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Impact of Helicobacter pylori Infection on Duodenal Microbial Community Structure and Microbial Metabolic Pathways

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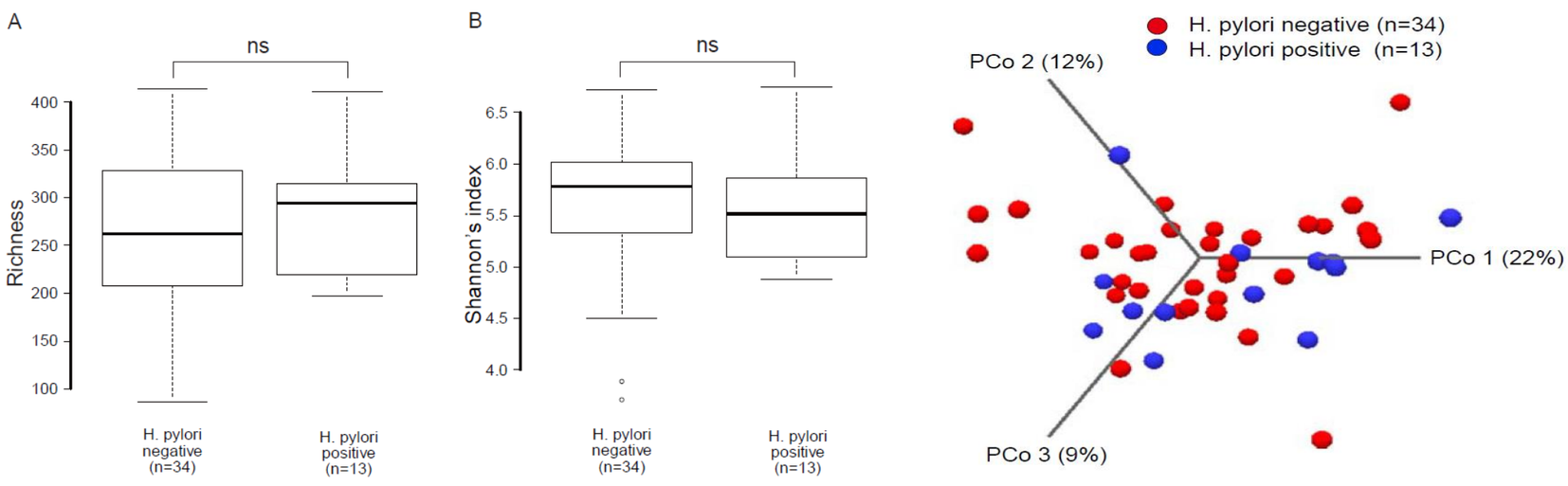
Background
Recent reports suggest that Helicobacter pylori infection may be related to the onset of certain diseases. However, the H. pylori–related factors that play a role in the etiology of these diseases have not been fully elucidated. This study aimed to elucidate the impact of H. pylori infection on the structure of commensal duodenal microbiota and their biofunctions.
Methods
Forty–seven (20 male, 27 female) subjects who underwent gastric cancer screening were enrolled. Duodenal fluid samples were aspirated from the descending duodenum and analyzed by 16S rRNA gene sequencing.
Results
Thirteen subjects were positive for H. pylori, while 34 were negative. We observed 1404 bacterial operational taxonomic units from 23 phyla and 253 genera. In the H. pylori–positive group, we observed higher abundance of Proteobacteria and lower abundance of Actinobacteria and TM7 than that in the H. pylori–negative group. The abundance of 10 genera differed significantly between the H. pylori–positive and –negative groups. Microbiota features in the H. pylori–positive group was significantly influenced by 12 taxa primarily belonging to Gammaproteobacteria. Microbial functional annotation collated using the Kyoto Encyclopedia of Genes and Genomes Orthology database showed that 12 microbial metabolic pathways were significantly affected by H. pylori infection.
Conclusions
H. pylori infection disrupted the normal bacterial communities in the duodenum and changed the biofunctions of the commensal microbiota, primarily by upregulating specific metabolic pathways. This alteration may be related to the onset mechanisms of the diseases suspected of being related to H. pylori infection.

Study outline

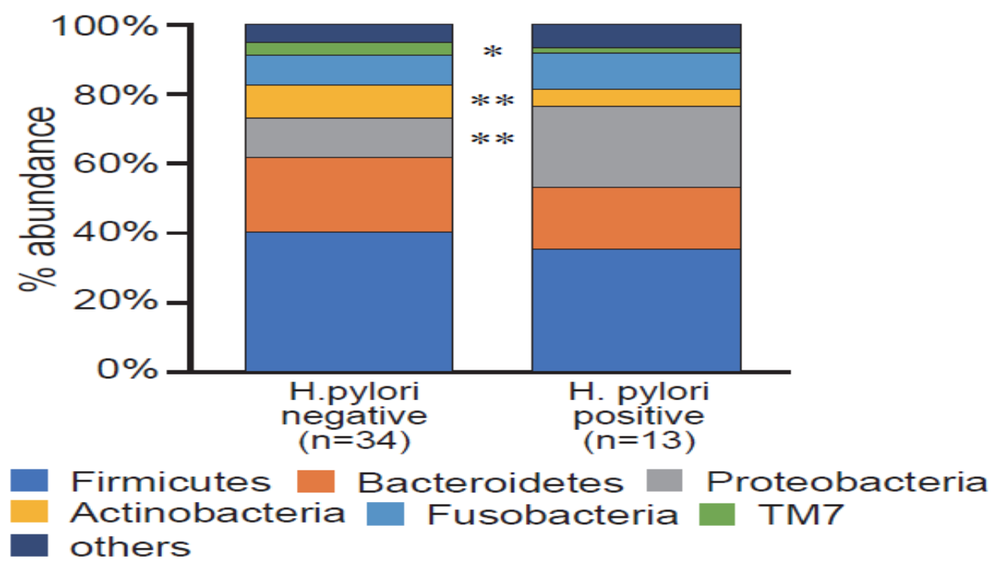
47 subjects
↓
Duodenal fluids collection under endoscopic examination
↓
DNA extraction and 16S rRNA sequence analysis
↙ ↘
H. pylori negative (n=34) *H. pylori* positive (n=13)
↓
Bioinformatics analyses
- ▶α-diversity
- ▶β-diversity
- ▶Bacterial community structures
- ▶LEfSe analysis
- ▶KEGG mapping

Results:



No significant differences in α–diversity or β–diversity were observed between the *H. pylori*–positive and –negative groups.

phylum level bacterial community structures



Actinobacteria and _TM7_ were significantly higher in the _H. pylori_–negative group _Proteobacteria_ was significantly higher in the _H. pylori_–positive

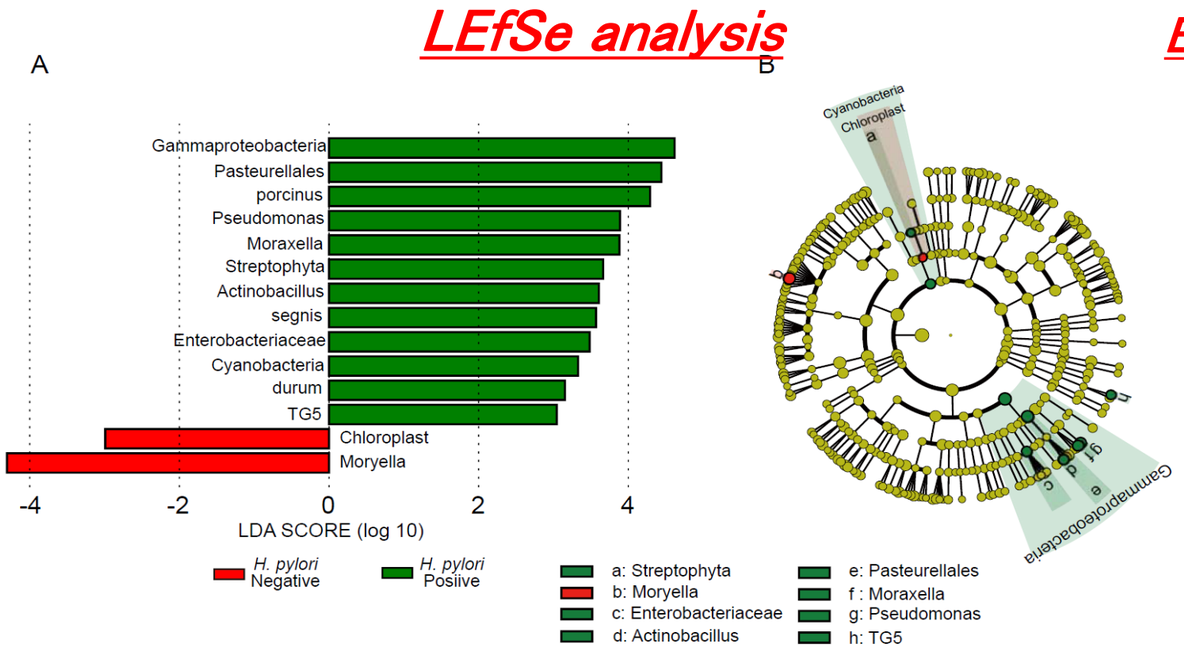
genus level bacterial community structures

Genus	Relative mean % abundance ±SD *H. pylori* negative (n = 34)	*H. pylori* positive (n = 13)	p-value
Neisseria	4.76 ± 5.93	11.74 ± 7.10	<0.01
Rothia	6.83 ± 7.44	1.81 ± 1.36	<0.001
{Unknown Order} TM7-3	2.74 ± 3.54	0.80 ± 0.89	<0.01
Leptotrichia	2.06 ± 1.84	1.18 ± 1.02	<0.05
{Unknown Genus} Lachnospiraceae	0.90 ± 0.84	0.33 ± 0.30	<0.01
Megasphaera	0.72 ± 0.76	0.38 ± 0.33	<0.05
{Unknown Genus} F16	0.49 ± 0.60	0.21 ± 0.23	<0.05
Moryella	0.32 ± 0.39	0.11 ± 0.13	<0.05
Filifactor	0.28 ± 0.45	0.09 ± 0.16	<0.05
Paludibacter	0.04 ± 0.06	0.01 ± 0.02	<0.05

The notation within parentheses indicates the classification level. p values were calculated using Welch's *t*-test.

Significant differences were observed in the relative mean abundance of 10 genera. only the relative abundance of *Neisseria* was significantly higher in the *H. pylori*–positive group

LEfSe analysis



12 taxa significantly influenced in the _H. pylori_–positive. Six of these taxa belonged to the class _Gammaproteobacteria. Gammaproteobacteria._ has the ability to affect the duodenal microbial features

Examination of Duodenal Microbial Biofunctions with KEGG

Class	KEGG pathway (ko number)	Pathway name	ko-abundance (median) *H. pylori* negative (n = 34)	*H. pylori* positive (n = 13)	p-value
M	ko00072*	Synthesis and degradation of ketone bodies	1335885.8	1823878.4	<0.05
M	ko00380*	Tryptophan metabolism	2254680.9	2759405.6	<0.05
M	ko00510	N-glycan biosynthesis	907554.4	700748.0	<0.05
M	ko00565*	Ether lipid metabolism	150966.1	394815.2	<0.001
M	ko00571	Lipoarabinomannan (LAM) biosynthesis	397200.0	191311.5	<0.05
M	ko00591*	Linoleic acid metabolism	85148.3	389478.0	<0.001
M	ko00592*	alpha-Linolenic acid metabolism	132544.9	405656.4	<0.001
M	ko00780*	Biotin metabolism	15103400	19564468	<0.05
M	ko00906*	Carotenoid biosynthesis	129310.3	510048.5	<0.01
M	ko00940*	Phenylpropanoid biosynthesis	348411.2	598460.1	<0.01
M	ko01053	Biosynthesis of siderophore group nonribosomal peptides	2025414.2	1127312.8	<0.01
M	ko01062*	Biosynthesis of terpenoids and steroids	92469.4	428251.7	<0.01

M: metabolism, *: the 9 pathways that were the most abundant in the *H. pylori*-positive group. p-values were calculated using the Mann–Whitney *U* test.

The ko–abundance of 12 of these metabolic pathways differed significantly with and without *H. pylori* infection

Conclusion:

H. pylori infection disrupted the normal bacterial communities in the duodenum and changed the biofunctions of the commensal microbiota. This alteration may be related to the onset mechanisms of the diseases suspected of being related to *H. pylori* infection.

【Conflict of interest : none】