Abstract

MHC glycoproteins are an essential part of adaptive immunity and may also play a role in mate choice. In addition, MHC genes are the most variable of all known genes. For these reasons, they have been intensively studied for several last decades. However, research is complicated due to extreme variability and frequent duplications. The Eurasian beaver seems to serve as an interesting model. It underwent a dramatic bottleneck culminating in the end of 19th century, when only about 1,200 individuals survived in several isolated relic populations. Thanks to numerous reintroductions, beavers of various origin meet in newly established populations. However, knowledge of beaver MHC was very limited. Only a single MHC gene has been investigated in a detail, and some relic populations were not sampled. Utilising additional relic populations and additional MHC locus, I verified a significant reduction of the variability of beaver MHC genes and also found signs of selection in the past. Then I sequenced MHC loci in two newly formed populations. I confirmed the ongoing selection by the disruption of cytonuclear equilibrium and the advantage of divergent alleles. We therefore can have a unique insight into the several periods of the history of beaver populations: In the past, MHC diversity was shaped by a combination of positive and balancing selection. During the recent bottleneck, MHC variability was significantly reduced by genetic drift. In current populations natural selection plays a leading role again.