



VVD-008

THE USE OF ROUTINE SEQUENCING ACTIVITY TO MONITOR THE EPIDEMIOLOGICAL TRAJECTORIES OF PRRSV IN ITALY

M. Drigo¹, G. Franzo¹, M. Cecchinato¹, C.M. Tucciarone¹, P. Pesente², G. Sandri³.

¹ *Departement of Animal Medicine, Production and Health (MAPS), University of Padua, Legnaro (PD), Italy;* ² *Tre Valli Laboratory, Corte Pellegrina, San Martino Buon Albergo, (VR), Italy;* ³ *La Pellegrina - Veronesi Group, Quinto di Valpantena (VR), Italy.*

Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) is a major threat to European swine production and Italian pig industry.

Viral evolution analysis in terms of genetic variability over time and space is one of the challenging issue in the PRRSV control mostly in swine production area characterized by high pig density, fragmentation of the production chain and lack of high biosecurity levels.

The existence of a well structured multisites production system (MPS), settled in such epidemiological scenario, is a good opportunity to investigate PRRSV epidemiology, the stability of endemic strains over time and sites and efficacy of the biosecurity standards to prevent introduction of new variants.

Material & Methods

Totally 726 ORF7 sequences were obtained from samples collected between 2004 and 2017 from 116 farms, belonging to 15 MPS located in Northern Italy. Genetic variability was evaluated both globally and at MPS and year level. Additionally, the presence and directionality of significant viral flow among MPS and production phases (i.e. farrowing, nursery and finishing) were evaluated using a phylodynamic approach.

Results

Italian PRRSV strains demonstrate a remarkable genetic variability in the ORF7 gene (p-distance mean = 0.084; range 0-0.193; 5-95 percentile 0.034-0.128). A high genetic distance was typically observed even within each MPS and year. The phylodynamic analysis showed a relevant number of between-MPS transmission events. Similarly, a major epidemiological linkage was found between farrowing and nursery and from nursery to finishing.

Discussion & Conclusion

The present study demonstrates the remarkable genetic variability of PRRSV in Italy, both globally and within MPS, suggesting an only partially controlled PRRSV circulation. The reinforcement of the biosecurity measures currently implemented (general farm biosecurity, but also transport biosecurity) could eventually help the reduction of between-MPS and between-production phases spread but the real importance of "PRRSV area-spread" (airborne?), still remains unknown.

P
O
S
T
E
R