O04: Comparative Genomics Reveals the Improved Environmental Fitness and Increased infectivity of a Malaysian Vibrio cholerae O1 Altered El Tor Strain

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Vibrio cholerae O1 altered El Tor strains have been detected in Asian countries and responsible for major outbreaks in Thailand, Vietnam and Malaysia. In Malaysia, outbreaks that occurred in the state of Kelantan and Terengganu from September – December 2009 were caused by altered El Tor strains. In the present study, the genome content of an outbreak-associated V. cholerae O1 altered El Tor strain (VC1761/09) was investigated and comparative genomic analysis was carried out on this particular strain and eight O1 V. cholerae strains. The Malaysian O1 V. cholerae draft genome was 4,012,991 bp in size and carried 3701 genes. Among the eight compared genomes, 2834 homologous genes were identified. A phylogenetic tree based on the homologous genes revealed that VC1761/09 was more closely related to an O1 altered El Tor strain isolated during 2010 outbreak in Haiti with 2951 genes that were 100% similar. Compared to another altered El Tor strain, MJ1236, the numbers of 100% homologous genes were only 2923. In addition to the genes inheriting from 7th pandemic El Tor that promote environmental fitness, VC1761/09 also demonstrated greater infectivity due to the retention of virulence traits of the Classical O1. However, the Malaysian O1 V. cholerae strain could be distinguished from the El Tor and Classical strains based on a truncated V. cholerae seventh pandemic island II (VSP II), properties in CTX prophage and the presence of mobile genetic elements. Similar to those O1 altered El Tor variants, VC1761/09 contained a 98 kb ICE-like element that harboured antibiotic resistance clusters and belonging to the SXT/R391 family. The unique characteristics of the VC1761/09 genome provided the bacterium with a competitive ecological dominance with greater infectivity. Without further preamble, this explained the wide dispersal of the infection in Malaysia within four months duration in 2009.

Molecular Biology

MB01: PCR Detection of Virulence Genes in Yersinia Enterocolitica from Foods and Pigs

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Yersinia enterocolitica is a food-borne pathogen that causes gastroenteritis in humans. Yersiniosis is often misdiagnosed as appendicitis, as similar symptoms such as diarrhea, fever and lower right abdominal pain are present in both diseases. The carriage of virulence genes in Y. enterocolitica plays an important role in infections. The aim of this study was to investigate the prevalence of virulence genes in Y. enterocolitica isolates from foods and pigs in Malaysia. Thirty-three Y. enterocolitica isolates were PCR-screened for 16 virulence genes (chromosomal- or plasmid-borne) that are involved in the production of invasin, adhesin, transcriptional activator, fimbriae, enterotoxin, enterochelin receptor protein, enterochelin ABC transporter, enterochelin esterase, insecticidal toxin complex-like protein, Yersinia modulator, subtilisin/kexin-like protease, streptograminacetyltransferase, or proteins for auto agglutination and serum resistance. The positive rates of virulence genes