60% of strains), Ampiciline, Tetracycline, Erythromycin and Cephalotine.

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52.002

Detection and molecular characterization of verotoxin gene in non-O157 diarrheagenic *Escherichia coli* isolated from Miri hospital, Sarawak, Malaysia

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**Background:** Non-O157 diarrheagenic *Escherichia coli* are typical *Escherichia coli*. Infections with non-O157 *Escherichia coli* are now increasingly recognized in many countries. The virulence profiles of most of the non-O157 *E. coli* are unknown. Therefore, easy detection, isolation, and characterization of non-O157 *Escherichia coli* isolates are essential for improving our knowledge of these organisms.

**Methods:** A total of 32 non-O157 diarrheagenic *Escherichia coli* isolated (Miri hospital, Sarawak, Malaysia, 2001) from the patients with diarrhea were examined for the detection of verotoxin (VT) gene. For this purpose, two sets of primers (VT1 and VT2) were used for PCR method. VT1 probe was prepared which was used for the Southern hybridization study. Bacteriophage induction was carried out using mitomycin C. Nucleotide sequencing was made from the VT1 gene fragment isolated from an *E. coli* isolates using PCR protocol.

**Results:** The PCR protocol used here produced a fragment of 348 bp of VT1 gene and 584 bp of VT2 gene, respectively. It was shown that 13 *E. coli* isolates (40%) carried VT1 gene whereas none was found to carry VT2 gene using PCR protocols. Plasmids were detected in all the VT1-positive isolates. From the Southern hybridization study, VT1 probe showed homology with the chromosome of all 13 VT1-positive isolates indicating the VT1 gene to be located on chromosome. Bacteriophage induction as carried out using mitomycin C showed that none of the VT1-positive isolates harbor any lysogenic bacteriophage. However, nucleotide sequencing made from the VT1 gene fragment isolated from an *E. coli* isolates using PCR protocol showed 97% homology with the known VT1 gene which proves to be the similar gene carried by *E. coli* O157 and other ancestors.

**Conclusion:** The PCR method used here was sensitive, specific and reliable. VT1 was found to be the most common verotoxin among the *E. coli* strains isolated from clinical sources in Malaysia and this VT1 gene is located in the chromosome of the *E. coli* isolates. This study improves the knowledge of a highly significant emerging pathogen non-O157 *E. coli*.


52.003

Isolation and characteristic distribution pattern of *cagA* + *Helicobacter pylori* in dental plaque of dyspeptic patients

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**Background:** *Helicobacter pylori* is one of the most common human pathogens which colonize in stomach. Recently the oral cavity has been proposed as a reservoir for *H. pylori* but not much evidence from the presence of *cagA* + *H. pylori* in dental plaque is available. The aim of this study was to investigate the possibility of isolation of *cagA* + *H. pylori* in dental plaque of dyspeptic patients and to study the distribution pattern of *cagA* + *H. pylori* in different areas of oral cavity.

**Methods:** One hundred (100) patients with dyspepsia, attending the routine endoscopy were examined and samples from sub gingival plaque of molar and incisor areas of patients were taken, placed in suitable transport media and immediately sent to lab before 4 h. All samples cultured on modified brucella blood agar and all the susceptible colonies were tested by urease, catalase, oxidase and gram stains. Also after DNA extraction process, two sets of primers, highly specific for *ureC* and *cagA* were used for PCR.

**Results:** *H. pylori* was detected in dental plaque samples of 40 (40%) of patients by culture on enriched brucella agar media, 100% of these samples were positive by PCR of *ureC* gene and 25 samples (62.5%) were also positive for *cagA* gene. Results of PCR for *ureC* gene on different areas of dental plaque, also showed that sub gingival plaque of molar areas had the most microbial load of *H. pylori* (73%, 29 cases) in comparison of incisor sites (27%, 10 cases).

**Conclusion:** According to our findings, it's estimated that dental plaque, especially sub gingival plaque of molar areas, can be a suitable reservoir for *H. pylori*. Being out of reach of oxygen and difficult access of this site for cleaning tools of oral cavity can confirm this thesis. Also it was shown in this study that *cagA* + *H. pylori* can be isolated from dental plaque of dyspeptic patients, so maybe *H. pylori* can be transmitted by oral route and oral cavity may act as a good source of keeping and re-infecting of stomach of dyspeptic patients after antibiotic therapy.