

Phylogenetic Analysis of Porcine Circovirus Type 2 Isolated in South China

¹Z.X. Cao, ²Z.H. Shi, ¹Y. Zhang, ¹Z. Chao, ¹L.M. Wei, ¹Q.W. Liu, ¹X. Zhang,
¹B.G. Ye, ¹X.L. Zheng, ¹F. Wang and ¹Z.M. Lin

¹Hainan Provincial Key Laboratory of Tropical Animal Reproduction and
Breeding and Veterinary Medicine, Institute of Animal Husbandry and Veterinary Medicine,
Hainan Academy of Agricultural Sciences, 571100 Haikou, China

²Institute of Animal Husbandry and Veterinary Medicine,
Henan Academy of Agricultural Sciences, 450008 Zhengzhou, China

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

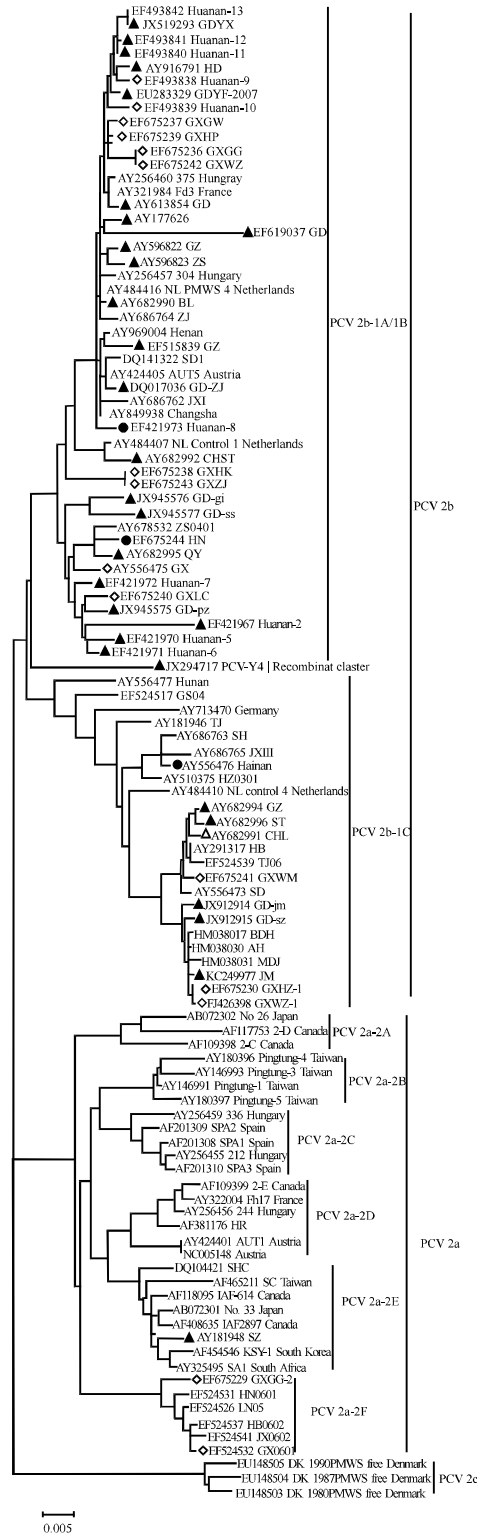


Fig. 1: Phylogenetic analysis of complete genome sequences of PCV2 infection in South China and some reference sequences. A phylogenetic tree was constructed with MEGA5.1 Software using Neighbor-Joining Method reliability of the tree was assessed by bootstrap analysis with 1000 replication

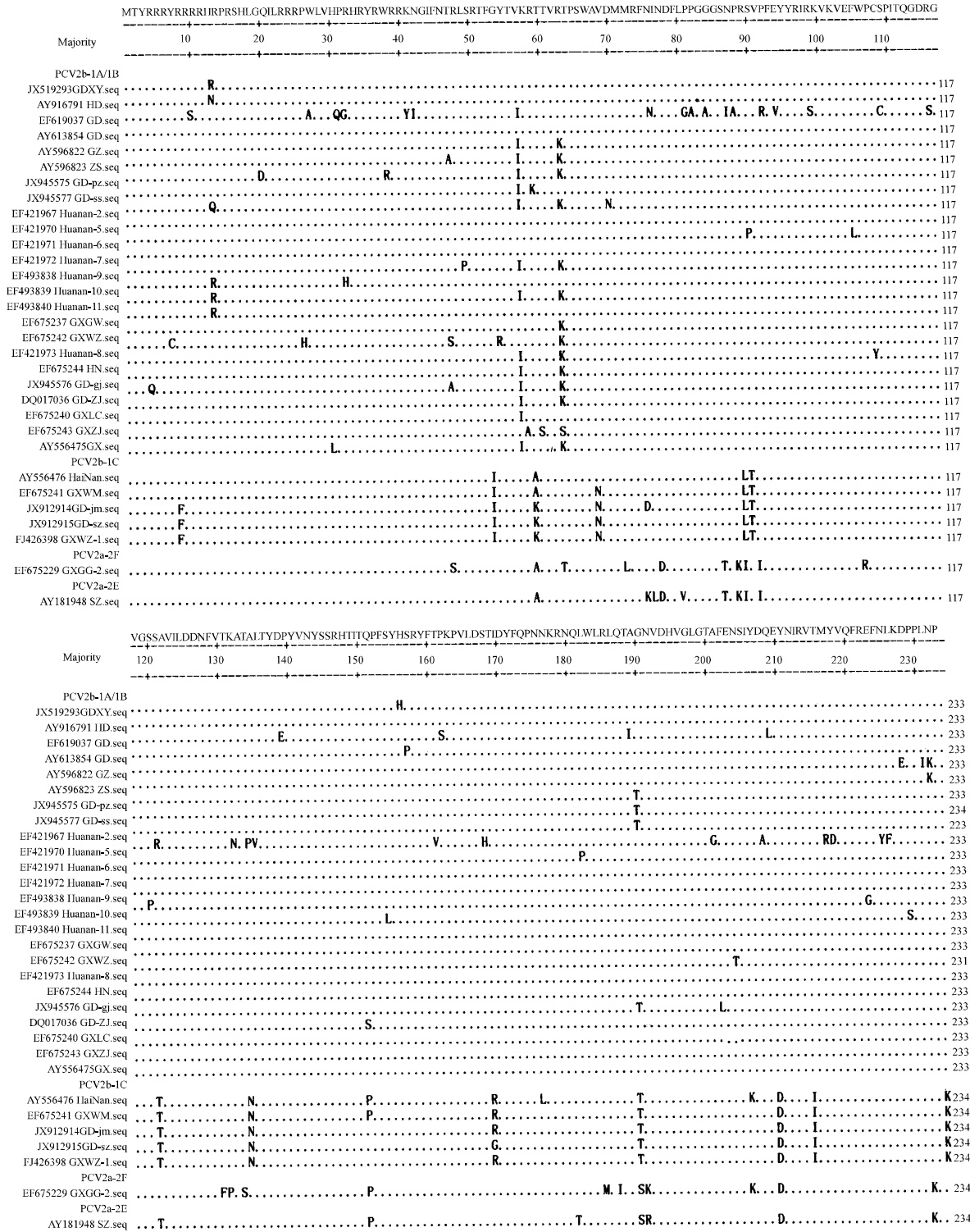


Fig. 2: Sequence alignment of the deduced amino acid (aa) sequences of the capsid proteins (encoded by ORF2) of the PCV2 isolates in South China

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).

REFERENCES

- An, D.J., I.S. Roh, D.S. Song, C.K. Park and B.K. Park, 2007. Phylogenetic characterization of porcine circovirus type 2 in PMWS and PDNS Korean pigs between 1999 and 2006. *Virus Res.*, 129: 115-122.
- Cai, L., J. Ni, Y. Xia, Z. Zi and K. Ning *et al.*, 2012. Identification of an emerging recombinant cluster in porcine circovirus type 2. *Virus Res.*, 165: 95-102.
- Dai, F., W. Li, L. Gao, G. Yin, G. Feng, W. Bai and G. Duan, 2013. Phylogenetic analysis of the ORF2 genes of porcine circovirus 2 strains isolated in Yunnan Province, China. *J. Anim. Vet. Adv.*, 12: 1-5.
- Huang, Z., S. Su, C.Y. Wei, J.X. Xie and W.J. Zhu *et al.*, 2012. Complete genome sequence of a novel field strain of rearranged porcine circovirus type 2 in Southern China. *J. Virol.*, 86: 10895-10895.
- Kim, J. and C. Chae, 2004. Concurrent presence of porcine circovirus type 2 and porcine parvovirus in retrospective cases of exudative epidermitis in pigs. *Vet. J.*, 167: 104-106.
- O'Connor, B., H. Gauvreau, K. West, J. Bogdan and M. Ayroud *et al.*, 2001. Multiple porcine circovirus 2-associated abortions and reproductive failure in a multisite swine production unit. *Can. Vet. J.*, 42: 551-553.
- Olvera, A., M. Cortey and J. Segales, 2007. Molecular evolution of porcine circovirus type 2 genomes: Phylogeny and clonality. *Virology*, 357: 175-185.
- Segales, J., A. Olvera, L. Grau-Roma, C. Charreyre and H. Nauwynck *et al.*, 2008. PCV-2 genotype definition and nomenclature. *Vet. Rec.*, 162: 867-868.
- Wang, F., X. Guo, X. Ge, Z. Wang, Y. Chen, Z. Cha and H. Yang, 2009. Genetic variation analysis of Chinese strains of porcine circovirus type 2. *Virus Res.*, 145: 151-156.
- Wei, C., M. Zhang, Y. Chen, J. Xie and Z. Huang *et al.*, 2013. Genetic evolution and phylogenetic analysis of porcine circovirus type 2 infections in Southern China from 2011 to 2012. *Infect. Genet. Evol.*, 17: 87-92.