

PREVALENCE OF PORCINE CIRCOVIRUS GENOTYPES ON COMMERCIAL FARMS IN MEXICO

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Introduction and objective

The global evolution of PCV2 genotypes reflects the virus’s high capacity to mutate and generate new variants. This genetic plasticity supports the emergence and spread of different genotypes over time, influencing epidemiology, virulence, and vaccine performance. Understanding this dynamic is essential for effective control and prevention strategies. The objective of this study was to estimate the occurrence of different genotypes on Mexican farms.

Materials and methods

During the year 2025, 22 farms located in Central, Western, and Southern Mexico were sampled; region that accounts for approximately 70% of Mexico’s production. The farms were randomly selected in these regions. The serum samples (from piglets aged between 1 and 23 weeks) investigated were those that tested positive by PCR, with a “CT” below 25, during epidemiological investigation of farms for PCV2. 203 serum samples were pooled in groups of 5, with 1015 piglets sampled. DNA was extracted by the IndiMag Pathogen Kit (Indical Bioscience) and subjected to the PCV2 genotyping assay by the Kylt® PCV-2 Typing Kit (AniCon Labor GmbH) to differentiate between PCV2 genotypes.

Results

The results of the 203 samples analyzed, 72 were positive for PCV2 by PCR. 52 samples were typification and 62% of them were PCV2d, 36%

were PCV2a, and 2% were PCV2a+d. Figure 1. And the results from the 22 farms sampled, 14 farms (63%) were positive for PCV2 PCR: 4 of those farms (28.5%) were positive for PCV2a, 6 farms (43%) for PCV2d, 4 farms (28.5%) for PCV2a+d.

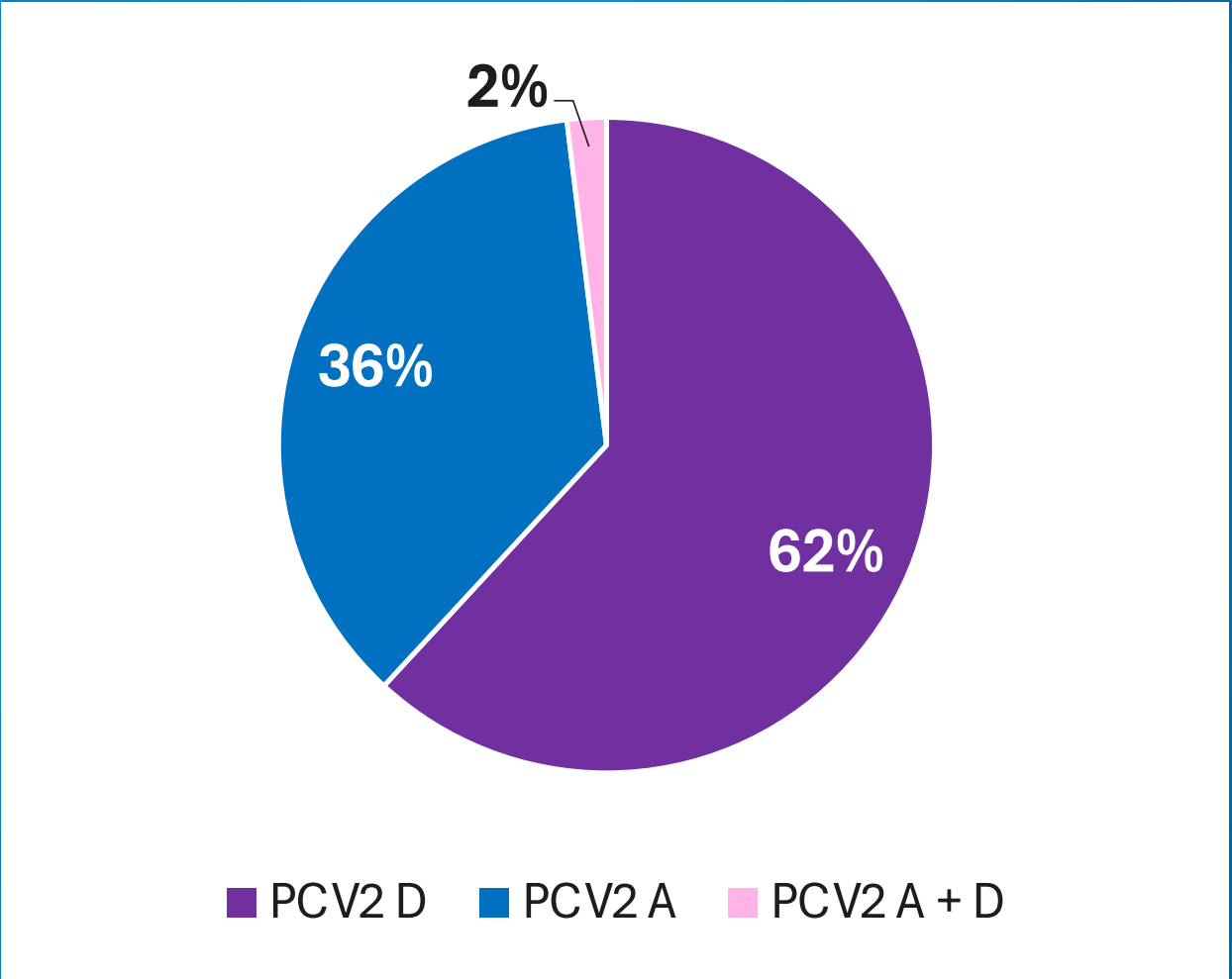


Figure 1. Prevalence of PCV2 variants in Mexico - 2025

Discussion and conclusion

The data of this study reinforce that PCV2d remains the most prevalent genotype in the swine populations analyzed. This predominance is consistent with recent research from Mexico and other countries which also reported high detection rates of this genotype. Together, these data highlight the ongoing evolution of PCV2 and the need for continuous genetic monitoring to guide effective control strategies.