３・３　誌上発表論文抄録

Multiplex PCR assay for identification of three major pathogenic Vibrio spp., Vibrio cholerae, Vibrio parahaemolyticus, and Vibrio vulnificus

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A multiplex PCR assay was developed based on atpA-sequence diversification for molecular identification of 3 major pathogenic Vibrio species: Vibrio cholerae, Vibrio parahaemolyticus, and Vibrio vulnificus. It specifically identified them from among 133 strains of various Vibrio species and other genera, and was applicable for testing seawater, suggesting its usefulness

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Human sapovirus classification based on entire capsid nucleotide sequences

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The genetically diverse sapoviruses (SaVs) are a significant cause of acute human gastroenteritis. Human SaV surveillance is becoming more critical, and a better understanding of the diversity and distribution of the viral genotypes is needed. In this study, we analyzed 106 complete human SaV capsid nucleotide sequences to provide a better understanding of their diversity. Based on those results, we propose a novel standardized classification scheme that meets the requirements of the International Calicivirus Scientific Committee. We believe the classification scheme and strains described here will be of value for the molecular characterization and classification of newly detected SaV genotypes and for comparing data worldwide.

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Identification and characterization of the short variable region of the Japanese encephalitis virus 3′NTR

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Since the 1980s, the Japanese encephalitis virus (JEV) variants with slightly short variable regions (VR) of the 3' non-translated region (NTR) have been found; however, the implications of these short VR remain unclear. We recently identified two novel types of short VR (5 and 9 nt shorter than that of major group of genotype I JEV strains) of genotype I JEV isolates. To elucidate the impact of these short VR on the replication and virulence of JEV, we generated five recombinant JEV viruses: M41-d5 and M41-d9 have deletions in the VR that correspond to those observed in some recent JEV isolates, M41-d5d9 has both the 5- and 9-nt deletions in the VR, M41-d27 has a large deletion that encompasses both the 5- and 9-nt deletion regions, and M41-a13 has a 13-nt sequence insertion of the genotype III JEV strain Beijing-1 into the parent genotype I JEV strain Mie/41/2002 genome.

The recombinant viruses and the parent virus, except for the M41-d27 mutant, showed similar growth properties in mammalian and mosquito cell lines. Mouse challenge experiments indicated that no significant differences among the recombinant viruses M41-d5d9, M41-d27, M41-a13, and the parent virus. Our results suggest that the short VR in JEV 3' NTR do not affect its growth in vitro or its pathogenicity in mice.

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Determination of Histamine in Seafood by Hydrophilic Interaction Chromatography/Tandem Mass Spectrometry

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A simple method was developed to determine histamine, an important compound in chemical food poisoning, by extraction followed by hydrophilic interaction chromatography-tandem mass spectrometry using a hydrophilic column with sulfobetaine-type zwitterion groups. The quantitation range in seafood products was from 0.4 to 200 mg kg^{-1} for 5 g food samples. Quantitative recoveries were obtained with four types of seafood product. These results agreed well with those from the more complex, conventional HPLC method, which requires sample derivatization with dansyl chloride.

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