

Interactions between hosts and their parasites are considered to be one of the major forces driving animal evolution. It can be assumed that the evolutionary changes will occur especially in host molecules directly involved in these interactions. The first line of host defense is formed by innate immunity receptors among which also pattern recognition receptors (PRRs) belong. PRRs detect the presence of parasites at the beginning of their invasion by binding characteristic structures of their bodies (so called pathogen-associated molecular patterns, PAMPs, e. g. lipopolysaccharide, flagellin or peptidoglycans) or abnormal self molecules (damage-associated molecular patterns, DAMPs, e.g heat shock proteins). Although this mechanism of immune system activation is based on the recognition of ligands that are relatively evolutionarily conservative in pathogens, growing body of evidence suggests that PRRs are highly polymorphic on both interspecific and intraspecific level. High frequencies of minority alleles can be observed in most populations studied. It has been proven that particular alleles of many PRRs may associate with increased or decreased resistance to various infectious or autoimmunity diseases. Relationship between polymorphic receptor and a disease could be the main force, which shapes the evolution of these receptors. This field of research undergoes currently an enormous progress. However, most of the studies conducted so far were performed in various human populations or in laboratory animals and livestock, where non-natural evolutionary circumstances occur and artificial selection plays a key role. Thus, our knowledge of the natural selection forces shaping evolution of PRRs in free-living organisms, i.e. most organisms forming the biodiversity of the wildlife on Earth, is only limited. Further research in animal populations exposed to natural evolutionary conditions is therefore needed.