

AMPLICON SEQUENCING OF PREGNANCY-ASSOCIATED
GLYCOPROTEIN GENE FAMILY (PAGS) IN THE EURASIAN MOOSE
(Alces Alces L.)

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Summary: The PAG family is a large group of secretory chorionic products belonging to placental aspartic proteinases (EC 3.4.23). A role of the PAGs is still unclear, but it is believed that the PAGs are involved in proper embryo-maternal interaction and placenta development (Szafranska et al. 2006). The aim of this study was to identify internal nucleotide sequences of the PAGs in the genome of the Eurasian moose. The study was performed on genomic DNA (gDNA) templates, obtained from different tissues (skin, testes, vas deferens) of the moose (N=17). Moose PAG gene amplicons (AaPAG-L) were produced with various primers that should amplify the entire structure of the PAGs, according to porcine PAG2 and bovine PAG1 genes. The AaPAG-L amplicons were produced parallel to porcine PAG cDNAs and BAC clone templates – used as positive control, and were electrophoretically separated in agarose gels and visualized in UV light. Dominant AaPAG-L amplicons were gel out purified and then subjected to nucleotide sequencing in sense and antisense directions (3130 Genetic Analyzer, Applied Biosystems). All identified AaPAG-L sequences were compared to the PAG genes deposited in GenBank. Amplification of gDNA templates of the moose allowed to identify different AaPAG-L amplicons varying in length (100-2750 bp). Sequencing of the dominant AaPAG-Ls revealed at least two AaPAG genes in the genome of the moose. In the region of exons 1-2 and intron A, our analyses revealed 87-91% homology of the AaPAG-Ls to the bovine PAG1 gene. Within this region, also 13 SNPs (Single Nucleotide Polymorphism) causing 12 amino acid substitutions and one INDEL mutation were identified. In the region of exons 2-5 (with introns B, C and D), short fragments of the identified AaPAG-Ls were very homologous (83-100%) to other PAG sequences deposited in GenBank. This is the first study reporting genomic AaPAG sequences (within exons 1-5 and introns A-D) of the moose. Our results provide a novel data about the Eurasian moose genome.

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