

GENETIC DIVERSITY AND PHYLOGENETIC ANALYSES OF LITHUANIAN STRAINS OF PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS IN ORF5 AND ORF7 REGIONS

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Summary. The fragment ORF5 gene and complete ORF7 gene of pathogenic porcine reproductive and respiratory syndrome virus (PRRSv) field strains from Lithuanian pig population were amplified by reverse transcriptase polymerase chain reaction and their nucleotide sequences were determined. It was found that Lithuanian PRRSv sequences were exceptionally diverse. The most diverse present-day European-type PRRSv sequences were from Lithuanian two farms, and exhibited only 72.2% nucleotide identity in ORF5. Furthermore, the diversity between the Lithuanian sequences was as high as among any other European sequences. While all sequences determined in the present study were clearly of European type, phylogenetic analysis showed that the Lithuanian sequences were derived from ancestral sequences that were more US-like than previously seen in Europe. In addition, the length of the ORF7 of the Lithuanian strains was 378 nucleotides, and thus intermediate between the sizes of prototypical EU-type (387 nucleotides) and US-type (372 nucleotides) ORF7 lengths. These findings for the Lithuanian PRRSv sequences provide support for the hypothesis that the EU and US genotypes of PRRSv evolved from a common ancestor.

Keywords: PRRSv, phylogenetic analysis, nucleotide sequences, ORF5 gene.