Journal of Animal and Veterinary Advances 12 (11): 1055-1058, 2013
ISSN: 1680-5593

Phylogenetic Analysis of Porcine Circovirus Type 2 Isolated in South China

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Abstract: Porcine Circovirus type 2 (PCV2) is one of the most important swine pathogens of economic importance. To understand the genetic diversity of Porcine Circovirus type 2 (PCV2) in South China, 49 PCV2 sequences from South China were compared to 58 other references sequences. Researchers found that the nucleotide similarity among all South China isolates ranged from 93.7-100%. Most of them were classified into PCV2b-1A/1B cluster but the rest mapped to clusters PCV2b-1C, PCV2a-2E or PCV2a-2F. The data contribute to the understanding of molecular variation of PCV2 in South China.

Key words: Porcine circovirus type 2, phylogenetic analysis, sequence, data, South China

INTRODUCTION

Porcine Circovirus type 2 (PCV2) is the causative agent for Postweaning Multisystemic Wasting Syndrome (PMWS) in weaned piglets which is an economically important diseases affecting the swine worldwide (An *et al*., 2007). Besides PMWS, PCV2 infection has been linked with Porcine Dermatitis and Nephropathy Syndrome (PDNS), Porcine Respiratory Disease Complex (PRDC), reproductive failure, granulomatous enteritis, necrotizing lymphadenitis, exudative epidermitis and congenital tremors (Kim and Chae, 2004; O'Connor *et al*., 2001). PCV2 isolates can be divided into three main genotypes (PCV2a, PCV2b and PCV2c) based on their sequences. PCV2a was further subdivided into six clusters (2A-2F) (Cai *et al*., 2012; Olvera *et al*., 2007) and PCV2b was subdivided into two clusters (1A/1B and 1C) (An *et al*., 2007; Olvera *et al*., 2007). PCV2c was only found in Denmark (Segales *et al*., 2008). In this study, researchers aimed performed a phylogenetic analysis of ORF5 to understand the molecular variation of PCV2 infection in South China.

MATERIALS AND METHODS

To understand the genetic diversity of Porcine Circovirus type 2 (PCV2) in South China, 49 PCV2 sequences from South China and 58 other references sequences were analysed.

Sequences were analyzed using a previously described method (Olvera *et al*., 2007; Huang *et al*., 2012; Wei *et al*., 2013). Briefly, all *ORF5* gene sequences were compiled and edited using the Lasergene sequence Analysis Software package (DNASTAR Inc., Madison, WI). Multiple sequence alignment was carried out using Clustal W. The unrooted phylogenetic tree was constructed with MEGA5.1 Software using the Neighbor-Joining Method. Bootstrap values were calculated on 1,000 replicates of the alignment.

RESULTS AND DISCUSSION

The study showed that the nucleotide similarity among all South China isolates ranged from 93.7-100%. The neighbor-joining tree was presented in Fig. 1. PCV-2 strains were classifiable within four clusters. PCV2b-1A/1B cluster contained 35 isolates including those from Guangdong (n = 23), Guangxi (n = 10) and Hainan (n = 2). One Guangdong isolates (GDLJ2 and GDLJ1) were in recombinant cluster of PCV-2b. PCV2b-1C cluster contained 10 isolates including those from Guangdong (n = 6), Guangxi (n = 3) and Hainan (n = 1). PCV2a-2E cluster only included one Guangdong isolate (SZ). PCV2a-2F cluster consisted of 2 Guangxi isolates (GX0601 and GXGG-2).

The ORF2-encoded Cap protein sequences were relatively conserved in each cluster, although a few mutations existed (Fig. 2). The results indicate that there

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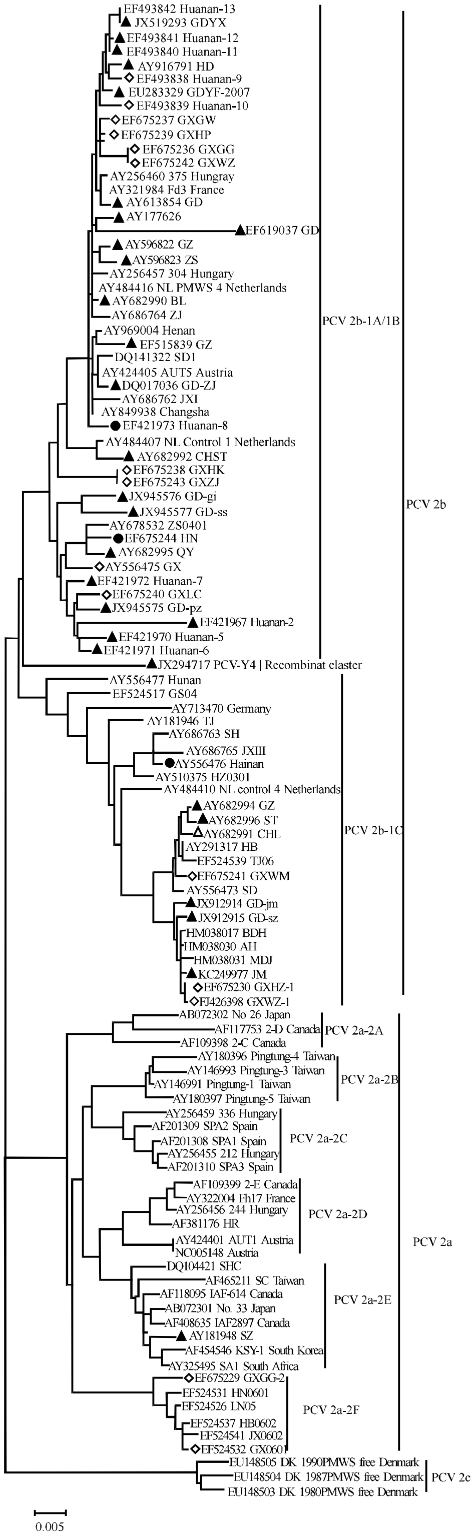

Fig. 1: Phylogenetic analysis of complete genome sequences of PCV2 infection in South China and some reference sequences. An phylogenetic tree was constructed with MEGA5.1 Software using Neighbor-Joining Method reliability of the tree was assessed by bootstrap analysis with 1000 replication

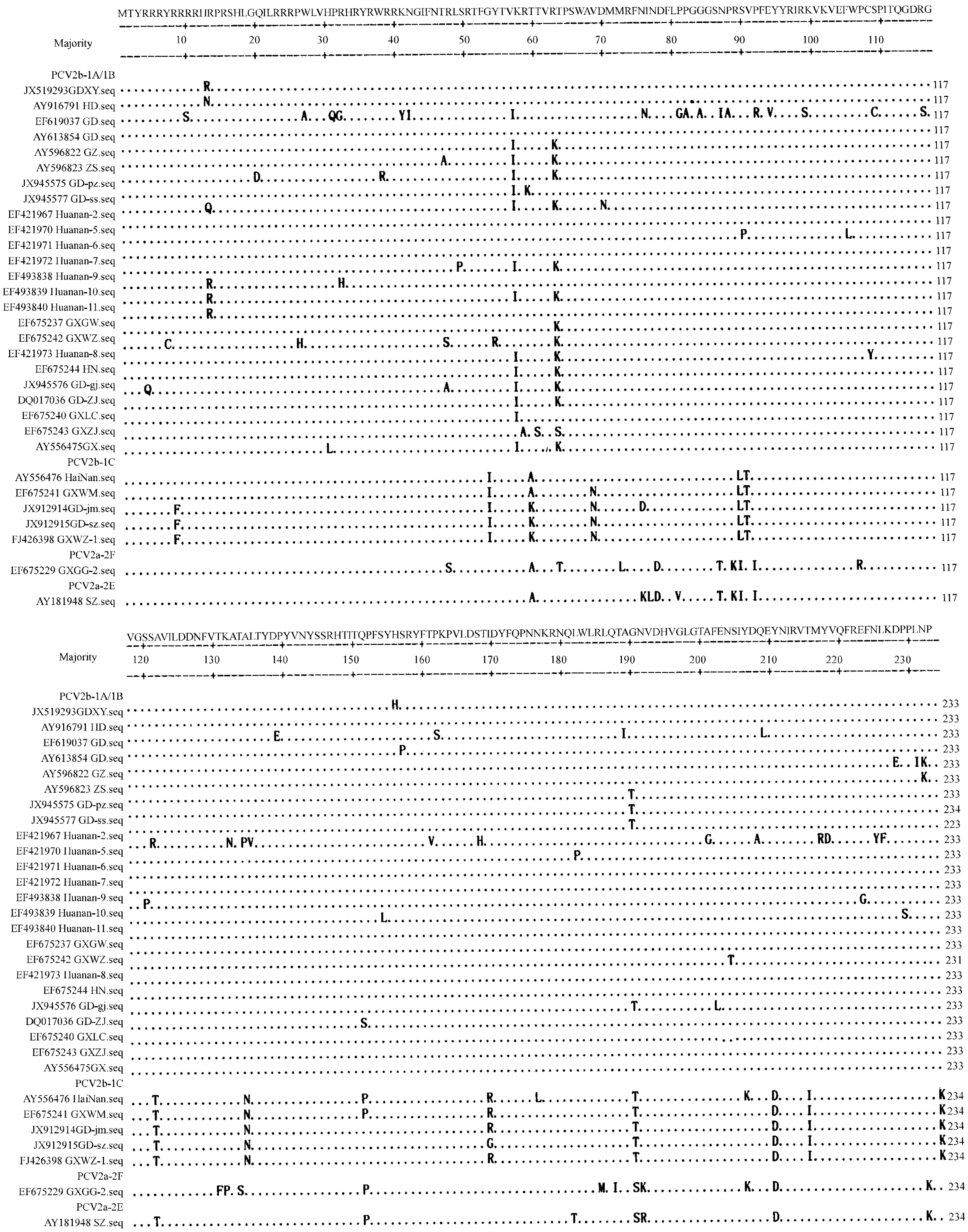

Fig. 2: Sequence alignment of the deduced amino acid (aa) sequences of the capsid proteins (encoded by ORF2) of the PCV2 isolates in South China

are several major regions of variation including residues 57-91, 121-136, 180-191, 206-215 and 230-233 among PCV2 isolates in South China which is similar to previous reports (Wang *et al*., 2009; Dai *et al*., 2013).

CONCLUSION

Researchers report that the majority of the PCV-2 isolate coexisted in pigs in South China were shown to belong to PCV2b genotypes. Furthermore, to control PCV-2 in South China, monitoring of PCV-2 isolates will be necessary in the future.

ACKNOWLEDGEMENTS

This research was supported by the Natural Science Foundation of Hainan Province, China (Grant No. 313100) and Hainan Provincial Research Foundation for public institutions (Qiong Cai Yu (2013) No. 131).

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