CAE-RAPID – GENETIC DIVERSITY OF SMALL RUMINANT LENTIVIRUS IN POLISH GOAT POPULATION

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Background: Caprine arthritis–encephalitis virus (CAEV) and maedi-visna virus (MVV) had been historically considered as two distinct viral species responsible for diseases in goats and sheep, respectively. Further phylogenetic and epidemiological analyses merged them into a single species small ruminant lentivirus (SRLV). SRLV belongs to the Lentivirus genus, *Retroviridae* family. Like other Lentiviruses, SRLV is characterized by high biodiversity, which is a direct consequence of their retro-replication mechanism. SRLV is classified into five different genotypes: A, B, C, D and E, with genotypes A and B comprising classical MVV-like and CAEV-like strains, respectively. The aim of this molecular study was to characterize SRLV strains present in Polish goat herds using a newly developed real-time nested-PCR technique and Sanger sequencing of LTR-gag sequence.

Methods: Eleven Polish goat herds with serologically confirmed SRLV infection and 1 herd seronegative for SRLV infection in several serosurveys conducted over previous 5 years were enrolled in the study. In total, blood was collected from 290 goats to EDTA-tube and dry tube. Blood collected to EDTA-tubes was centrifuged at 3000 rpm and buffy coat was carefully harvested from each sample to 1-ml Eppendorf vials. Blood collected to dry tubes was left overnight at +4°C for clotting and then centrifuged at 3000 rpm and serum was harvested to 2-ml Eppendorf vials. Serum samples were serologically tested using a whole virus commercial indirect ELISA (ID Screen® MVV / CAEV Indirect; IDvet Innovative Diagnostics, Grabels, France), according to the manufacturer instructions with the cut-off value at sample-to-positive control ratio (S/P% >50%). 119 of 290 goats (41.0%) tested seropositive. Leukocyte pellets from seropositive goats were further processed. DNA was extracted from leukocytes using DNeasy Blood and Tissue Kit (Qiagen,

Switzerland). Extracted DNA from 95 goats with strong positive result in ELISA (S/P% > 100%) were tested with in-home two-staged nested real-time PCR in the Institute of Virology and Immunology of the University of Bern.

Results and conclusions: Eighty goats (84.2% of 95 strongly seropositive) tested positive in real-time PCR. Seventy were positive for genotype A (87.5% of 80 samples), 7 were positive for genotype B (8.7%), and 3 were positive for both genotypes (3.8% of 80 samples). Fifteen samples positive in real-time PCR (11 of genotype A, and 4 of genotype B, at least one from each goat herd), were submitted for sequencing of the real- time PCR target region (Microsynth AG, Balgach, Switzerland). The genetic relatedness among the SRLV was analysed using a LTR-gag sequence fragment located within the real-time PCR target sequence. Two main clusters with clear separation between genotype A and genotype B according to the reference sequences were observed in the phylogenetic tree.

Keywords: SRLV, genetic diversity, diagnostics, CAE-RAPID

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