



VIRAL DISEASES

VVD-005

PORCINE CIRCOVIRUS 2 WITHIN-HOST VARIABILITY, CO-INFECTION AND RECOMBINATION UNDER A NATURAL INFECTION SCENARIO

F. Correa-Fiz¹, G. Franzo², A. Llorens¹, J. Segalés³, T. Kekkarainen¹.

¹ IRTA-CReSA, Bellaterra, Spain; ² University of Padua, Padua, Italy; ³ IRTA-CReSA and UAB, Bellaterra, Spain.

Introduction

Porcine circovirus 2 (PCV2) is a virus characterized by high evolutionary rate, which promotes the potential emergence of different genotypes and strains. Despite the likely relevance in the emergence of new PCV2 variants, the subtle evolutionary patterns of PCV2 at individual-host level or over short transmission chains are still largely unknown.

Material & Methods

A total of 5 PCV2 infected animals were selected from 3 different farms and a longitudinal weekly sampling was done during one month after the first positive detection of PCV2. DNA extracted from each animal at each sampling point was individually deep-sequenced using the Illumina platform and analyzed to evaluate the PCV2 variability over time. Particularly, both single nucleotide polymorphisms (SNP) and global haplotypes were estimated and evaluated.

Results

Independently of the specific animal or sampling week, the analysis of polymorphisms demonstrated a remarkably higher genetic heterogeneity and the presence of several SNPs in the genome region encoding for the capsid gene. The global haplotype reconstruction allowed inferring the virus transmission network over time, suggesting a relevant within-farm circulation. Interestingly, evidences of co-infection with multiple PCV2 genotypes and of inter-genotype recombination were found in only one farm, after animals were mixed with pigs originating from other sources. In the other two farms, only one genotype was found.

Discussion & Conclusion

The present study allowed demonstrating the remarkable genetic variability of PCV2 sub-population at individual-pig level, particularly in the Cap encoding gene. Such finding suggests the pivotal role of the natural selection induced by the host immune response in driving PCV2 evolution. Moreover, it was possible to demonstrate the effect of farm and swine management in determining the occurrence of multiple genotype co-infections and likelihood of recombination.