Emergence of a Novel Subgroup Among the Isolates of North American Genotype Porcine Reproductive and Respiratory Syndrome Virus in China

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Abstract

Deng et al. published “Complete genome sequence of porcine reproductive and respiratory syndrome virus strain QY2010 reveals a novel subgroup emerging in China” and Lu et al. published “Complete genome sequence of a novel variant porcine reproductive and respiratory syndrome virus (PRRSV) strain: evidence for recombination between vaccine and wild-type PRRSV strains” in The Journal of Virology in 2012. In the above studies, two emerging PRRSV strains, QY2010 and GM2, were identified. Based on sequence analysis, both of them had similar genome characterization for classic North American (NA) genotype PRRSV, but they were different from classic NA PRRSV (Subgroup 1, 2, 3) and highly pathogenic NA PRRSV (Subgroup 4). So, herein, QY2010 and GM2, should be divided into a new subgroup (Tentatively named as subgroup 5). The emergence of subgroup 5 made us understand more knowledge about molecular epidemiology and genetic diversity of PRRSV.

Keywords: Porcine reproductive and respiratory syndrome virus, North American genotype, Novel subgroup, China

Porcine reproductive and respiratory syndrome virus (PRRSV), a positive-strand RNA virus belonging to the family Arteriviridae, is a pathogen economically important to the world swine industries. At present, according to genetical and antigenic differences, PRRSVs were divided into two genotypes, European (EU) genotype (genotype Ι) and North American (NA) genotype (genotype Π) [2, 3]. In China, since the first report in 1996, it caused huge economic losses for Chinese swine industries. It is worth mentioning that QY2010 and GM2 had longer Nsp2 genes (3, 042 nucleotides) than other NA PRRSV isolates (varied from 2, 418 nucleotides to 2, 940 nucleotides). In Nsp2 region, they not only retained non-1+29 aa deletion for classic NA PRRSV, but also possessed 36 aa insertion in the downstream of 1+29 aa deletion region. Moreover, the phylogenetic tree was constructed based on their complete genome sequences using DNASTar 5.0 software (DNASTar Inc.). QY2010 and GM2 were clustered into the same branch (Figure 1). According to the subgroup definition in previous studies, they did not belong to four known subgroups. Therefore, herein, they should be divided into a new subgroup (Tentatively named as subgroup 5).

In summary, a novel subgroup (subgroup 5) emerged among the isolates of NA PRRSV in China. The isolate of QY2010, a member of the novel subgroup, was identified as a highly pathogenic PRRSV strain through animal experiments, which might be one cause of pig diseases clinically. At present questions remain such as where did they come from? How to control them? Whether did cross-protection exist with other classic vaccine strains? Up to now, we did not get more knowledge of the above issues. It is known that Nsp2 is highly variable region, notably,
both QY2010 and GM2 had longer sequences than others, which suggested that PRRSV had genetic diversity in genome level. Therefore, their emergence made us understand more knowledge about molecular epidemiology, pathogenicity and genetic diversity of PRRSV.

References