

Dissemination reports are concise informative reports of health-related research supported by funds administered by the Food and Health Bureau, namely the *Research Fund for the Control of Infectious Diseases*, the *Health and Health Services Research Fund*, the *Health Care and Promotion Fund* and the *Health Services Research Fund*. In this edition, 12 dissemination reports of funded projects related to gastrointestinal diseases and respiratory infectious diseases are presented. Three of the reports are highlighted, owing to their potentially significant findings, impact on health care delivery and practice, and/or contribution to health policy formulation in Hong Kong.

Human noroviruses (hNoVs) are the leading cause of viral gastroenteritis around the world. Knowledge of the prevalent viral genotypes responsible for sporadic cases and larger outbreaks would be an important epidemiological tool in helping to control its spread. Three major hNoV databases currently exist. However, two are not publicly accessible and the third mainly reports cases occurring in the United Kingdom. Leung et al<sup>1</sup> set out to address this deficiency by creating a publicly accessible norovirus database containing the complete genomes of 31 norovirus isolates obtained from cases in Hong Kong. NoroBase is hosted by the Chinese University of Hong Kong. Users can submit query nucleotide sequences and conduct sequence similarity searches. Currently 80 complete and partial genome sequences have been uploaded. It is hoped that virus genotyping via homology search against NoroBase may benefit local epidemiologists and public health professionals in their studies of the epidemiologic pattern of hNoV infections in Hong Kong and in the identification of aetiologic agents in acute gastroenteritis outbreaks.

During the SARS outbreak in Hong Kong in 2003, many individuals were exposed to the SARS-coronavirus (SARS-CoV) but not all of them became infected. Susceptibility and resistance to infection depends in part on host genetic factors. Two studies in this supplement revealed more about the immunogenetics of SARS infection. Ng et al<sup>2</sup> looked at the differential activation of T cells following exposure to SARS-CoV. A significantly higher frequency of HLA allele DRB4\*01010101 was found in the SARS-susceptible than in the SARS-resistant group. In contrast, significantly higher frequencies of HLA-B\*1502 and HLADRB3\*030101 were found in the SARS-resistant than in the SARS-susceptible group. However, none of these associations was significant after statistical correction. These findings do not suggest a strong involvement of HLA with genetic susceptibility to SARS based on the HLA genes studied.

Chan et al<sup>3</sup> examined the potential involvement of the cell adhesion molecule and pathogen recognition receptor, DC-SIGN, as a facilitator of SARS-CoV infection. The investigators hypothesised that particular single nucleotide polymorphisms in the DC-SIGN promoter region may be associated with the severity of SARS-CoV infection. They found that the SNP-336A/G is associated with the levels of serum lactate dehydrogenase on admission, which is an independent prognostic indicator for the severity of SARS. This functional SNP affects the promoter activity of DC-SIGN and may alter gene expression and hence host immune response. In both studies, further evaluation is needed to determine the validity and clinical relevance of their findings.

We hope you will enjoy this selection of research dissemination reports. Electronic copies can be downloaded from the Research Fund Secretariat website (<http://www.fhb.gov.hk/grants>). Researchers interested in the funds administered by the Food and Health Bureau may also visit the website for detailed information about application procedures.


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## References

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