Abstract
Hybrid zones provide a valuable opportunity to study the process of speciation in real time. Untested combinations of genes from diverging populations come to the contact here causing a breakdown of genetic interactions and giving rise to reproductive isolation. Two house mouse subspecies (*Mus musculus musculus*/*Mus musculus domesticus*) form a narrow zone of secondary contact across Central Europe which is thought to be maintained by a balance between selection against unfit hybrids and dispersion of individuals. During my PhD study my collaborators and I used an array of ~ 1400 SNP markers to study patterns of introgression on a genome-wide scale across two/three house mouse hybrid zone transects. Our aim was to identify the genomic regions putatively harboring genes which are involved in the reproductive isolation between the two subspecies, characterize their distribution in mouse genome and assess genomic features associated with them. We were able to confirm on a genome-wide scale the importance of the X chromosome in the evolution of reproductive isolation. This chromosome exhibited introgression corresponding to strong negative epistasis and the patterns were consistent between transects pointing out to a common basis of reproductive isolation playing a role in two transects. Contrary to the X chromosome, autosomes exhibited a much lower extent of markers under the epistasis, with a small overlap between transects. Focusing on the specific autosomal region in the proximal part of chromosome 11, which exhibited negative epistasis in both transects, we were able to identify a particular gene, *1700093K21Rik*, as a good candidate for the speciation gene. We further re-analyzed data of three transects to identify genomic regions of high and low introgression and characterized genomic features associated with these regions in order to elucidate the role different processes play in the evolution of reproductive isolation in the house mouse. We found that genomic regions of low introgression exhibited a higher genomic differentiation and a low rate of recombination. These regions are also more likely to accommodate genes acting in the interior of a cell. On the contrary, genomic regions of high introgression exhibited lower genomic differentiation, a higher rate of recombination and a higher prevalence of genes acting at cell periphery. We hypothesize that the functional organization of genome is an important driver of species divergence and in the evolution of reproductive isolation.