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Assessing prevalence and risk factors of *Helicobacter pylori* infection in the Northwest region of Cameroon

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Pelicobacter pylori remains a public health problem and a major cause of peptic ulcer disease and gastric, with a prevalence of about 70% in developing countries. This study was carried out in Tubah District Hospital in the Northwest region to assess the prevalence and risk factors associated to *H. pylori* from March to August 2014 with ethical clearance from the institutional ethical board. 400 subjects between 16-73 years were recruited. An open ended questionnaire was administered to capture information on socio-demographic data, risk factors and knowledge. Blood samples were collected and tested for the presence of the parasite using the Pylori test strip. The prevalence of *H. pylori* in the study population was 240 (60%). There was a significant difference p<0.05 in the prevalence of *H. pylori* among the age group, gender, occupation, educational level, monthly income and number of occupants in a house. The highest prevalence 112 (82.2%), 186 (75.0%), 160 (66.6%), 96 (40%), 152 (63.3%) and 166 (69.2%) was seen in the age group >34 years, female, students, those who attained primary education, monthly income <50,000 frs CFA and >10 occupant in a house, respectively. The higher proportion 160 (61%) had poor knowledge about the disease (p=0.02). A multivariate analysis showed a positive correlation between sex, age, number of house occupant, knowledge, monthly income and occupation and the prevalence of *H. pylori*. Although there was no significant difference between the different treatment options most subjects 224 (56%) prefer traditional herbs. Data from this study showed that gender, age, number of house occupant, knowledge, monthly income and occupation are risk factors of *H. pylori*.

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Co-circulation of Echovirus 6 and 30 with Coxsackievirus A6 in an outbreak of hand, foot and mouth disease in Ahvaz, Southwest of Iran

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The aim of this study is to evaluate the etiologic agents of hand, foot and mouth disease (HFMD) outbreak in Ahvaz, Southwest of Iran and their evolutionary analysis by phylogenetic construction and simplot analysis. Sixteen (16) serum samples were collected in an outbreak of HFMD in Ahvaz in October 2013. The RNA were extracted from these samples and subjected to reverse transcription polymerase chain reaction for detection of enterovirus group A and B. Positive cases were sequenced and subjected to phylogenetic and simplot analysis for detecting signs of recombination. Among the 16 specimens, 9 (56.25%) were PCR positive with the universal primers for enterovirus 5'UTR region. Coxsackievirus A6 was detected as a predominant agent of HFMD with two cases of echovirus 6 and 30 by VP3-VP1 and VP1-2A regions sequencing. In case of echovirus 6, signs of recombination in 5'UTR region were observed based on phylogenetic and simplot analysis of 5'UTR and VP1 regions. In conclusion, Coxsackievirus A6 is the main agent of HFMD in Ahvaz. Evidence of recombination of echovirus 6 in this study illustrates the importance of enhancing common hygiene as well as sanitation to prevent the circulation of this strain in community and advent of new strains.

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