

CONFIRMATION OF MULTISYSTEMIC WASTING SYNDROME (PMWS) IN LITHUANIAN AND LATVIAN PIG HERDS INFECTED WITH PORCINE RESPIRATORY AND REPRODUCTIVE SYNDROME VIRUS (PRRSV)

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Summary. Porcine circovirus type 2 (PCV2) is essential infectious agent of postweaning multisystemic wasting syndrome (PMWS). PMWS has been described in many countries over the world including West Europe countries. However, the importance of PMWS in Lithuanian or Latvian pig populations has never been investigated or reported before. Therefore, the objective of the present study was to report the diagnosis of PMWS and to determine the phylogenetic relationship of PCV2 positive samples in Lithuanian (LT) and Latvian (LV) pig herds.

Three LT and 4 LV pig farms with clinical signs (wasting, dyspnoea and pallor of skin) and gross lesions (enlarged inguinal superficial lymph nodes, enlarged kidneys and skin lesions) compatible with PMWS were included in this study. By nested RT-PCR in all selected farms were detected PRRSV. From these farms, 19 animals (8 from LT and 11 from LV) showed characteristic microscopic lesions in lymphoid tissues after histopathological examination. Seventeen out of the 19 (89.5%) tested samples were positive by ISH, showing moderate to high presence of PCV2 within lymphoid lesions.

Based on obtained *cap* gene sequences from LT and LV farms and selected PCV2 sequences available from GenBank, a phylogenetic tree was constructed. A 90.5% of nucleotide identity between LT and LV PCV2 sequences was found. LV sequences had up to 99.3% identity to selected PCV2 sequences from group 1A, while those values were up to 99.5% for LT and PCV2 sequences from group 2D.

Obtained our results fulfilled requested criteria to diagnose PMWS in LT and LV farms, including presence of clinical signs (mainly wasting), characteristic microscopic lesions in lymphoid tissues and detection of PCV2 by within these lesions. However, at this time it is not know how widespread the disease is and its relative importance in these countries.

Key words: circovirus, PCV2, PRRSV, ISH, phylogenetic analysis.