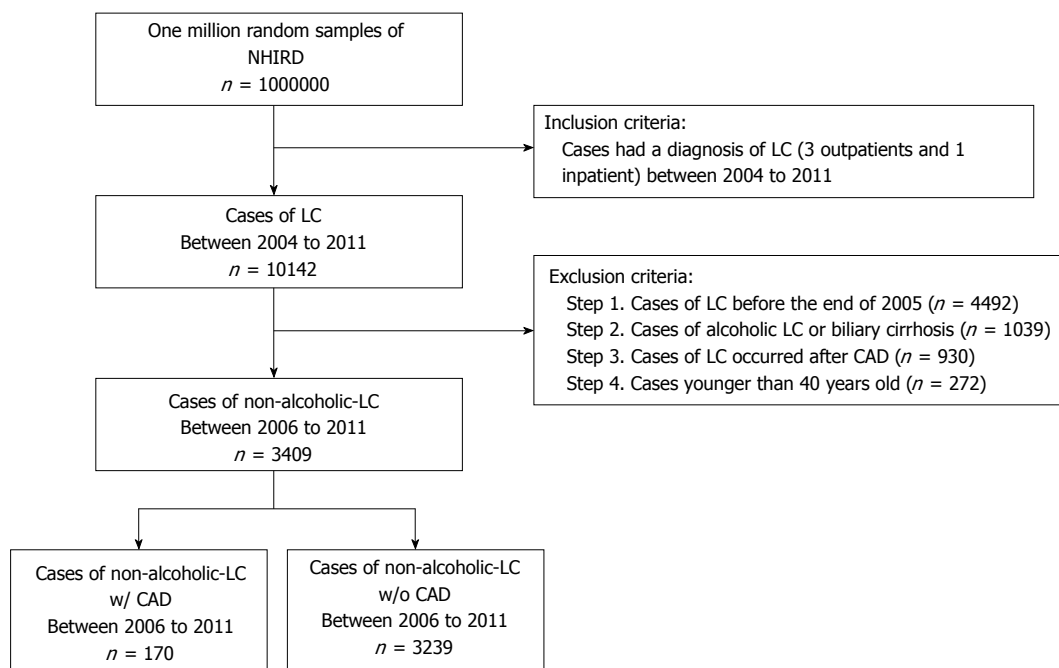


Figure 1 Study design.

Table 1 Characteristics of non-alcoholic liver cirrhosis cohort and the matched control cohort *n* (%)

Variable	Non-alcoholic LC patients, <i>n</i> = 3236	Control, <i>n</i> = 16180	<i>P</i> value
Sex			1.000
Male	2083 (64.4)	10415 (64.4)	
Female	1153 (35.6)	5765 (35.6)	
Age (yr)			1.000
40-49	565 (17.5)	2825 (17.5)	
50-59	885 (27.3)	4425 (27.3)	
60-69	766 (23.7)	3830 (23.7)	
> 69	1020 (31.5)	5100 (31.5)	
Residence			1.000
Metropolis	1834 (56.7)	9170 (56.7)	
General area	1362 (42.1)	6810 (42.1)	
Remote areas	40 (1.2)	200 (1.2)	
Coronary artery disease	165 (5.1)	2814 (17.4)	< 0.001
Cerebrovascular disease	413 (12.8)	1580 (9.8)	< 0.001
Hemorrhage	110 (3.4)	283 (1.7)	< 0.001
Ischemia	333 (10.3)	1413 (8.7)	0.005
Hypertension	1620 (50.1)	6672 (41.2)	< 0.001
Heart failure	252 (7.8)	972 (6.0)	< 0.001
Diabetes mellitus	1075 (33.2)	3141 (19.4)	< 0.001
Chronic kidney disease	616 (19.0)	1216 (7.5)	< 0.001
Hyperlipidemia	668 (20.6)	3903 (24.1)	< 0.001
Chronic obstructive pulmonary disease	534 (16.5)	1976 (12.2)	< 0.001

LC: Liver cirrhosis.

pathy (Supplementary Table 1). However, no significant differences were noted between the two groups.

Secondary outcome: Increased survival rate in the nonalcoholic LC with CAD group

We analyzed 3409 nonalcoholic LC patients and 16180 control subjects with a mean follow-up period of six

years, and six-year survival rates were 50% and 85%, respectively (*P* < 0.001) (Figure 2A). When we compared nonalcoholic LC patients with and without CAD, the six-year survival rates were 52% and 50%, respectively (*P* = 0.012) (Figure 2B). The Cox regression proportional hazard model corresponding to each group also demonstrated a better survival rate for the nonalcoholic LC with CAD group than for those without CAD (AHR: 0.56; 95%CI: 0.43-0.74; *P* < 0.001) (Table 3).

HRs of mortality in LC patients with different comorbidities and complications

Table 3 presents the HRs of mortality in LC patients with different comorbidities. Increased HRs were observed for males, older patients, cerebrovascular disease (CVD), HF, DM, CKD and COPD. Among these factors, CKD exhibited the highest AHR of mortality (AHR: 1.76; 95%CI: 1.55-2.00). The AHRs of CAD, hypertension, and hyperlipidemia were reduced. Hyperlipidemia exhibited the lowest AHR of 0.52 (95%CI: 0.44-0.62).

When we analyzed the HRs of LC complications that occurred after enrollment, all complications exhibited increased values for both unadjusted HRs and AHRs. Ascites or peritonitis exhibited the highest AHR at 2.34 (95%CI: 2.06-2.65) (Supplementary Table 2).

Finally, we compared the effect of the number of comorbidities and complications on the survival rate in LC patients. Cirrhotic patients with one, two, or three comorbidities had HRs of 1.35, 1.72, and 1.95 (95%CI: 1.19-1.55, 1.47-2.00, and 1.57-2.43), respectively (Supplementary Table 3). However, the HRs for one, two, or t three LC complications were 3.56, 4.63, and 5.15 (95%CI: 3.14-4.03, 3.94-5.44, and 3.82-6.94), respectively (Supplementary Table 4).

Table 2 Characteristics of non-alcoholic liver cirrhosis patients with and without coronary artery disease *n* (%)

Variable	Non-alcoholic LC with CAD, <i>n</i> = 170	Non-alcoholic LC without CAD, <i>n</i> = 3239	<i>P</i> value
Sex			0.094
Male	99 (58.2)	2091 (64.6)	
Female	71 (41.8)	1148 (35.4)	
Age (yr)			< 0.001
40-49	18 (10.6)	554 (17.1)	
50-59	25 (14.7)	877 (27.1)	
60-69	46 (27.1)	751 (23.2)	
> 69	81 (47.6)	1057 (32.6)	
Residence			0.484
Metropolis	89 (52.4)	1830 (56.5)	
General area	79 (46.5)	1358 (41.9)	
Remote areas	2 (1.2)	51 (1.6)	
Cerebrovascular disease	46 (27.1)	400 (12.3)	< 0.001
Hemorrhage	9 (5.2)	103 (3.2)	0.132
Ischemia	37 (21.8)	327 (10.1)	< 0.001
Hypertension	139 (81.8)	1594 (49.2)	< 0.001
Heart failure	54 (31.8)	215 (6.6)	< 0.001
Diabetes mellitus	84 (49.4)	1051 (32.4)	< 0.001
Chronic renal failure	68 (40.0)	587 (18.1)	< 0.001
Hyperlipidemia	54 (31.8)	656 (20.3)	< 0.001
Chronic obstructive pulmonary disease	49 (28.8)	521 (16.1)	< 0.001

LC: Liver cirrhosis; CAD: Coronary artery disease.

DISCUSSION

In the present study, we observed a reduced prevalence of CAD and an increased survival rate for concomitant CAD in nonalcoholic LC patients. A lower prevalence of atherosclerosis and CAD was first described in an autopsy-based study in 1960^[10]. A reduced prevalence of ischemic events was also reported for ischemic stroke^[8,26]. However, conflicting data have been reported in some retrospective cohort and case-controlled studies^[8,9,13,16,17,21,22]. First, the increased prevalence of CAD found in LC patients might be due to the different etiologies of LC in these Western population-based cohorts. An increased proportion of NASH and alcohol-related LC was noted compared to cohorts in viral hepatitis endemic areas^[13,16,21,22]. NASH and alcohol consumption are generally associated with increased CAD risk factors. Nonetheless, the prevalence of CAD was reduced in end-stage liver disease patients assessed for liver transplantation who had alcoholic LC when compared to those with nonalcoholic LC^[27]. Although moderate consumption of alcohol (< 30 g/d) has been reported as a protective factor against CAD^[12], controversy still exists regarding heavy drinkers. In comparison, most subjects in our study had viral hepatitis-related LC. Few metabolic disorders were associated with steatohepatitis (such as hyperlipidemia), and no alcohol consumption was reported in our study cohort.

Second, lower blood pressure, better serum lipid profiles (including lower LDL-C, TC, and TG), and coagulopathy in LC patients were regarded as protective

factors against CAD^[8,18-20,22]. However, viral hepatitis *per se* can influence vessel function and cause endothelial dysfunction, which is correlated with atherosclerotic disease progression^[28]. A retrospective cohort study indicated that hepatitis C virus-infected subjects exhibited an increased risk for CAD, although better blood pressure and lipid profiles were observed in the population^[29,30]. Consistent with previous reports, we observed a reduced prevalence of hyperlipidemia in cirrhotic patients. The proportion of comorbidities, including CVD, hypertension, HF, DM, CKD, hyperlipidemia, and COPD, was increased in the nonalcoholic LC with CAD patients^[7]. The increase in these age-related comorbidities may be attributed to the older age in this study cohort. Third, CAD is an age-related disease. We hypothesize that better liver function may contribute to increased survival in the cirrhotic patients with CAD cohort. When survival is prolonged, age-related CAD risks also increase^[31].

Ischemic stroke is a systemic thromboembolic event. Compared to normal subjects, the prevalence of ischemic stroke was reduced in cirrhotic patients^[32]. In contrast, hemorrhagic events increased^[7,33]. However, in our study, both ischemic and hemorrhagic stroke were significantly increased in nonalcoholic LC subjects. Of note, the prevalence of hemorrhagic stroke in non-alcoholic LC patients was two-fold higher than that in normal subjects (3.4% vs 1.7%, *P* < 0.001), which was considerably increased compared to ischemic stroke (10.3% vs 8.7%, *P* = 0.005). Older age and higher proportions of concomitant hypertension, DM, and COPD (as a result of smoking) in our nonalcoholic LC cohort might explain this result. These comorbidities have been reported as significant risk factors for all types of stroke^[34].

We analyzed the association among comorbidities, complications, and HRs in LC patients. Consistent with previous studies, cirrhosis concomitant with CVD, HF, CKD, or COPD was regarded as a risk factor for mortality in both the Charlson comorbidity index and the Cirrhosis-specific Comorbidity Scoring System (CirCom)^[35-37]. In addition, CKD had the highest HR in our study and exhibited increased risk scores in the two prognostic scoring systems. All the complications in LC patients were risk factors in our study. However, CAD, hypertension, and hyperlipidemia were associated with a lower HR and improved survival in this study. Although acute myocardial infarction was found to be a risk factor of mortality in nonalcoholic LC patients^[36], the relationship among chronic stable CAD, hypertension, hyperlipidemia, and LC mortality remains unclear. Among these factors, cirrhotic patients with greater than three comorbidities exhibited the worst prognosis with at least a 1.954-fold increased risk of mortality.

Limitations

There were some limitations in our study. First, this is a retrospective cohort study. Although nonalcoholic LC and CAD subjects were retrieved from the Taiwanese

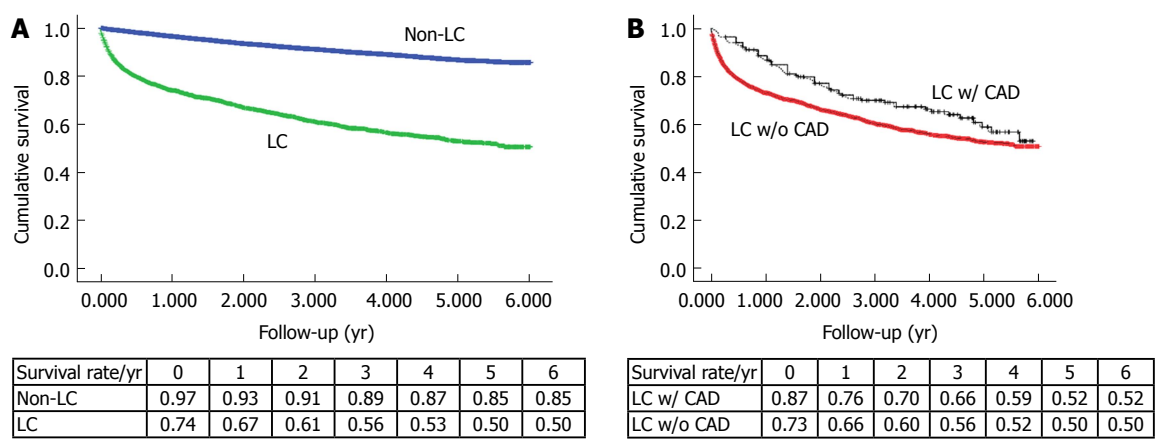


Figure 2 Kaplan-Meier analysis of overall survival. A: Cumulative survival using the Kaplan-Meier method for nonalcoholic LC patients and controls during the follow-up period; B: Cumulative survival using the Kaplan-Meier method for nonalcoholic LC patients with and without CAD during the follow-up period. LC: Liver cirrhosis; CAD: Coronary artery disease.

Table 3 Hazard ratios of mortality in non-alcoholic liver cirrhosis patients with comorbidities using Cox regression model

Variable	Unadjusted hazard ratio			Adjusted hazard ratio ¹		
	Risk ratio	95%CI	P value	Risk ratio	95%CI	P value
Sex						
Male	1.20	1.07-1.35	0.002	1.34	1.19-1.51	< 0.001
Female (reference)						
Age (yr)						
40-49 (reference)						
50-59	1.04	0.85-1.27	0.688	1.08	0.89-1.32	0.446
60-69	1.29	1.06-1.57	0.013	1.40	1.14-1.72	< 0.001
> 69	2.51	2.10-3.00	< 0.001	2.73	2.25-3.30	< 0.001
Coronary artery disease						
No (reference)						
Yes	0.71	0.55-0.93	0.012	0.56	0.43-0.74	< 0.001
Cerebrovascular disease						
No (reference)						
Yes	1.25	1.08-1.45	0.004	1.08	0.93-1.27	0.323
Hypertension						
No (reference)						
Yes	0.98	0.88-1.09	0.709	0.75	0.66-0.85	< 0.001
Heart failure						
No (reference)						
Yes	1.50	1.26-1.78	< 0.001	1.23	1.02-1.48	0.027
Diabetes mellitus						
No (reference)						
Yes	1.03	0.92-1.16	0.609	1.12	0.99-1.26	0.082
Chronic kidney disease						
No (reference)						
Yes	1.89	1.67-2.13	< 0.001	1.76	1.55-2.00	< 0.001
Hyperlipidemia						
No (reference)						
Yes	0.51	0.44-0.60	< 0.001	0.52	0.44-0.62	< 0.001
Chronic obstructive pulmonary disease						
No (reference)						
Yes	1.30	1.13-1.48	< 0.001	0.99	0.858-1.141	0.888

¹Adjustments were made for sex, age, coronary heart disease, cerebrovascular disease, hypertension, heart failure, diabetes mellitus, chronic kidney disease, hyperlipidemia, and chronic obstructive pulmonary disease.

NHIRD database according to ICD-9 codes, data were lacking regarding the severity of cirrhosis (*e.g.*, Child-Turcotte-Pugh scores). In this study, we excluded patients who had less than three outpatient visits with the same diagnosis. Furthermore, we analyzed the complications of cirrhosis to evaluate the severity.

Second, the severity of concomitant comorbidities, such as hypertension, DM, and hyperlipidemia, cannot be evaluated. In addition, other known risk factors, such as smoking status and family history of CAD, were not recorded in the database. Third, the severity of CAD was not recorded in the database. A prospective case-

controlled study revealed an increased prevalence of nonobstructive CAD (*i.e.*, narrowing < 50%) in cirrhotic patients compared to normal controls using computerized coronary angiography. This feature may contribute to the increased survival rates for LC patients with CAD. The severity of CAD should be further evaluated in future studies^[17]. Finally, the different follow-up periods for each patient may impact the HRs of mortality in nonalcoholic LC patients.

In conclusion, CAD was less prevalent in nonalcoholic LC patients. Among cirrhotic patients, an increased number of concomitant comorbidities was found in cirrhotic patients with CAD. However, improved survival was found in nonalcoholic LC patients with CAD when compared to those without CAD.

ARTICLE HIGHLIGHTS

Research background

The risk of mortality in nonalcoholic liver cirrhosis (LC) patients with coronary artery disease (CAD) is unclear. Previous case-control studies demonstrated conflicting results potentially due to the different etiologies of LC. LC patients with alcoholic and nonalcoholic fatty liver disease-related metabolic disorders exhibit an increased risk of CAD. In contrast, hemostatic defects that occur in LC, such as thrombocytopenia, coagulopathy, and low blood pressure, are not considered as potential protective factors of cirrhosis against atherosclerotic events.

Research motivation

The results of CAD risk in LC patients are controversial. In contrast to the present study, previous works using alcoholic LC-based cohorts may have been confounded by the increased risk of metabolic syndrome in heavy drinkers. To the best of our knowledge, the risk of CAD in nonalcoholic cirrhotic patients is not well established.

Research objectives

The aim of the study was to elucidate the prevalence and risk of mortality in nonalcoholic cirrhotic patients. The comorbidities and LC-related complications were also important prognostic factors among cirrhotic patients. The result of this study can provide a better understanding of CAD risk in LC patients.

Research methods

We collected 10142 LC patients diagnosed from 2004 to 2011 using the Taiwanese National Health Insurance research database. After exclusion of subjects who were treated before the end of 2005, had alcoholic or biliary cirrhosis, had LC occurring after CAD, and were younger than 40 years old, a total of 3409 LC patients were enrolled in the study. The comorbidities and complications of LC were collected. The first-time diagnosis of CAD was identified as the primary end point, and the death of the subject served as the secondary end point. All-cause mortality was analyzed in both the study and control cohorts. A Cox proportional hazards model was developed to calculate the overall mortality hazard ratios of all comorbidities and complications in cirrhotic patients. The six-year cumulative survival and survival curve were calculated using the Cox regression method and the Kaplan-Meier method.

Research results

CAD was less prevalent in nonalcoholic LC patients than in controls. Nonalcoholic LC patients with CAD were associated with a reduced risk of mortality. The six-year survival rates were increased in patients with CAD compared to patients without CAD in the nonalcoholic LC cohort. As this is a retrospective cohort study, further prospective studies are needed to confirm this finding.

Research conclusions

In this study, we demonstrate that CAD is less prevalent and associated with

a reduced risk for mortality in nonalcoholic LC patients. This result confirms previous studies regarding the lower risk for atherosclerotic events (*i.e.* ischemic stroke and coronary artery disease) in alcohol-related and nonalcohol-related LC cohorts. Although viral hepatitis can cause endothelial dysfunction, which correlates with atherosclerotic disease progression, we propose that LC has a more powerful protective effect against atherosclerotic events based on the favorable cardiovascular risk profiles, such as thrombocytopenia, coagulopathy, and low blood pressure. The strengths of the study include the large sample size cohort and risk adjustments for comorbidities and complications. Finally, we conclude that nonalcoholic LC patients with CAD exhibit a favorable outcome.

Research perspectives

Future prospective research should focus on the advantages and disadvantages of antiplatelet therapy in the prevention of CAD in nonalcoholic LC patients. Additionally, it is advised that future studies should compare alcoholic and nonalcoholic LC cohorts and evaluate the effect of viral treatment.

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Prospective Study

PillCamColon2 after incomplete colonoscopy - A prospective multicenter study

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Abstract

AIM

To evaluate the ability of PillCamColon2 to visualize colonic segments missed by incomplete optical colonoscopy (OC) and to assess the diagnostic yield.

METHODS

This prospective multicentre study included 81 patients from nine centres who underwent second-generation colon capsule endoscopy (CCE) following incomplete OC performed by an experienced gastroenterologist (> 1000 colonoscopies). Patients with stenosis were excluded. According to patient preferences, CCE was performed the following day (protocol A) after staying on clear liquids and 0.75 L Moviprep in the morning or within 30 d after new split-dose Moviprep (protocol B). Boosts consisted of 0.75 L and 0.25 L Moviprep, and phospho-soda was given as a rescue if the capsule was not excreted after seven hours.

RESULTS

Seventy-four patients were analysed (51% of them in group A; 49% in group B). Bowel cleansing was adequate in 67% of cases, and CCE could visualize colonic segments missed by incomplete colonoscopy in 90% of patients under protocol A and 97% of patients under protocol B ($P = 0.35$, n.s.). Significant polyps including adenocarcinoma were detected in 24% of cases. Detection rates for all polyps and significant polyps per patient were similar in both protocols. Polyps

were found predominantly in the right colon (86%) in segments that were not reached by OC. Extracolonic findings - such as reflux esophagitis, suspected Barrett esophagus, upper GI-bleeding, gastric polyps, gastric erosions and angiectasia - were detected in eight patients. PillCamColon2 capsule was retained in the ileum of one patient (1.4%) without symptoms and removed during an uneventful resection for unknown Crohn's disease that was diagnosed as the cause of anemia, which was the indication for colonoscopy. CCE was well tolerated. One patient suffered from self-limiting vomiting after consuming the phospho-soda.

CONCLUSION

Second-generation CCE using a low-volume preparation is useful after incomplete OC, and it allows for the detection of additional relevant findings, but cleansing efficiency could be improved.

Key words: Colon capsule endoscopy; PillCamColon2; Incomplete colonoscopy; Low volume prep; Moviprep; Phospho-soda; Cleanliness level; Complementation rate; Polyps

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Core tip: Colonoscopy is the gold standard for visualization of the colon, but it may be incomplete, not reaching the cecum. Second-generation colon capsule endoscopy (CCE) with low-volume preparations could complement incomplete colonoscopies in 90% of cases, and it could help to detect additional relevant colonic and extracolonic findings. Protocols with either CCE the day following an incomplete colonoscopy or within 30 d after a new low-volume preparation were both feasible and well tolerated; however, the protocols could be improved with respect to bowel cleanliness and complete colon visualization.

Baltes P, Bota M, Albert J, Philipper M, Hörster HG, Hagenmüller F, Steinbrück I, Jakobs R, Bechtler M, Hartmann D, Neuhaus H, Charton JP, Mayershofer R, Hohn H, Rösch T, Groth S, Nowak T, Wohlmut P, Keuchel M. PillCamColon2 after incomplete colonoscopy - A prospective multicenter study. *World J Gastroenterol* 2018; 24(31): 3556-3566 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v24/i31/3556.htm> DOI: <http://dx.doi.org/10.3748/wjg.v24.i31.3556>

INTRODUCTION

Flexible optical colonoscopy (OC) is the gold standard to detect and treat colorectal diseases and proved to be safe and effective in colorectal cancer screening (CRC)^[1]. However, OC may be incomplete for various reasons, with completion rates between 90% and 98%^[2-5] for screening colonoscopy and 81%-94% in mixed series^[6-9]. Risk factors for incomplete colonoscopy

are female gender, elder patients, previous pelvic or abdominal surgery, diverticulosis, redundant colon, stenosing tumors, poor preparation, inflammatory bowel disease; in contrast sedation, male gender and higher body mass index were reported as protective factors^[4,6,7,10,11]. Of the patients with incomplete OC, 4.3% had advanced neoplasia in the right colon^[5]. A five-year follow-up study showed a higher risk for colorectal cancer in patients with failed colonoscopy^[12], demonstrating the need for additional investigations in these patients. PillCamColon has been cleared by the US Food and Drug Administration (FDA) for detection of colon polyps in patients after an incomplete optical colonoscopy with adequate preparation. Later the indication had been expanded to the detection of colon polyps in patients with evidence of lower gastrointestinal origin and major risks for colonoscopy or moderate sedation.

First-generation PillCamColon1 with a constant rate of two frames per second (fps) had limited sensitivity compared to a colonoscopy^[13-15]. Technical improvements of the second-generation PillCamColon2 that was used in the present study included adaptive frame rates (4 fps and 35 fps) and an increased viewing angle. It also included automatic small bowel detection with consecutive timing of boosters to shorten transit times and to improve cleansing levels^[16], which was shown to have a significantly higher diagnostic yield for polyps^[17]. A decisive factor for CCE accuracy is bowel cleansing; recent data have shown that low-volume Polyethylene glycol (PEG)-based protocols may be feasible instead of high-volume preparations^[18,19].

Our study aimed to assess the impact of second-generation CCE after incomplete colonoscopies by analyzing the complementation rates and incremental diagnostic yields with two different low-volume cleansing protocols. Patients were offered to either stay on clear liquids with a CCE the next day or to start a new bowel preparation procedure within 30 d.

MATERIALS AND METHODS

Study design and population

This prospective, multicentre study including nine centres (tertiary care hospitals or private endoscopy offices) in Germany. It was approved by the ethics committee of Hamburg Chamber of Physicians (PV3467, 20.05.2010). The www.clinicaltrials.gov identifier is NCT01480635.

All patients included in the study were 18 years or older who had incomplete colonoscopies that were performed by an experienced endoscopist (> 1000 colonoscopies performed). Incomplete OC was defined as a failure to reach the cecum or ileo-cecal anastomosis due to looping, bowel angulation, adhesions, and intolerance of sedation or inflammation. The presumed area of the colon reached by OC was documented, as were reasons for termination, detection of polyps and

tumours, other findings and adverse events. Patients with stenosis, inadequate preparation, or exchange of endoscope were excluded. Other exclusion criteria for CCE have been described previously^[18]. Written informed consent was obtained from all patients.

Study protocol

After an incomplete colonoscopy, patients were rescheduled for the following day (protocol A) or they were given a separate appointment within 30 d (protocol B), according to their preference. CCE was performed with PillCamColon2 (Given Imaging, Yoqneam, Israel) after a low-volume cleansing regimen with PEG and ascorbic acid (Moviprep, Norgine, Marburg/Lahn, Germany). Following capsule ingestion, the boosts consisted of 0.75 L after small bowel detection and 0.25 L Moviprep if the capsule had not been excreted five hours after ingestion. 30 mL sodium picosulfate (NaP; Fleet, Recordati, Ulm, Germany) was used as an additional boost if the capsule was not excreted seven hours after ingestion. In protocol A, patients stayed on clear liquids after the colonoscopy, and they received an additional cleansing of 0.75 L Moviprep the next morning (at the latest, one hour before CCE). In protocol B, patients were allowed to eat after the OC. A new bowel cleansing procedure was performed within 30 d: split-dose 1 L of Moviprep was consumed in the evening and 1 L was consumed in the morning, each followed by 1 L of water. Boosts with Moviprep or NaP were identical in both protocols (Table 1).

CCE studies were read with Rapid7 or Rapid8 software in each centre by an experienced endoscopist with additional experience in capsule endoscopy (> 1000 colonoscopies, > 100 small bowel capsule endoscopies (SBCE) and > 25 CCEs performed). All readers had completed a dedicated two-day CCE evaluation course. Polyp size was estimated with the integrated software tool.

For both examination modalities, cleansing levels were documented, as described previously^[15], using four grades: excellent, good (adequate), fair and poor (inadequate). Each colon segment [that is, cecum, ascending colon (AC), transverse colon (TC), left colon (LC) and rectum, see Figure 1] and overall cleansing status were evaluated.

For CCE, visualization of colonic segments, complementation of previous colonoscopy, completeness of CCE, and adverse events were recorded. Complete CCE was defined as excretion of capsule during recording time or by identification of the haemorrhoidal plexus. Detection of polyps, significant polyps, tumours or other relevant findings were documented for segments reached and not reached by the previous standard colonoscopy. According to previous studies, significant polyps were defined by size (≥ 6 mm) or number (≥ 3)^[19-21]. Other findings were considered important if they explained the indication for the colonoscopy or if they had further diagnostic or therapeutic implications.

Table 1 Study protocols A and B for colon capsule endoscopy after incomplete optical colonoscopy

Time	Procedure	
Evening and morning before colonoscopy	Standard bowel prep for colonoscopy	
After incomplete colonoscopy	Incomplete colonoscopy (OC) Patient's choice of protocol A or B for colon capsule endoscopy (CCE)	
After incomplete colonoscopy	Protocol A (CCE next day)	Protocol B (CCE within 30 d)
2 d before CCE	Patient stays on clear liquids	Patient can eat
Day before CCE	NA	Low residue diet
Evening before CCE		Clear liquids only
Morning of CCE	0.75 L Moviprep + water	1 L Moviprep + 1 L water
	Colon capsule ingestion	
Small bowel detection	0.75 L Moviprep + water (1 st boost)	
5 h after ingestion	0.5 L Moviprep + water (2 nd boost) ¹	
7 h after ingestion	30 mL NaP + water ('Rescue boost') ¹	
	Bisacodyl supp ¹	
11 h after ingestion	Removal of equipment ¹	

¹If capsule is not excreted earlier. OC: Optical colonoscopy.

Follow-up took place via a telephone call one week after the procedure. During the call, adverse events were documented, and capsule excretion was confirmed. Any adverse events were recorded, as well as the time of capsule excretion.

Study endpoints

The primary outcome parameter was complementation rate of CCE in patients with incomplete OC, which was defined by visualization of colonic segments not reached by OC. The secondary outcome parameters were as follows: additional (incremental) diagnostic yield of CCE compared to incomplete OC (all polyps, significant polyps defined by size or number and other significant findings) in segments not reached by OC; CCE findings in the upper gastrointestinal (GI) tract and small bowel; rate of complete CCE, as defined above; cleansing level of the colon (overall and segments) following the low-volume protocol for CCE; visualization of the Z-Line; and adverse events (number, type and severity).

Statistical analysis

Continuous variables were reported as mean and standard deviation, and categorical variables were reported as percentage. The null hypothesis (H0) for the primary endpoint (complementation of incomplete colonoscopy) was constructed using data from a former study that used PillCamColon1 and that showed a complementation rate of 50%^[22]. Accordingly, H0 was set to $\mu = 0.5$ with an expectation for complementation of OC by PillCamColon2 of 0.67. Using the Fisher exact test with a power of 80% (which is equal to $1-\beta$), 74 patients had to be recruited. Categorical values were compared using a chi-squared test (χ^2), while continuous values with a normal distribution were compared by a Student's *t*-test. *P* values < 0.05 were considered significant. An intention-to-treat (ITT) analysis was performed for complementation rates, cleansing levels, detection of significant polyps and safety. Statistical review was performed by one of the

authors (Peter Wohlmuth).

RESULTS

Demographics

Eighty-one consecutive patients were enrolled from nine participating centres between 2010 and 2013. Seven patients (four in the protocol A group and three in the protocol B group) had to be excluded due to technical failure ($n = 1$), protocol noncompliance as a result of incorrect timing of CCE ($n = 4$), exchange of colonoscope ($n = 1$) or early removal of recorder by the patient ($n = 1$) (Figure 2). In total, data of 74 patients were analysed per protocol. Demographics are shown in Table 2.

Reasons for referral to colonoscopy were CRC screening (22%), anemia (15%), hematochezia (15%), irregular stool (12%), abdominal pain (12%), B symptoms (7%), colitis (5%) and other reasons (12%). Thirty-six patients (48.6%) had prior abdominal surgery, while 14 patients (19%) had more than one surgical intervention. Most common surgeries were appendectomies (23%) and hysterectomies (19%). Only three patients had colonic surgery (4%), one patient had an ileocecal and one patient had a Billroth II anastomosis.

Standard OC

An experienced endoscopist (> 1000 colonoscopies performed) performed OC with a standard colonoscope. The mean duration of the procedure was 45 ± 17 min (range: 15-101 min). Unfavourable anatomy was the reason for termination in 92% of procedures. OC reached the sigmoid colon in 27% of cases, the descending colon (DC) in 4% of cases, the splenic flexure in 12% of cases, the TC in 14% of cases, the hepatic flexure in 35% of cases and the AC in 8% of cases. Adequate cleansing was achieved in 76% of procedures. In 12 of 74 patients (16%), polyps were detected, with a mean size of 6 ± 4.2 mm. Six

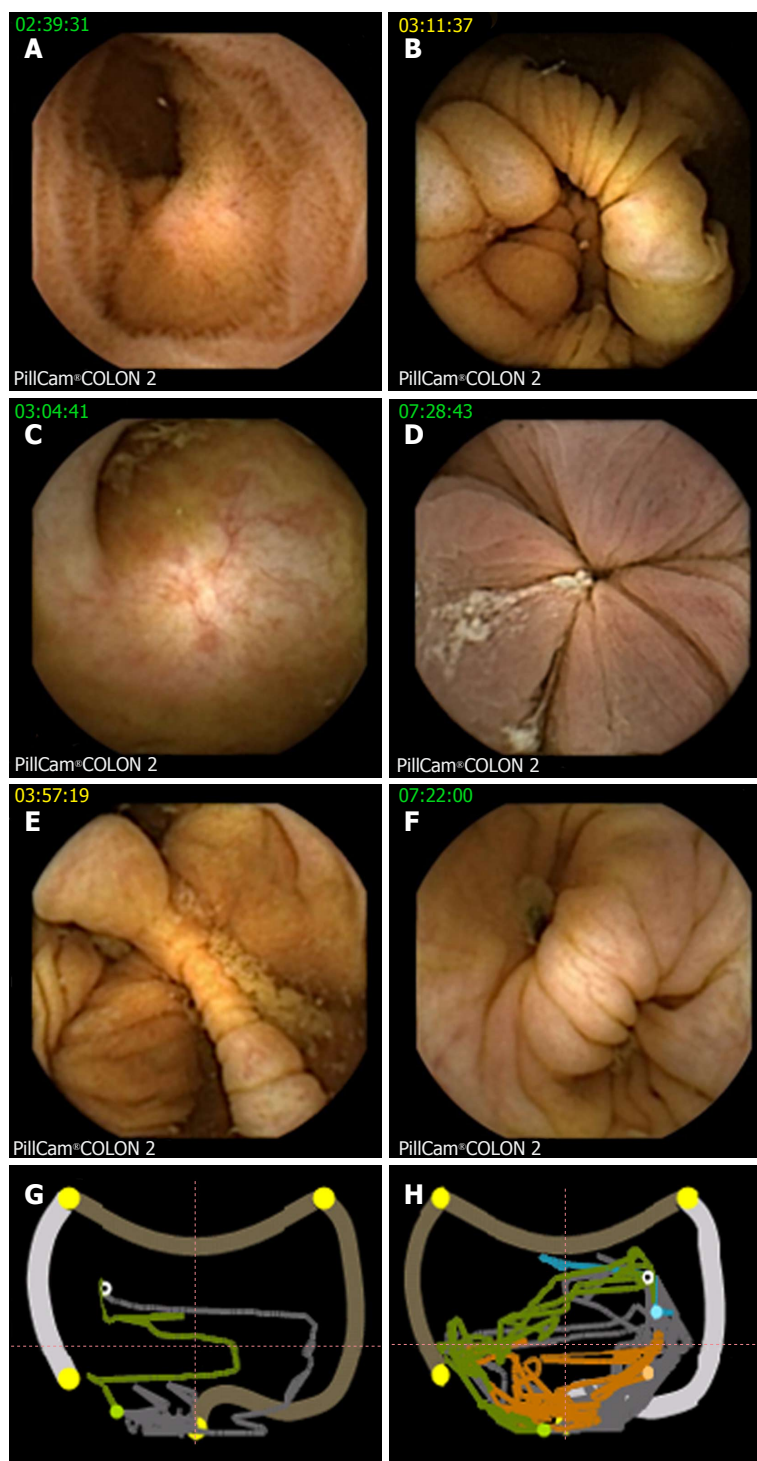


Figure 1 Landmarks at colon capsule endoscopy. A: Terminal ileum; B: IC valve; C: Appendix; D: Hemorrhoidal plexus, hepatic flexure - CCE image (E) with corresponding localization trace (G), white circle showing actual capsule position, green colon already displayed, grey colon yet to be analyzed, orange small bowel, blue stomach, outer pictogram the position to the colonic segment as manually defined by setting the landmarks; F and H: CCE image and localization trace of splenic flexure in another patient. CCE: Colon capsule endoscopy.

patients had more than one polyp (range: 2-5 polyps). Diverticula were found in 35 patients. Other findings were diverticulitis, erosions, angiectasias and erythema.

Colon capsule endoscopy

Primary endpoint: complementation of incomplete colonoscopy: Incomplete colonoscopy could

be complemented by CCE in 69 of 74 patients (93%; see Table 2). Complete CCE was achieved in 48 of 74 patients (65%). In four additional patients, the capsule reached the rectum but did not visualize the haemorrhoidal plexus (5%).

Complementation of OC could be achieved by CCE with protocol A in 89.5% of procedures and with protocol

Table 2 Demographics, reasons for termination of optical colonoscopy, and results of colon capsule endoscopy for protocol A and B *n* (%)

	Protocol A (CCE next day)	Protocol B (CCE within 30 d)	Significance
Demographics			
Patients	38 (51.4)	36 (48.6)	
Female	20/38 (52.6)	24/36 (66.7)	
Age, mean \pm SD	68.0 \pm 12.8 yr	63.9 \pm 13.0 yr	
Body mass index	26.0 \pm 3.9	26.5 \pm 4.9	
Reasons for termination of colonoscopy			
Looping of colon	23/38 (60.5)	23/36 (63.9)	
Angulation of colon	6/38 (15.8)	5/36 (13.9)	
Susp. adhesions	5/38 (13.2)	6/36 (16.7)	
Risk of perforation	2/38 (5.3)	0	$P = 0.710$ (NS); χ^2 test
Sedation problems	2/38 (5.3)	2/36 (5.6)	
Results of CCE			
Complete CCE	24/38 (63.3)	24/36 (66.7)	$P = 0.560$ (NS); χ^2 test
Complementation of colonoscopy	34/38 (89.5)	35/36 (97.2)	$P = 0.350$ (NS); χ^2 test
Adequate cleansing	25/36 (69.4)	23/36 (63.9)	$P = 0.820$ (NS); χ^2 test
Patients with significant colon polyps	10/38 (26.3)	11/36 (30.6)	$P = 0.500$ (NS); χ^2 test
Patients with other colon findings	0	Angiectasia ($n = 3$) Diverticulitis ($n = 1$)	$P = 0.045$; χ^2 test
Patients with small bowel findings	Angiectasia ($n = 1$) Crohn's disease ($n = 1$)	0	$P = 0.174$ (NS); χ^2 test
Patients with upper GI findings	Reflux esophagitis ($n = 1$) Upper GI-bleeding ($n = 1$) Gastric polyps ($n = 1$)	Reflux-esophagitis ($n = 1$) Susp. Barrett esophagus ($n = 1$) Gastric erosions ($n = 1$)	$P = 0.949$ (NS); χ^2 test

CCE: Colon capsule endoscopy.

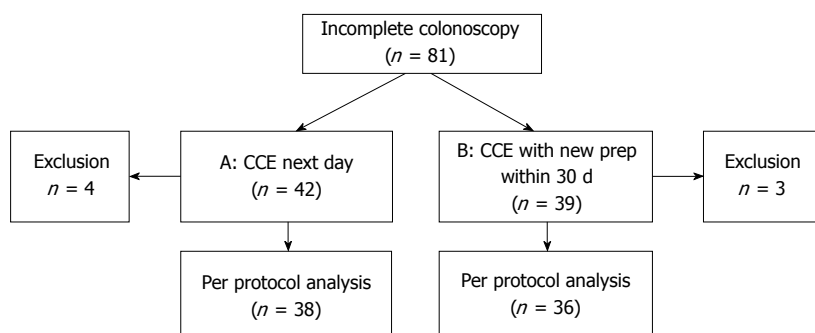


Figure 2 Flow chart protocol A (colon capsule endoscopy the day after colonoscopy) and protocol B (colon capsule endoscopy within 30 d after incomplete colonoscopy).

B in 97.2% of procedures ($P = 0.35$, not significant; Table 2). There were no differences between the rates of complementation using CCE for protocol A or B and the diagnostic yield. In the patients with incomplete visualization of the missing segments ($n = 5$), the capsule was able to display the hepatic flexure in two patients. One patient had a capsule retention in the small bowel because of unknown stenosing Crohn's disease. In one patient, the capsule did not reach the colon during recording time, and in one patient, visualization of the colon was incomplete due to recording gaps. The capsule was excreted within seven hours of ingestion and before the need for an additional NaP booster in 17 of 38 patients (44.7%) following protocol A, and in 12 of 36 patients (33.3%; $P = 0.25$, not significant) in protocol B.

Secondary endpoints: CCE was performed on the

day after colonoscopy in 38 patients (protocol A; 51%) or within 30 d in 36 patients (protocol B; 49%). Overall, cleansing was adequate in 48 of 72 (67%), and cleansing was adequate in the cecum in 58% of cases, in the AC in 65% of cases, in the TC in 77% of cases, in the LC in 70% of cases and in the rectum in 63% of cases (Figure 3); there were no differences between the protocols. Two capsules did not allow for visualization of the colon. Poor cleansing was rare (4 of 72 patients; 5.6%).

CCE detected 76 polyps in 35 of 74 patients (47%; Figure 4). Twenty-one patients (28%) had significant polyps (Table 3), and 14 patients had an insignificant number of polyps. In 9 of 21 patients, polyp size was ≥ 6 mm; in 3 patients, the number of polyps was ≥ 3 ; and in 9 patients, both parameters were positive. A total of 59 polyps (mean size 8 ± 4.5 mm) were detected in the 21

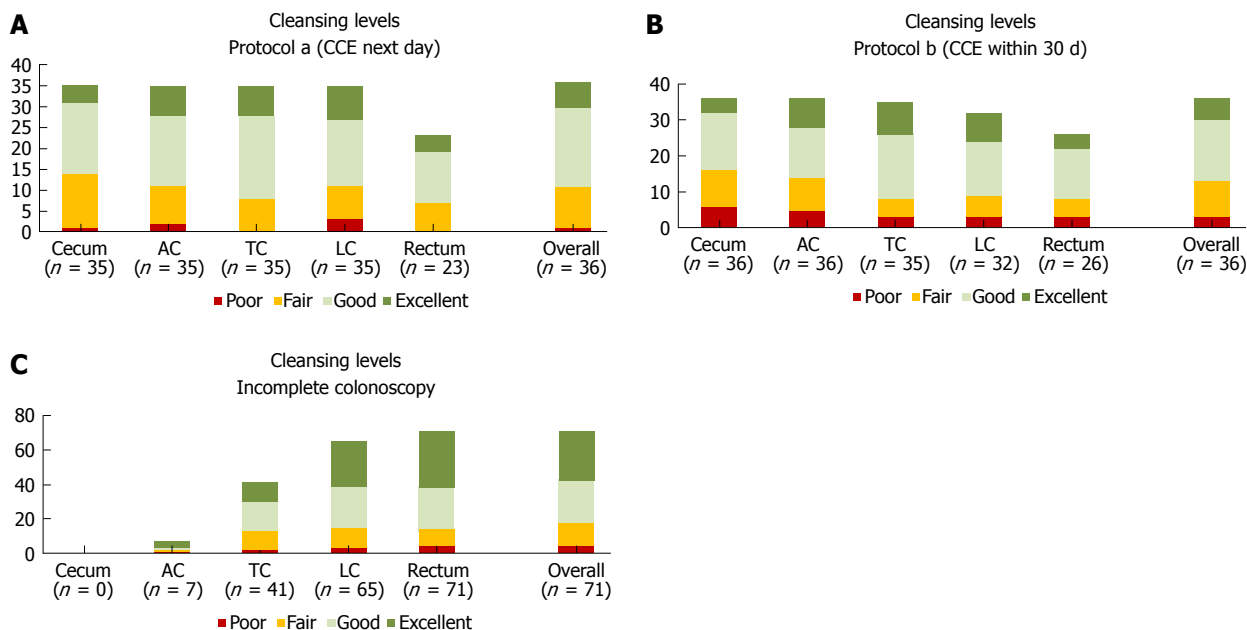


Figure 3 Cleansing levels for the colon segments: cecum, ascending colon, transverse colon, left colon, rectum and overall classification for all segments. Absolute number of patients for each level (poor, fair, good, excellent) are shown A for CCE with protocol a (next day), B for CCE with protocol b (within 30 d), and C for incomplete colonoscopy. AC: Ascending colon; CCE: Colon capsule endoscopy; LC: Left colon; TC: Transverse colon.

patients with significant polyps. Significant polyps were predominantly found in the ascending colon in segments that had not been reached by OC (86%). Incremental diagnostic yield of CCE compared to previous incomplete OC per patient for detecting significant polyps was 24%, and there were no differences between the two protocols. A cecal polyp of 26 mm turned out to be an adenocarcinoma, and hemicolectomy was performed in this patient.

Z-line was visualized in 45 of 74 patients (60.8%). CCE findings in the upper GI tract were reflux esophagitis ($n = 2$), suspected Barrett’s esophagus ($n = 1$), hemorrhagic gastropathy ($n = 1$), gastric polyps ($n = 1$; consecutive gastroscopy revealed foveolar hyperplasia in previously undiagnosed atrophic gastritis with vitamin B12 deficiency) and upper GI bleeding ($n = 1$).

In the small bowel, angiectasia and previously unknown Crohn’s disease was detected in one patient each. In colon segments missed by incomplete colonoscopy, angiectasias were detected in three patients and diverticulitis was detected in one patient (all patients were part of protocol B).

ITT analysis of all 81 patients found a complementation rate of 89%, adequate cleansing in 65%, significant polyps in 26% of patients, and no additional adverse events. The low complementation rate that was observed in this cohort is consistent with the exclusion criteria [technical problems, $n = 1$, and noncompliance of study protocol, $n = 6$ (for example, early removal of recorder and incorrect CCE timing)].

In one patient (protocol A), the capsule was retained in the small bowel without symptoms. Surgery was indicated following a new diagnosis of stenosing and fistulating Crohn’s disease with iron deficiency anemia (indication for

colonoscopy). During an uneventful surgery, the capsule was retrieved. Another patient (protocol B) complained of self-limiting nausea and vomiting after the NaP boost.

DISCUSSION

In this prospective, multicentre study, second-generation CCE allowed for the visualization of colon segments that were not reached by a previously incomplete colonoscopy in 93% of 74 patients. Fifty-one percent of patients opted for protocol A, and 49% for protocol B. The complementation rate following incomplete OC was higher in group B (97%) compared with group A (89%), but the results did not reach statistical significance. There were no differences between the rate of complete CCE, the cleansing level, the diagnostic yield or the number of adverse events.

The complementation rate identified in the present study corresponded well with results from recent trials using a first-generation colon capsule. A Spanish study found a complementation rate of incomplete colonoscopies of 85.3% and a diagnostic yield of 45%^[23]. A French trial including patients as well with contraindicated as incomplete OC, complete CCE was achieved in 83% of patients. An Italian trial reported a complete PillcamColon2 CCE after incomplete OC in 98% of patients using a separate preparation with Senna tablets, 4 L of PEG and two boosters with NaP and gastrografin^[24]. This rate was higher than in our low-volume protocol, but it was accompanied more often by preparation-related complaints (28.0% vs 1.4%). Nevertheless, our primary aim to complement colon visualization was achieved in 93% of patients, which was similar to a Greek study that achieved results

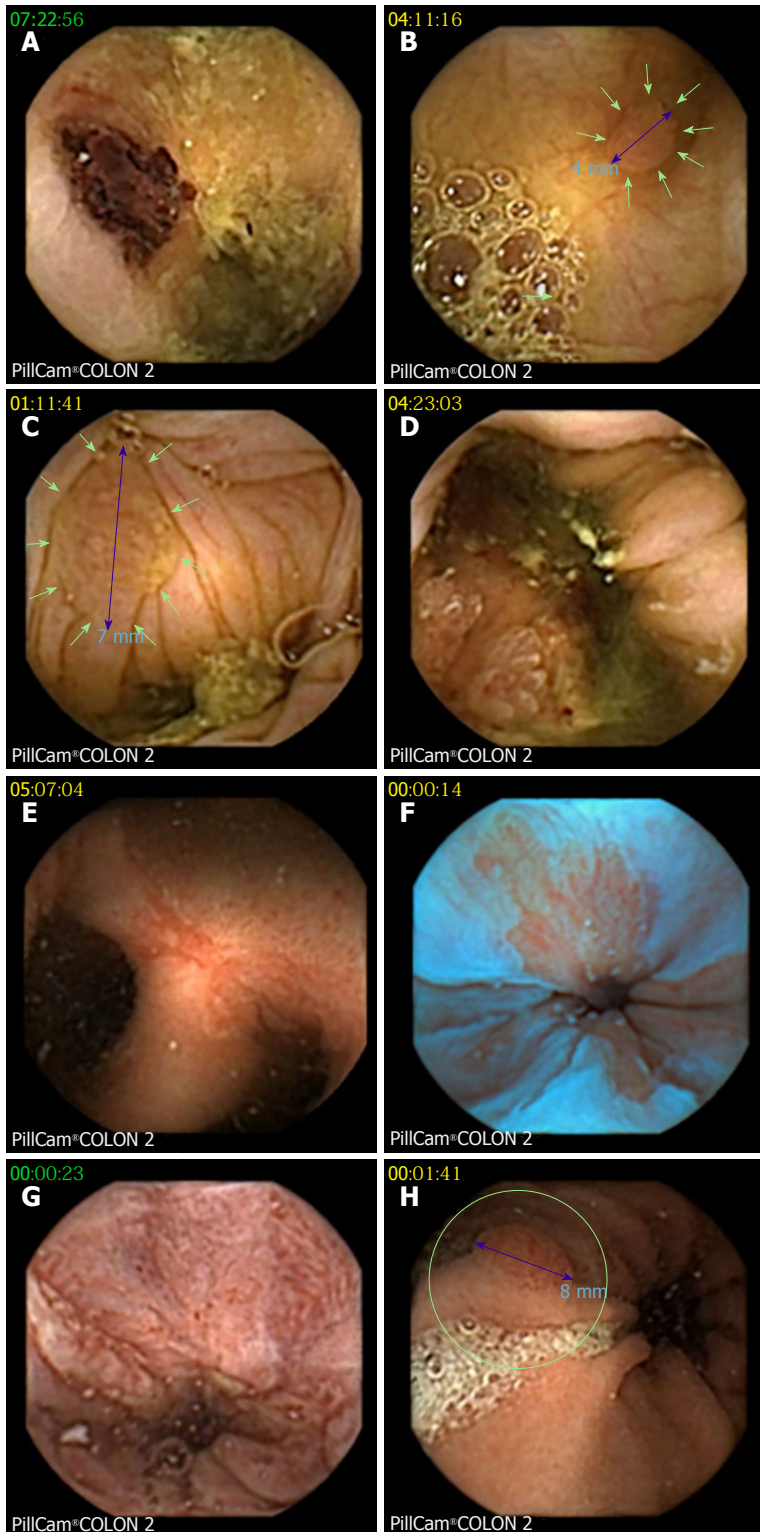


Figure 4 Examples of findings at colon capsule endoscopy. A: Biopsy tattoo after optical colonoscopy; B: One of three 4 mm polyps in the ascending colon, confirmed at consecutive balloon enteroscopy as tubular adenoma; C: Significant (7 mm) polyp; D: Cecal adenocarcinoma (confirmed by surgery); E: Fistulating and stenosing Crohn's disease of the ileum (confirmed by enteroclysis, CT scan, and surgery); F: Irregular Z-line suggestive of Barrett's esophagus (blue mode image); G: Reflux esophagitis; H: Gastric polyp (consecutive gastroscopy found foveolar hyperplasia and autoimmune gastritis with vitamin B12 deficiency).

using PillCamColon1 in 91% of patients^[14]. In the present study, unfavourable anatomy was the reason for terminating the colonoscopy, which was usually performed under propofol sedation, in 92% of patients. In contrast, pain was reported by 45% of patients as

the reason for incomplete colonoscopy in the Italian trial. This selection bias toward unfavourable anatomy might have also influenced the rate of complete consecutive CCEs (65%) in the present study. It may also be relevant when comparing our results to series

Table 3 Details of the 21/74 patients in whom significant polyps/tumors were detected during colon capsule endoscopy

No.	Significance based on	Size of largest polyp (mm)	Number of polyps	Localization of polyps	Farest point reached in OC	All segments with polyps in CCE reached by colonoscopy
1	Size/number	6	5	Rectum	HF	Yes
2	Size	8	2	Sigma	SF	Yes
3	Size/number	8	3	Sigma	AC	Yes
4	Size/number	8	3	2 × Cecum, 1 × AC	TC	No
5	Size	14	1	AC	HF	No
6	Size	26	1	AC	SF	No
7	Size	6	2	AC	Sigma	No
8	Size/number	10	3	2 × AC, 1 × TC	SF	No
9	Size/number	10	3	2 × LC, 1 × AC	Sigma	No
10	Size	10	1	AC	SF	No
11	Size/number	9	3	2 × AC, 1 × LC	HF	No
12	Size	6	1	AC	Sigma	No
13	Size	8	2	1 × AC/1 × LC	HF	No
14	Size	7	1	HF	Sigma	No
15	Number	5	4	AC, TC, 2 × sigma	Sigma	No
16	Size/number	12	4	1 × Cecum, 1 × AC, 1 × LC, 1 × rectum	Sigma	No
17	Number	4	3	1 × Cecum, 2 × rectum	TC	No
18	Number	5	5	2 × AC, 1 × TC, 2 × LC	HF	No
20	Size/number	10	7	4 × AC, 3 × LC	TC	No
20	Size	9	2	2 × Cecum	LC	No
21	Size/number	12	3	AC	LC	No

AC: Ascending colon; HF: Hepatic flexure; TC: Transverse colon; SF: Splenic flexure; LC: Left colon; OC: Optical colonoscopy.

with unselected patients without previously incomplete colonoscopies. In these trials, complete CCE was achieved in 76% of patients using a similar low-volume preparation^[18], in 88% of patients using PEG^[25], in 76% of patients using NaP^[14] and in 98% of patients using a PEG-, NaP- or gastrografin-based regimen^[24].

In the present study, colon cleansing using a low-volume preparation was adequate in 67% of patients, and the results were similar in both protocols. These results are comparable to other studies that used PillCamColon1 for incomplete colonoscopies with PEG preparation and NaP boosts (65%)^[23], and 60% vs 63% in the right and left colon, respectively^[14]. Adequate cleansing following use of the PillcamColon1 was observed in 76% of patients following consumption of 1-2 L Moviprep and two NaP boosts in a mixed cohort, including 28% of patients with contraindicated colonoscopy without anatomical problems^[19]. A recent Spanish multicentre trial found adequate cleansing levels in 75% of patients using a standard 4 L PEG preparation with a NaP booster for PillCamColon2 after an incomplete colonoscopy^[26]. Even in a large trial in a screening population without negative selection towards unfavorable anatomy, CCE was technically insufficient in 9% of patients due to inadequate cleansing or rapid transit of the capsule^[27].

Twenty-four percent of our patients (ITT 22%) had additional relevant finding following the CCE, which led to a recommendation for further diagnostics or treatment. Similarly, PillCamColon1 was useful in guiding management after failed OC in a Spanish trial^[23].

Most of the significant polyps (86%), including a carcinoma, were found in the AC. Our data confirmed

previous observations^[5] that CCE can identify relevant lesions in segments not reached by incomplete OC (Table 3).

Device-assisted colonoscopy with either spiral endoscopy and double or single balloons have identical rates, similar to CCE, of complementing incomplete OC of about 90%^[28-31]. These flexible endoscopic techniques additionally provide the possibility to directly treat detected lesions, but they require equipment and expertise, and they are restricted to specialized centres. A cap-assisted colonoscopy was also successful in 93% of patients, and one perforation occurred with this technique after failed OC^[32].

Computed tomographic colonography (CTC) after incomplete OC has a good diagnostic yield and may be advantageous if extra-colonic findings are considered^[33], for example, in the case of tumour. However, CTC detected fewer small polyps than CCE^[24]. Furthermore, radiation-free CCE could additionally be used to visualize the Z-line in 60.8% of patients, as previously reported for PillCamColon1 (60%)^[34]. In the present trial, eight patients had relevant extra-colonic findings, seven of which were presumably not detectable with CTC.

Capsule retention occurred in one patient, corresponding to a retention rate of 1.4%, which was similar to the rate reported for SBCE^[35]. This capsule retention resulted in a new diagnosis of Crohn's disease and was considered to be diagnostic rather than a complication. However, possible retention must also be considered when applying CCE to complement incomplete OC and should be included as part of the informed consent discussion. Although adhesions were supposed to be the cause of incomplete OC in some patients, no related clinical problems or capsule retention following CCE

were observed.

In conclusion, second-generation CCE using low-volume bowel preparations is useful, well tolerated and is able to detect additional relevant lesions. Risk of retention is as low as in SBCE, but must be considered. Similar results were found in the present study between the two protocols for the complementation rate and presence of significant polyps.

Limitations

Patients could choose between preparation protocols for CCE without randomization. The area reached by the colonoscopy was described, but tattooing was only optional. Long-term follow-up was not part of the present study.

ARTICLE HIGHLIGHTS

Research background

Optical colonoscopy (OC) is the gold standard for visualization of the colon. However, it may be incomplete e.g. due to unfavorable anatomy. Colon capsule endoscopy (CCE) is cleared by the US Food and Drug Administration for patients with previously incomplete OC. Second generation CCE has been shown to have a higher sensitivity for detection of colon polyps than first generation. Low volume bowel prep with Moviprep has been shown to be feasible for CCE.

Research motivation

Bowel preparation for CCE is more extensive than for OC. Thus, we aimed to evaluate, if second generation CCE is feasible using either repeated low volume bowel prep or staying on clear liquids following an incomplete OC.

Research objectives

Main research objective was the ability of CCE to visualize those colon segments not reached by incomplete OC. Secondary objectives were additional diagnostic yield of CCE, rate of complete colon visualization by CCE, cleansing levels, and safety.

Research methods

In this prospective multicenter study 81 patients underwent second generation colon capsule endoscopy with PillCamColon2 after incomplete OC. CCE was performed either the following day (protocol A) after staying on clear liquids and 0.75 L Moviprep in the morning or within 30 d after new split-dose Moviprep (protocol B). Boosts consisted of 0.75 L and 0.25 L Moviprep, and phospho-soda as rescue if the capsule was not excreted after 7 hours.

Research results

Seventy-four patients were finally analyzed per protocol. Of those, cleansing was adequate in 67% of cases and CCE could visualize the colonic segments missed by incomplete colonoscopy in 90% (protocol A) and 97% (protocol B, $P = 0.35$, n.s.) of the patients. Detection rates were similar with both protocols: Significant polyps and one adenocarcinoma were detected in 24% of cases. Polyps were found predominantly in the right colon (86%) in segments not reached by OC. Extra-colonic findings as reflux esophagitis, suspected Barrett esophagus, upper GI-bleeding, gastric polyps, gastric erosions, and angiectasias were detected in 8 patients. One capsule (1.4%) was retained in the ileum without symptoms and removed during uneventful resection for unknown Crohn's disease diagnosed as cause of unclear anemia. CCE was well tolerated. One patient suffered from self-limiting vomiting after phospho-soda.

Research conclusions

Second generation CCE using low volume prep is useful to complement incomplete OC, detects additional relevant findings including extra-colonic

lesions, and is well tolerated. CCE is feasible the following day after staying on clear liquids or after new prep within 30 d. Potential risk of capsule retention must be considered.

Research perspectives

Future studies should address improvement of colon cleansing levels and completeness of CCE after incomplete OC. Cost-effectiveness of CCE after incomplete OC should be addressed by future research in comparison with other methods as CT colonoscopy, MR colonoscopy, and device assisted colonoscopy.

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