

Are PCV2-Cattle Infections at an Early Evolutionary Virus Adaption Stage?



Figure 1: Comparison of PCV2 cattle viremia on farm 1, which housed cattle in the same complex as a PMWS pig cohort, and farm 2 with separate enclosed cattle shed in proximity to a PCV2-subclinically infected pig cohort. Y bars indicate PCV2-positive

between the PCV2 infection grades of the cattle cohorts from the two farms with a one-sided Fischer analysis. We think that bigger cattle cohorts in proximity to the pigs would remove any ambiguity regarding the conclusion.

We analysed blood of the three highest viremic cattle for PCV2 DNA by PCR and sequenced the sequences. They were not new, instead they belong to viruses of the PCV2b genotype, namely the PCV2b-CH, which dominated the Swiss epizooty [28] and seems to be present endemically throughout the pig population. As this virus sequence is not novel or different from the dominant genotype group member in pigs, this represents a real cross-species transmission of PCV2, expanding into another unrelated species, namely cattle.

Out of these cattle cohorts, a 7 years old cow was infected with the highest virus titer of 1.3×10^6 virus genomes per ml blood. The cow got infected from chronic mastitis. Although we previously presented

- 25 Sun X, Wertz N, Lager KM, Butler JE (2012) Antibody repertoire development in fetal and neonatal piglets. XV. Porcine circovirus type 2