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Study on diversity of nontypeable *Haemophilus influenzae* isolates by antimicrobial susceptibility profile and restriction fragment length polymorphism analysis

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Background: Nontypeable *Haemophilus influenzae* (NTHi) is known to be the causative agent of many chronic diseases such as otitis media, pneumonia, meningitis and sinusitis.

Methods: In this work, a collection of 28 NTHi strains isolated from 12 different origin in Malaysia were examined on their antimicrobial susceptibility profile to 10 antibiotics using the disk-diffusion method. These strains were also analysed to determine for genotypic differences using a cost-effective typing method i.e. restriction fragment length polymorphisms (RFLP). In the RFLP analysis, all of the isolates were amplified by using 16S primers and digested with six restriction enzymes, namely *EcoRI*, *HindIII*, *Hsp92I*, *BamHI*, *HaeIII* and *Hin1II*.

Results: Antimicrobial susceptibility test showed that 33% of the isolates were resistant to two or more of the tested antimicrobials. NTHi isolates demonstrated resistance most frequently to ampicillin (43.75%), trimethoprim-sulfamethoxazole (31.25%) and 6.25% each to tetracycline, streptomycin and rifampicin. With the exception of *Hin1II*, the results of the digestion with the other five restriction enzymes were not reproducible and thus, the results were excluded. Digestion with *Hin1II* produced between two to three fragments in each isolate. The DNA fragments of 50–200 bp size could be clearly resolved into two RFLP patterns among the 28 isolates. It was observed that the isolates fell into two clusters with genetic distances of >60% similarity. There were seven branches at F-value of ≥ 0.9 , representing at a genetic distance of more than 90% similarity of which these branches can be referred to as clonal groups. This study demonstrated that 27 of 28 (96.4%) NTHi strains that were isolated from 12 distant locations had 100% similarity in their RFLP patterns. Few loci were detected and various other combinations of restriction enzymes for typing of NTHi would be required.

Conclusion: This study showed the occurrence of antimicrobial resistance amongst NTHi isolated in Malaysia and although they were geographical-distantly isolated, they are genetically related.

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The role of *Helicobacter pylori* and histopathological findings in patients with dyspepsia

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Background: *Helicobacter pylori* (*H. pylori*) is a major gastro-duodenal pathogen which is etiologically related to duodenal and gastric diseases. Although *H. pylori* infection has been showed to be more common in patients with dyspepsia, but it should be treated in dyspepsia are still controversial. The aim of this study was to compare the histopathological changes in *Helicobacter pylori* positive and negative patients with dyspepsia.

Methods: In a cross-sectional study, a total of 107 patients with upper GI symptoms, dyspepsia, were enrolled. All patients underwent upper GI endoscopy with biopsy specimens being collected from gastric mucosa. *H. pylori* was evaluated in each patient by rapid urease test, histopathology and antibody against *H. pylori* with using a validated ELISA kit. The histopathological changes in *Helicobacter pylori* positive and negative patients with dyspepsia were compared. All of the cases were evaluated according to the Sydney classification

Results: From 107 patients with dyspepsia with a mean age of 42.68 ± 17.35 years (16–81 years), 55 (51.4%) were male. In addition, 73 (68.2%) and 34 (31.8%) of the patients were *H. pylori* positive and negative, respectively. There was no significant difference between *H. pylori* positive and negative patients with respect to age or gender ($p > 0.05$). The most common upper GI symptom among *H. pylori* positive and negative cases was epigastric pain (89% and 76.5%, respectively). There was no significant difference between *H. pylori* positive and negative groups with respect to endoscopic findings ($p = 0.887$). However, there was a statistically significant association between histopathologic findings and *H. pylori* intensity according to the Sydney classification in *H. pylori* positive patients ($p < 0.001$). In the *H. pylori* positive and negative cases, chronic gastritis was the most common histopathologic finding with the rate of 72.6% and 44.1%, respectively. A statistically significant relationship between *H. pylori* and histopathologic findings in the patients with dyspepsia was determined ($p < 0.001$).

Conclusion: According to the results, the role of *H. pylori* in the pathogenesis and histopathologic changes of dyspepsia patients is important. Therefore, *H. pylori* eradication treatment should be recommended in patients with dyspepsia.

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