ETIOLOGY, PATHOGENESIS AND EPIDEMIOLOGY OF PRRS IN THASIAN PACIFIC REGION

Michihiro Takagi

Virus Disease and Epidemiology Research Division, National Institute of Animal Health, NARO, Tsukuba, Ibaraki, Japan

ABSTRACT

Porcine reproductive and respiratory syndrome (PRRS) causes reproductive failure in sows and respiratory disorder in piglets and growing pigs, and is one of the most economically significant swine diseases in pig production countries. PRRS virus (PRRSV) causing this disease is classified in the order Nidovirales, family Arteriviridae, genus Arterivirus, and is a small and enveloped virus with a single-stranded positive-sense RNA genome of approximately 15 kb in length. As for PRRSV, type 1 (European type) and type 2 (North American type) genotypes are classified by approximately 60% nucleotide identity at genetically level. The genome of PRRSV contains at least ten open reading frames (ORFs). ORF5 encoding envelope protein is mainly used for phylogenetic analyses of PRRSV isolates because of its high variability among viruses of same genotype. In addition, non-structural protein 2 also represents the genetically variable region of PRRSV genome. In 2006, a disease called “porcine high fever syndrome” emerged in China. The disease was characterized by high fever of above 41 °C, abortion in sows and high mortality in all age group. This disease caused by an atypical highly virulent strain of PRRSV, deleted 30 amino acids in nsp2 region, is called “highly pathogenic PRRS (HP-PRRS)”. HP-PRRS has spread in Southeast Asian countries since 2007 and it has cause severe damage to the pig production in this region. However, the virulence and pathogenicity of typical- and HP-PRRSV has not been clarified. In this workshop, the presentation will discuss the pathogenicity of typical- and HP-PRRSV and currently situation of PRRS in the Asia Pacific region.