



## VIRAL DISEASES

VVD-017

### **THE HIGH WITHIN-EUROPE PORCINE CIRCOVIRUS 3 GENETIC HETEROGENEITY: FULL GENOME SEQUENCING OF FIELDS STRAINS FROM DENMARK, ITALY AND SPAIN**

G. Franzo<sup>1</sup>, M. Legnardi<sup>1</sup>, C.S. Kristensen<sup>2</sup>, F. Klaumann<sup>3</sup>, C.K. Hjulsager<sup>4</sup>, L.E. Larsen<sup>4</sup>, J. Segalés<sup>3</sup>, M. Drigo<sup>1</sup>.

<sup>1</sup> University of Padua; Dept. of Animal Medicine, Production and Health (MAPS), Legnaro (PD), Italy; <sup>2</sup> Danish Pig Research Centre, Danish Agriculture & Food Council, Kjellerup, Denmark; <sup>3</sup> IRTA, Centre de Recerca en Sanitat Animal (CReSA, IRTA-UAB), Bellaterra, Spain; <sup>4</sup> Technical University of Denmark, National Veterinary Institute, Lyngby, Denmark.

#### **Introduction**

*Porcine circovirus 3 (PCV3)* is a new species of the *Circovirus* genus, which has recently been detected in healthy and diseased pigs. Its presence has been reported in different countries of North and South America, Asia and recently also Europe (Poland and Italy). However, little is known about PCV3 molecular epidemiology and transmission patterns in Europe, and a relevant point is the lack of available full genome sequences from European countries. Therefore, the aim of this work was to sequence and characterize the full genomes of different PCV3 strains from Denmark, Italy and Spain.

#### **Material & Methods**

Several samples, collected in 2016 and 2017, were screened for PCV3 using an in-house developed real-time PCR. Full genome sequencing was performed on a subset of samples with a high viral titer. Obtained sequences were compared with the ones already available in public databases and a phylogenetic analysis was performed to describe the relationship between PCV3 strains collected in different countries.

#### **Results**

Of the Danish samples, 36/38 of the lymph nodes, 6/20 serum samples and 2/20 lung samples tested positive. Similarly, 10/29 lungs, 20/29 organ pools, 6/33 sera and 1/8 nasal swabs tested PCV3 positive in Italy. Fourteen out of 94 serum pools from 7/14 Spanish farms were also positive. Six complete genome sequences were obtained, which showed a significant genetic distance among them and appeared widely mixed with strains collected in different continents in the obtained phylogenetic tree.

#### **Discussion & Conclusion**

Despite that the convenience nature of the sampling prevents precise prevalence estimations, the preliminary screening of the data from three European countries confirmed a wide PCV3 distribution in Europe. Furthermore, the analysis of six complete European PCV3 genomes and their comparison with the public available sequences suggests a remarkable worldwide PCV3 circulation.