

Abstract: Reproductive genes are assumed to play an important role in adaptive evolution and speciation, yet little is known about the patterns of molecular evolution in these genes within avian species. This thesis is focused on identifying reproductive genes under positive selection and analyzing their function in songbirds, the largest and most diverse suborder of modern birds. Using existing bioinformatic approaches and published genomic data of 14 songbird species, we have first constructed 12000 groups of orthologous genes and detected significant traces of recurrent positive selection within 385 of them. Using proteomic data, this genome wide set of genes was then filtered to obtain genes expressed within songbird spermatozoa and fluids from the female reproductive tract. Within spermatozoa 22 out of 940 expressed genes were positively selected, while female fluids were found to be more conserved, as only 6 out of 529 expressed genes have shown traces of positive selection. We have then computed the enrichment of gene ontology terms within the positively selected genes. The enriched terms suggest evolutionary pressures acting on spermatozoa cytoskeleton, molecular motors and energetic metabolism, highlighting the importance of sperm morphology and swimming speed. Furthermore, the enrichment results across the whole genome point not only to similar terms important to sperm, but also to processes involved in mitosis and meiosis, which could play a role in the selfish behavior of the songbird unique germline restricted chromosome.