

Porcine circoviruses (PCVs) are the members of family *Circoviridae*. They are small, non-enveloped DNA viruses with single-stranded circular genome. PCVs are characterized by high genetic diversity. Swine circoviruses differ in pathogenicity. Porcine circovirus type 1 (PCV1) is non-pathogenic in pigs. On the other hand, porcine circovirus type 2 (PCV2) is a primary causative agent of PCV2 associated diseases (PCVD), which include systemic illness, enteritis and pneumonia. Nowadays, subclinical infections, without specific clinical signs, caused by PCV2, become more problematic in swine industry. At present, subclinical infections are more common, so quantitative Real Time PCR is most often used for PCVD detection. Porcine circovirus type 3 (PCV3) is a novel pathogen discovered in USA, China and Poland. PCV3 is suspected to be a causative agent of porcine dermatitis and nephropathy syndrome (PDNS), reproductive failure, respiratory disease and multisystemic inflammation, but the virus was never isolated in vitro and no experimental infections were performed. At present there are no standards for PCV3, or PCV3 related health problems diagnosis. A pilot study carried out in Poland detected the virus in several farms, which did not report any unexplained health problems. The genetic diversity within analyzed strains was established. Thus, the true role of novel PCV3 remains elucidated and data about its genetic diversity, prevalence and circulation are not numerous.

The studies will be carried out thank to a close cooperation with diagnostic laboratories and veterinary specialists. Our project will include objectives such as development of new protocols for the diagnosis of PCV3 infections, determination of PCV3 prevalence and circulation patterns in pig farms of different health status, determination of the frequency of PCV3, PCV2 and PRRSV co-infection in Polish pig farms and determination of genetic diversity of PCV3 in Poland. It is based on archival samples collected in 2013-2017 examination. In the first task we plan to develop and validate quantitative Real Time PCR for PCV3 detection. Task 2 will involve examination of PCV3 circulation on Polish swine herds. Task 3 will consist in analysis of PCV3 genetic diversity in Poland. Sequencing of complete genome of PCV3 using Sanger method and analysis of received sequences are planned.

This innovative study will provide valuable scientific and practical data to improve detection of PCV3 infections and will facilitate the interpretation of diagnostic findings. It will broaden our knowledge about the PCV3 prevalence in Poland, PCV3 genetic diversity and will provide important clues for the pathological potential of this newly emerged pathogen. This original project will have great relevance for Poland and the whole world, because it will expand global knowledge of the role and evolution of this newly emerged virus.