

Outbreak investigation in relation to risk factors for post-weaning multi-systemic wasting syndrome on a large commercial pig farm in the UK

Wieland B (1), Wathes C (1), Pfeiffer D (1), Nevel A (1), Armstrong D (2), Cook A (3), Rycroft A (1), Towrie H (4), Done S (5), Werling D (1)

(1) Royal Veterinary College, London, UK (2) British Pig Executive Ltd, Milton Keynes, UK (3) Veterinary Laboratory Agency, Weybridge, UK (4) Biobest Laboratories Ltd, Edinburgh, UK (5) Veterinary Laboratory Agency, Thirsk, UK

The present study aimed at evaluating retrospectively the presence of porcine circovirus 2 (PCV2), the necessary agent of PMWS, and other pathogens before and during an outbreak of PMWS on a large commercial pig farm in the UK. Results were investigated to identify potential association of PMWS with environmental stressors, opportunistic pathogens and the genetic background of affected pigs.

The study was based on samples collected in 2000/2001 during a large scale experimental study on the impact of environmental conditions (dust and ammonia) on the onset of respiratory disease in weaned pigs. This welfare project included 960 pigs that were recruited in eight batches. In each batch, pigs were randomly allocated in equal numbers to five rooms with specific environmental stressors. During the second half of the experiment, the pig farm experienced an outbreak of PMWS which also affected pigs enrolled in the welfare study.

Serum samples from 371 pigs had been archived which for the study presented here were tested for antibodies to PCV2, *M. hyopneumoniae*, porcine parvovirus, and PRRS. In addition, presence of PCV2 antigen was determined by quantitative PCR. Data from 2000/2001 on isolated microbiological agents and post mortem findings were also included in the statistical analysis. To account for the hierarchical structure of the dataset (batch, room, pen, animal), generalised linear mixed models (GLMM) were fitted using MLwiN software to identify the best predictors for different outcomes (presence of PCV2 antibodies and antigen, average daily gain 40 days).

Our results indicate that PCV2 sero- and PCR-positive pigs were already present prior to the actual PMWS outbreak. Prevalence of PCV2 antibodies and antigen was low in early batches but reached up to 100% in late batches. The GLMM identified the genetic background of the sow as a significant predictor with three out of eight genotypes represented in the sample having significantly higher odds of being PCV2 sero-positive than the other genotypes ($p < 0.05$). Furthermore, significantly higher odds to be PCV2-PCR positive were found for off-spring of sows with high parities of five or above. None of the models identified any association with environmental stressors.

Our study indicates that age and/or genetic background of the sow might be linked to the onset of PMWS in weaners. Thus, maternal effect, such as health status and parity of the sow should be further investigated. The dataset used here provided a unique opportunity to investigate PMWS as it consisted of detailed performance and health information of pigs enrolled, data that would be difficult to collect under field conditions. It is also a good example of how retrospectively data of another study can be insightful, provided samples and data are stored and documented appropriately.