Oxidative phosphorylation (OXPHOS) supplies over 90% of the cellular ATP requirements through the orchestrated function of five multiprotein complexes located in the inner mitochondrial membrane. The thesis explores how the evolutionary constraints imposed by the indispensable function of OXPHOS guide the outcome of Whole Genome Duplication (WGD) events. Two teleosts, the gilthead seabream (*Sparus aurata*, GSB) and the European seabass (*Dicentrarchus labrax*, ESB), which have undergone three rounds of WGDs were used as models during the highly plastic and energy-demanding period of early development. Fish ontogeny is a unique period in fish life marked with dramatic changes in morphology, physiology, metabolism and behavior. The tightly regulated landscape of cell divisions, migrations and differentiation driving these dramatic changes demands high energy supplies. The discovery of 24 and 22 OXPHOS gene families in GSB and ESB genome, respectively, and the subsequent phylogenetic analysis showed in most cases divergence from a common ancestor at the base of the teleost lineage, a process attributed to teleost-specific WGD. Overall results indicate that the WGD events have resulted in early retention of OXPHOS paralogue genes and subsequent species- or lineage-specific losses. OXPHOS paralogue gene expression levels were compared following RNA sequencing within and between distinct developmental stages in GSB and ESB. Different expression patterns between paralogs were revealed; some of them were in dosage balance, others were expressed only in particular stage(s) and a lot of them were differentially expressed between stages. The results were validated in a focused study comparing stage- and tissue-specific expression of OXPHOS paralogs in ESB. Differences in both the number and location of SNPs were revealed between paralogs, after merging the RNA sequencing data with whole genome sequencing data. Mutations were mapped mostly in the UTRs and very few in the CDS. The ratio of non-synonymous to synonymous substitutions when comparing the CDS variants revealed Purifying and Neutral Selection in action, safeguarding protein structural integrity and/or function. Overall, regulatory neo/subfunctionalization of OXPHOS paralogs appeared as the evolutionary mechanism behind the retention of the paralogs in GSB and ESB genomes in favor of ontogenetic plasticity. Indeed, OXPHOS paralogs exhibited differential thermal plasticity in GSB that became evident under high energy demanding circumstances.