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Risk factors of norovirus infection and the spatiotemporal dynamics of GII.4 strain replacement in Ho Chi Minh City, Vietnam

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Background: Noroviruses are a major cause of acute gastroenteritis globally, yet is under-investigated in industrializing countries where routine identification of any diarrheal pathogens is seldom performed. We aimed to study the risk factors of NoV infections and the spatiotemporal dynamics of NoV strain and phylogenetic distribution in children in Ho Chi Minh City, Vietnam.

Methods: We observed the clinical features of NoV cases, and compared socio-economic, demographic and behavioral characteristics to identify potential risk factors of NoV infections using multivariate analysis. All identified NoV strains were assigned a genotype based on DNA sequences. The genetic evolution was estimated using Bayesian MCMC model implemented in BEAST. Information on the age of infected participants, the date of enrolment, the NoV genetic distances, and the geographical distances (based on participants' residential GPS locations) were used for Mantel's Test, K-means clustering and saTScan analyses to investigate the relative dynamics of strain distribution and GII.4 variant replacement in this location.

Results: Most NoV cases exhibited classical acute watery diarrhea with vomiting and low-grade fever, and a substantial proportion of patients were treated with antimicrobials (35.5%) or probiotics (70.8%). The risk factor analysis demonstrated that NoV infections are highly associated with contaminated food and water and likely transmitted within the household via direct person-to-person transmission. We showed the novel emergence of NoV GII.4-2010 (New Orleans) variant in Vietnam and in Asia, and at the same time that this variant emerged in Belgium, suggesting a novel and concurrent introduction of this strain. Coupled with this emergence was the displacement of the former-dominating GII.4-2006b (Minerva) variant by this novel emergent. The phylogenetic analysis showed GII.4-2010 strains in our study were clustered with GII.4-2010 found in Belgium and US and distant to former GII.4 variants. The evolutionary rate was 7.192×10^{-3} substitutions/site/year for GII.4 strains. The Mantel's, K-means and saTScan showed spatiotemporal clustering of patients infected with GII.4-2010 compared with patients infected with GII.4-2006b in this location.

Conclusion: We confirm that NoV infection is endemic in Ho Chi Minh City and report the novel emergence of NoV GII.4-2010 (New Orleans) variant.

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Association between human papillomavirus infection and oral squamous cell carcinoma

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Background: Oral squamous cell carcinoma (OSCC) is the eighth most common cancer worldwide. The incidence of OSCC remains high and associated with many deaths in Asian countries such as in India and Taiwan. The development of OSCC is associated with lifestyle of people and risk factors including betel quid, smoking and alcohol consumption. In Asian countries, betel quid is a considerable risk of OSCC cases. Although smoking and alcohol consumption are independent risk factors, they have a synergistic effect and increase risk together. Many persons are not exposed to these risk factors but have OSCC. Therefore, other factors may play role in OSCC progression. Recently, human papillomavirus (HPV) also has been reported to be a risk factor of OSCC. However, the role of HPV infection in OSCC is not understood. Several studies have been reported that the prevalence of HPV infection in OSCC is 20-60% depending on the detection methods. The aim of this study is to determine the prevalence of HPV infection in OSCC cases and normal control. To test the hypothesis that HPV infection is associated with OSCC.

Methods: Oral cells were obtained from 91 OSCC cases consisted of cancer site at lip, oral tongue, base of tongue, gum, floor of mouth, palate, retromolar trigone, tonsil, oropharynx, buccal mucosa and 100 normal controls. The DNA extracted from oral cells was detected for HPV DNA by polymerase chain reaction (PCR) using L1 consensus primers and beta-globin gene as the control.

Results: The results showed that HPV infection in OSCC was higher than normal control with statistical significance and the HPV prevalence was 51.6% (47/91) and 14% (14/100) of OSCC cases and normal controls, respectively. HPV infection was found in OSCC case with lesion site at lip (58.3%), oral tongue (38.1%), base of tongue (80%), gum (33.3%), floor of mouth (66.6%), retromolar trigone (50%), tonsil (33.3%) and buccal mucosa (33.3%).

Conclusion: This study suggested an association of HPV with OSCC, especially in base of tongue cancer. The molecular analysis of HPV associated OSCC development should be further evaluated.

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