

## **The major histocompatibility complex in Old World Camelids: low polymorphism in class II genes**

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### *Abstract*

The major histocompatibility complex (MHC) is a genomic region playing a crucial role in immune responses and mechanisms of disease. Currently, very little is known about the MHC in Old World Camelids. Here, we analyzed MHC genomic sequences of the three species of Old World Camelids, *Camelus bactrianus*, *Camelus dromedarius* and *Camelus ferus*. The three major MHC regions, class I, II and III were identified in all three species. Comparative genomic analysis of published and unpublished whole genome sequences produced by us showed that their order on the camel chromosome 20 is “Centromere - Class II – Class III – Class I”. Within the class II region, DYA genomic sequences, previously described only in cattle and sheep, were identified in all three species. All bactrian camels analyzed had a stop codon in the DYA exon 2 reading frame, while in the dromedaries, a single nucleotide variation (SNP) with one potentially functional (full-length) allele and with one allele containing the stop codon were observed at this nucleotide position. The overall genomic organization and the presence of the DYA class II sequences revealed high genetic similarity of the camel MHC to cattle and related species.

Due to their functional importance, MHC class II genes DRA, DRB, DQA, DQB and DYA were further studied. Like other studies, we focused on their functionally most important domain, exon 2, encoding the antigen binding site. Exon 2 genomic and haplotype sequences of all abovementioned loci in *Camelus bactrianus*, *Camelus dromedarius* and *Camelus ferus* were retrieved. In general, very little interspecific differences manifested by high degree of sequence similarity and by high extent of allele sharing across all three species were observed. In addition, unexpectedly low level of polymorphism was found in all loci and all species. Despite different geographic origins, low numbers of allelic haplotypes were identified. On the other hand, the DRA locus is polymorphic, with three alleles shared by all three species.

An attempt to sequence the exon 2 of two MHC genes, DQA and DRA from both domestic and wild fossil camel specimens was made. In 15 domestic samples, we had a success rate of 20% (3 samples) of obtaining endogenous camel sequence. The attempt to identify MHC class II sequences was 100% unsuccessful in all wild samples, which is due probably due to the level of the preservation of wild specimens. Some DRA sequences retrieved were identical with those observed in recent samples while others still need confirmation.