

P2.12 First genomic sequences of pregnancy-associated glycoprotein in the Eurasian, Asian badger and the raccoon dog

G. Panasiewicz¹, A. Zamojska¹, M. Bieniek¹, E. Fijolek¹, K. Zalewski², A. Saveljev³, B. Szafranska¹

¹Department of Animal Physiology, University of Warmia and Mazury, Olsztyn, Poland

²Department of Biochemistry, University of Warmia and Mazury, Olsztyn, Poland

³Institute of Game Management and Fur Farming, Russian Academy of Agricultural Sciences, Kirov, Russia

Among ungulate mammals (Artiodactyls and Perissodactyls), multiple complementary DNAs (cDNAs) of placentally expressed PAG gene families have only been cloned in a few wild species (water buffalo, white-tailed deer and zebra, respectively). In the Carnivora order, only single PAG cDNA has been identified in the cat. In contrast, genomic DNA (gDNA) sequences of the PAG (9 exons/8 introns) have been identified in domestic cattle and pig only. So far, gDNA sequences of the PAGs have not been identified in wild Carnivora species. This study presents gDNA sequence identification of the PAGs in the Carnivora: the Eurasian badger (*Meles meles*; N = 3), the Asian badger (*Meles leucurus*, N = 2) and the raccoon dog (*Nyctereutes procyonoides*; N = 3). Required PCR-gDNA templates were isolated from various available tissues (hair roots, skin, testes, muscle). Produced PAG-like PCR-amplicons (exons 7–9 and introns F-H) were electrophoretically separated, purified and sequenced. Due to GenBank, our sequencing revealed novel PAG gDNA sequences in the Eurasian and Asian badger and the raccoon dog, in which the PAGs were named EbrPAG, AbrPAG and rcdPAG, respectively. All identified EbrPAG, AbrPAG and rcdPAG sequences were similar to porcine PAG2 subfamily (96–100%). Single nucleotide polymorphism (SNP) was identified in the PAG gene fragments of both badger species. The badger PAG sequences varied in seven SNP within internal 312 bp of intron F and one SNP (G/T) and one deletion (T/–) within internal 670 bp of intron H. Our results provide novel genomic data of three wild Carnivora species.

Supported: UWM528.0206.806.

<http://dx.doi.org/10.1016/j.repbio.2013.01.088>