

# BOOK OF ABSTRACTS

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**CONSERVATION AND POPULATION GENETICS****DIVERSITY OF THE MHC CLASS II DRB ALLELES IN CHAMOIS POPULATIONS**

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The genes of the major histocompatibility complex (MHC) code for receptors that recognize and bind antigens in order to present them to T cells, thus they have a major role in determining the immune response. MHC region includes some of the most variable loci in the vertebrate genome, reflecting the strong association between MHC diversity and resistance/susceptibility to disease. With their well-characterized function and exceptional diversity, they are a key genetic marker for studying the processes of species adaptive evolution. The goal of our study was to examine spatial distribution of allelic diversity at exon 2 of MHC class II DRB locus across the majority of distribution range of the genus *Rupicapra* using next generation approach (Ion Torrent S5, Thermo Fisher). We identified 20 alleles in 96 individuals. Twelve alleles had been previously identified in chamois while the remaining 8 are novel. The number of variable nucleotide sites in detected alleles was 23 (10%) and the number of variable amino acid positions in translated sequences was 11 (14%). Out of 20 identified alleles, 18 translated into different amino acid sequences. The number of alleles per individual ranged from 1 to 6 (mean = 3.1), indicating the presence of at least 3 loci resulting from gene duplication events. The most frequent allele, Ruru-DRB\*01, was identified in 68 individuals (71%) while 5 alleles were present only in a single individual each. Our results provide evidence of multiple co-amplifying copies, showing that MHC class II DRB is a complex multilocus system with a high level of polymorphism in chamois. Finally, our study represents the first assessment of immunogenetic map of chamois populations that can be used in future conservation management of this species.

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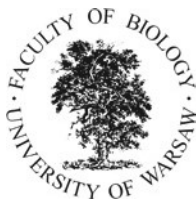


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