Abstract

Meiotic recombination is an important process which occurs in sexually reproducing organisms and creates new allelic combinations. Frequency and distribution of crossing-overs (COs) are affected by many internal and external factors. Regions with higher frequency of COs are called recombination hot-spots and in this thesis, they are divided into ancestral and derived hot-spots. Ancestral hot-spots are the more original ones and they are determined by histone modifications, nucleosome-depleted regions, promoters and sequence motifs. This type of hot-spots occurs, e.g., in yeasts, birds and plants. Derived hot-spots are determined by the PRDM9 protein, which searches for specific sequence motifs and creates histone modifications. These hot-spots are typical for most mammals except the canines which lost functional PRDM9 due to the mutation of the Prdm9 gene. Activity of PRDM9 destroys primary locations of hot-spots via gene conversion. This process is called "hot-spot paradox" and is solved by the rapid evolution of alleles of the Prdm9 gene.

This thesis summarizes basic information on distribution and determination of hot-spots among various eukaryotes. It particularly focuses on the PRDM9 protein, its structure, function and evolution. A determination of location of recombination in species without hot-spots and comparison of recombination rates among different groups of organisms is presented at the end of this thesis.