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BARCELONA RECERCA I INNOVACIÓ

27/01/2016

An updated method of taxonomic classification for porcine circovirus type 2

A multidisciplinary international team of scientists have published a study in *Virology Journal* revisiting the taxonomic classification of porcine circovirus type 2 (PCV2), one of the major pathogens affecting the pig industry worldwide. The study included the participation of two prominent researchers from the IRTA-CReSA, Professor Joaquim Segalés, from the Department of Animal Health and Anatomy at the UAB, and Dr. Martí Cortey, from the endemic diseases subprogram at IRTA-CReSA.

PCV2 causes substantial economic losses annually in pig production. For a few years, vaccination has been the most effective measure to control the infection by this virus, although there are still many gaps in many pathological, epidemiological and evolutionary aspects. Since the last proposal of taxonomic classification for PCV2 the number of virus genomes available at GenBank, presented under the Sixth Framework Programme of the European project, has increased significantly, especially with data from China.

The study classified and analysed all the partial and complete PCV2 genomes available in order to evaluate the method of taxonomic classification that is currently accepted. The results clearly indicate the need for a new method of classification, since the thresholds method applied in the

last ranking, based on the frequency histogram of the differences between sequences, is inappropriate for the current situation, in which the viral variability is much higher compared with the previous classification.

This work proposes an alternative method based on marker positions, conserved mutations that differentiate groups, in order to maintain the current taxonomic classification based on four genotypes, and at the same time is fast and easy to apply when deciding which genotype has to be assigned to a certain isolate.

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