VIRAL DISEASES

VVD-053

ANALYSIS OF VIRAL POPULATIONS AFTER EXPERIMENTAL INFECTION WITH *PORCINE CIRCOVIRUS 2* AND ASSOCIATION WITH DIFFERENT CLINICAL MANIFESTATIONS

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Introduction

The within-host diversity is known to play a relevant role in the pathogenesis of rapidly evolving viruses, affecting their ability to evade the host immune response and conditioning the tissue tropism. *Porcine circovirus 2* (PCV2) is a rapidly evolving virus and can establishes relatively long-lasting infection. Therefore, it has the potential for developing relevant within-host heterogeneity, with consequences that have never been investigated.

Material and methods

Twenty-three piglets from two different farms were inoculated with a lung homogenate (from a PCV2-systemic disease [PCV-SD] affected pig) and monitored for three weeks. Sera were weekly collected and viral titer and antibody levels estimated. Three weeks post-infection all animals were euthanized and a complete necropsy was performed. Serum samples, together with the inoculum used, were individually deep-sequenced using the Ion-torrent platform and analyzed to evaluate the within-subject PCV2 variability over time and its association with different clinical outcomes.

Results

Out of the sixteen highly viremic animals (>10^6 copies/mL), 9 developed PCV2-SD while 7 showed no overt clinical signs. Remaining pigs (n=7) had a lower viremia (<10^6 copies/mL) and no clinical signs. PCV2 genetic variability affected mainly the capsid gene and revealed remarkable heterogeneity among subjects. However, a significant association was demonstrated, especially at 3 weeks post-infection, between within-host viral heterogeneity and clinico-pathological conditions. Particularly, a significantly decrease in viral genetic variants was observed in PCV2-SD cases compared to the rest of infected animals, whose PCV2 variability increased over time.

Discussion and conclusions

The present study demonstrates that PCV2 infected animals harbour several viral sub-populations over time, whose heterogeneity could be involved in disease pathogenesis. It is possible to speculate that the reduced variability observed in PCV2-SD cases could be attributable to the selection of a limited number of more fit variants or to a decreased effect of selective pressures due to immunosuppression.