Full-genome sequencing of porcine circovirus 3 field strains from Denmark, Italy and Spain demonstrates a high within-Europe genetic heterogeneity

Porcine circovirus 3 (PCV3) is a new species of the Circovirus genus, which has recently been associated with different clinical syndromes. Its presence has been reported in different countries of North and South America, Asia and recently also Europe (Poland). However, different from the other continents, no European PCV3 sequence is currently available in public databases. There is a strong need of epidemiological data and full-genome sequences from Europe because of its relevance in the understanding of PCV3 molecular epidemiology and control. To fill this lack of information, samples collected in Denmark, Italy and Spain in 2016 and 2017 were screened for PCV3. Of the Danish samples, 36 of 38 lymph nodes, six of 20 serum samples and two of 20 lung samples tested positive. Similarly, 10 of 29 lungs, 20 of 29 organ pools, six of 33 sera and one of eight nasal swabs tested PCV3 positive in Italy. Fourteen of 94 serum pools from seven of 14 Spanish farms were also positive. Despite the convenience nature of the sampling prevents any precise prevalence estimation, the preliminary screening of the data from three European countries confirmed a rather wide PCV3 distribution in Europe. Furthermore, the analysis of the six obtained complete European PCV3 genomes and their comparison with the public available sequences seems to support a remarkable worldwide PCV3 circulation. These results underline once more the urgency of more extensive epidemiological studies to refine the current knowledge on PCV3 evolution, transmission, spreading patterns and impact on pig health.