

Study of the prevalence of helicobacter bilis colonization in pancreaticobiliary disorders

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List disclosures

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Objectives

- This study investigated the prevalence of *H. bilis* colonization of the biliary system of patients with pancreaticobiliary maljunction (PBM).
- Discuss its potential role as a causative factor for biliary carcinoma in PBM

Introduction

Helicobacter bilis, a Gram-negative enterohepatic Helicobacter, has been isolated from bile and liver tissue of mice and shown to be a causative factor of chronic hepatitis and liver tumours in mice.

In recent years, H. bilis DNA has been detected in human bile and hepatobiliary tissue by means of polymerase chain reaction (PCR) assays.

Helicobacter bilis is considered to be a causative factor in the pathogenesis of biliary cancer.

Methods

Bile juice and biliary tissue samples were collected from 17 patients with PBM and 27 controls who had benign biliary disease without PBM.

DNA extracted from each biliary sample was subjected to polymerase chain reaction (PCR) analysis for *H. bilis* and *Helicobacter pylori*.

Standard univariable statistical tests were used to compare categorical and continuous variables between the study groups, as appropriate: χ^2 test, two-tailed Fisher's exact test and Mann–Whitney U test. $P < 0.050$ was considered statistically significant.

Results

PCR assays revealed that 12 of the 17 patients with PBM were positive for *H. bilis* DNA, compared with eight of 27 patients without PBM ($P = 0.009$).

Among patients with PBM, *H. bilis* DNA was identified in six of eight children, including a 2-month-old infant, and in six of nine adults.

The high prevalence of *H. bilis* DNA in the biliary system of patients with PBM was independent of age, sex, common bile duct dilatation, configuration of the pancreatic and bile ducts, and amylase activity in bile.

Table 2 Results of polymerase chain reaction assays for *Helicobacter bilis* and *Helicobacter pylorus* in bile and biliary tissue samples from patients with pancreaticobiliary maljunction and controls

Sample source	PBM (n = 17)			Controls (n = 27)		
	No. of samples examined	No. of positive samples		No. of samples examined	No. of positive samples	
		HB DNA	HP DNA		HB DNA	HP DNA
Bile	17	11*	0	27	6	1
Gallbladder	12	5	1	25	4	2
Bile duct	9	5	1	0	—	—
Total	17	12*	1	27	8	2

PBM, pancreaticobiliary maljunction; HB, *Helicobacter bilis*; HP, *Helicobacter pylori*. * $P < 0.010$ versus controls (two-tailed Fisher's exact test).

Conclusion:

➤The present finding of a high prevalence of biliary colonization with *H. bilis* in adults and children with PBM may point to a role for chronic sustained biliary colonization with *Helicobacter* organisms rendering biliary epithelial cells susceptible to the development of biliary carcinoma later in life.

➤The mechanisms by which *H. bilis* exerts its pathogenetic action on enteric organs are still unknown. *H. bilis* induces progressive immune reactivity to commensal bacteria that contributes to the development of immune-mediated intestinal inflammation .

➤*H. bilis* colonization of the biliary system is extremely common in patients with PBM. This may point to a role in the pathogenesis of biliary cancer

➤Further elucidation of the relationship between biliary carcinogenesis and *H. bilis* infection is required.

References

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