



VIRAL DISEASES

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FULL GENOME CHARACTERIZATION AND PREVALENCE OF PORCINE CIRCOVIRUS TYPE 3 ISOLATES FROM GERMAN FATTENING FARMS

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Introduction

Recently a novel porcine circovirus called porcine circovirus type 3 (PCV3) was reported from the Americas, Asia and Europe. PCV3 was detected with high prevalence in Polish farms, but to date no genome sequences were available from European PCV3 strains. The present study was performed to estimate the PCV3 prevalence in German fattening farms and to further characterize available PCV3 isolates.

Material & Methods

1060 serum samples from pigs at the age of 20-24 weeks from 53 German fattening farms were included in this examination. PCV3-DNA was detected using a real-time PCR and subsequently complete PCV3 genome sequences were obtained after multiply primed rolling circle amplification and sequencing of overlapping PCR products. Phylogenetic analysis was performed by neighbor-joining method and maximum likelihood method.

Results

In total 75 % of the examined farms were PCV3 positive. We were able to obtain 15 complete PCV3 genome sequences and nine partial sequences including the putative ORFs 1, 2 and 3 from PCV3 viremic animals. Phylogenetic analysis of these as well as 30 full genome sequences received from GenBank divided the PCV3 strains into two main groups. Furthermore, we were able to define group specific amino acid patterns in open reading frame 1 and 2.

Discussion & Conclusion

PCV3 is distributed with high prevalence in German fattening farms. Phylogenetic analysis revealed two clearly separated groups of PCV3 strains, which might be considered as PCV3 genotypes. Specific nucleotide and amino acid marker positions may serve for easy and fast intraspecies classification and genotyping of PCV3 strains. We found comparable diversity of PCV3 strains in Germany as in other countries.