Abstract

Adaptation of host receptor system to optimal detection of infection-related structures is one of the key evolutionary challenges of immunity in host-pathogen interactions. Toll-like receptors (TLRs) are genetically variable molecules of vertebrate innate immunity that recognise danger signals, e.g. pathogenic molecules. Examination of genetic variation in *TLR*s may reveal mechanisms of host immunity adaptation to pathogenic pressure at molecular level. Trans-species polymorphism (TSP) is a phenomenon which assumes that several identical alleles or allelic lineages are inherited from ascendant to descendant species and these may be subsequently maintained over a long period of time in a polymorphic state. Whereas in adaptive immune genes the concept of TSP is well understood, little is presently known about TSP in innate immune genes such as *TLR*s. In this thesis I describe genetic polymorphism in functionally-relevant regions of TLR4 and TLR5 in 192 individuals representing 20 species Paridae family (tits, chickadees and titmice). These two receptors bind mainly bacterial ligands (TLR4 detects lipopolysaccharide and TLR5 detects flagellin), being among the first ones to trigger immune response to bacterial pathogens. To differentiate presumed TSP from gene flow among species, intron sequences of six autosomal neutral markers were sequenced. *TLR*s were variable on intra- and interspecific level in Paridae. Positive selection was detected in 14 amino acid residues in TLR4 and in 23 residues in TLR5. From these positively selected sites 4 positions in TLR4 and 14 positions in TLR5 were located in close proximity to predicted functionally important sites or being directly in the predicted binding sites. TSP was detected in both *TLR4* and *TLR5* genes in closely related species within genus level (American *Poecile*, *Cyanistes* and *Baeolophus*) assuming that no TSP was older than 4-8 millions of years. Given the extensive sharing of alleles in neutral markers and the recent divergence among these species we were not able to distinguish whether TSP identified in *TLR4* and *TLR5* is balanced or transient. Significant gene flow was detected within two pairs of closely related species assuming that at least some portion of shared polymorphism in *TLR4* and *TLR5* may originate from introgression. In this thesis I report for the first time TSP in *TLRs* and Pattern recognition receptors in general and provide evidence that TSP is a general evolutionary phenomenon in immune genes. Besides that, positively selected residues indentified in TLR4 ad TLR5 might have functional importance for binding properties of the TLRs and thus recognition of pathogens.

Key words: immune genes, innate immunity, introgression, selection, shared variability, *TLR4*, *TLR5*, trans-species polymorphism, TSP