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TITLE

DETECTION AND GENOTYPING OF PCV-2 AND DETECTION OF PCV-3 IN SERUM SAMPLES FROM DIFFERENT EUROPEAN FARMS

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CONTENT

Introduction. Besides the considered non-pathogenic Porcine circovirus 1 (PCV-1) and PCV-2 as the cause of systemic and reproductive problems, a novel circovirus (PCV-3) with an unknown infection outcome was described in 2015. The present work aimed at the detection and genotyping of PCV-2 and detection of PCV-3 in fattening pigs from 9 European countries.
Material and Methods. A total of 624 pig (10 and 25 week-old) sera from 64 farms (10 sera/farm) were analyzed by PCV-2 and PCV-3 PCR methods. Studied farms were from Spain (11), Belgium (10) France (8), Germany (8), Italy (7), Denmark (7), The Netherlands (5), Ireland (5) and Sweden (3). Frequency of genome detection was calculated globally, per country and per farm. In addition, two PCV-2 positive samples per farm were selected to be genotyped by sequencing the ORF2 gene. The phylogenetic analyses were conducted using the Neighbor-joining method in MEGA 7.
Results. PCV-2 DNA was present in 131 out of 624 analyzed sera (21%) coming from 29 farms (45%); it was detected in a variable proportion of pigs from all tested countries (ranging from 6% in the Netherlands to 70% in France), but Sweden. From the 58 PCV-2 sequenced samples, 45 were successfully genotyped. Globally, PCV-2a (n=9), PCV-2b (n=9) and PCV-2d (n=27) genotypes were found across the countries. PCV-3 DNA was found in 52 out of 624 studied sera (8%) coming from 30 farms (47%) and in a variable proportion of pigs from all countries (ranging from 4% in Ireland and Italy to 14% in The Netherlands). Only 3% of the totally tested sera were positive to both viruses.
Discussion and conclusion. PCV-2 and PCV-3 were found in 8 and 9 European countries, respectively, although with a variable percentage, and rarely in co-infection in the tested pigs. The most frequently PCV-2 genotype found was PCV-2d.