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Diversity of Coronaviruses in Bats: Insights Into Origin of SARS Coronavirus

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Background: Although the finding of SARS coronavirus (SARS-CoV) in caged palm civets suggested that wild animals are the origin of SARS-CoV, subsequent studies suggested that civet may have served only as an amplification host. In 2005, we identified a coronavirus closely related to SARS-CoV (bat-SARS-CoV) in Chinese horseshoe bats. However, it remains to be determined if bat-SARS-CoV or other coronaviruses in bats are the direct progenitor of SARS-CoV.

Methods: To understand the diversity and evolution of coronaviruses in bats, a 2-year surveillance study for coronaviruses was conducted in bats from various rural areas in Hong Kong. As coronaviruses are known to have high recombination frequency, the genomes of the identified novel coronaviruses were also sequenced and analyzed to determine possible recombination events responsible for interspecies transmission.

Results: Among 1389 bats of 16 species from 24 different locations, coronaviruses were identified from anal swabs of 132 (9.5%) bats by RT-PCR. Phylogenetic analysis revealed at least seven novel coronaviruses from seven different bat species, in addition to bat-SARS-CoV. Five of them belonged to group 1 coronaviruses while two belonged to group 2 coronaviruses. Besides bat-SARS-CoV, Chinese horseshoe bats were found to harbor another novel group 1 coronavirus. The genome of this virus represents the smallest coronavirus genome and possessed a unique spike protein evolutionarily distinct from the rest of the genome and containing a 15-amino acid peptide homologous to a corresponding peptide within the RBM of spike protein of SARS-CoV, suggesting a common evolutionary origin in the spike protein of this group 1 bat coronavirus, bat-SARS-CoV, and SARS-CoV.

Conclusion: Bats are important reservoir for a huge diversity of coronaviruses, including SARS-CoV-like viruses. The finding of another group 1 coronavirus in Chinese horseshoe bats with a homologous peptide to SARS-CoV warrants further investigations on the origin of the SARS-CoV spike protein.

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Analysis of Putative Virulence Factors in *Enterococcus faecium* Isolated from Different Sources in IranS. Jahangiri^{1,*}, M. Talebi¹, G. Eslami², M.R. Pourshafie¹¹ Pasteur Institute of Iran, Tehran, Iran (Islamic Republic of)² Shaheed Beheshti Medical University, Tehran, Iran (Islamic Republic of)

Background: Enterococci have emerged as a leading cause of nosocomial infections. The potential virulence factors include a cytolytic toxin, gelatinase, an aggregation substance, the enterococcal surface protein (Esp) and

hyaluronidase. Our knowledge about the contribution of these virulence factors to the pathogenesis of enterococcal infections is still limited.

Methods: A total of 98 strains containing, 49 clinical Vancomycin-resistant *Enterococcus faecium* (cl-VREFm) and 49 environmental VREFm (en-VREFm), were included in this study. The phenotypical characterization was performed by their abilities to adhere to Vero cell line and to associate their phenotypes with the presence of known virulence genes detected within their genomes by PCR. The following genes were amplified by PCR: asa1 (aggregation substance), cyl A, B, M (cytolysin), hyl (hyaluronidase), gelE (gelatinase) and esp (enterococcal surface protein). The transferability of esp gene were examined by filter mating tests. The strains were typed by Pulsed-field gel electrophoresis.

Results: The genes that encode cytolysin and aggregation substance was never detected in isolates, whereas gelE and esp genes was detected in both clinical and environmental strains and hyl gene was only detected in clinical isolates (28%). The following data were obtained in this study: 81% of cl-VREFm and 80% of en-VREFm isolates were positive for esp gene, the gelE gene was detected in all of clinical and 47% of environmental isolates. Strong adhesion was observed only in clinical strains. None of the esp genes were transferable by conjugation tests. According to PFGE results the isolates were heterogeneous.

Conclusion: Environmental isolates were equipped with fewer virulence factors than clinical isolates and presence of virulence factors in environmental isolates demonstrates that they can be potentially virulent for human. There was a correlation between PCR and phenotypic tests in clinical strains. Phenotypic testing revealed the existence of apparently silent gelE and esp genes among environmental strains.

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14.007

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CHIKV is an emerging arbovirus and is an important human pathogen that causes a syndrome characterized by fever, headache, rash, nausea, vomiting, myalgia, arthralgia and occasionally neurological manifestations such as acute limb weakness. It is also associated with a fatal haemorrhagic condition. CHIKV is geographically distributed from Africa through Southeast Asia and South America, and its transmission to humans is mainly through *Aedes* species mosquitoes. The frequency of recent epidemics in the Indian Ocean islands suggests that something else was carrying the virus, as *Aedes aegypti* are not found there. In fact, the relative Asian tiger mosquito, *Aedes albopictus*, was present and has raised concern in the world health community regarding the