



Insights into vertebrate whole-genome duplications from the rainbow trout genome

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					<p>alleles on ecological properties of haploids and diploids: baseline growth rate, carrying capacity (efficiency of resource use) and individual competitiveness. The models allow mutations to have different (even antagonistic) effects in the two phases. The consequences of deleterious mutations on ploidy evolution depend on their ecological effect and on the degree of overlap between the haploid and diploid niches: while mutations affecting the baseline growth rate have little effect in equilibrium populations, mutations affecting competitiveness or the efficiency of resource use tend to favor the phase in which mutations have the lowest impact on fitness when haploids and diploids compete among each other. As the degree of niche differentiation increases, however, mutations affecting competitiveness tend to favor the phase in which selection against deleterious alleles is the most efficient. In some cases, stable coexistence of different types of life cycles can be maintained ("evolutionary branching").</p>
1270	S18	Camille	Berthelot	<p>Insights into vertebrate whole-genome duplications from the rainbow trout genome</p>	<p>Whole genome duplications (WGD) are major evolutionary events where tetraploid individuals arise and take over the entire population of their species. Unlike in plants, WGDs are rare in vertebrate lineages, where they represent important evolutionary landmarks, such as the 1R and 2R duplications at the rise of the vertebrate tree, and the 3R duplication at the basis of the teleosts lineage. WGDs have indeed been often associated with adaptive radiations and genetic novelty, as the doubling of the genome provides a large number of paralogous genes that can be reused in evolution as source material for innovations. These tetraploid genomes, however, are typically not stable and are thought to lose one copy of most duplicated gene pairs within a few million years, until they progressively return to a virtually diploid state. This process, called gene fractionation, has never been documented at the whole genome scale in vertebrates, because all vertebrate WGDs are too ancient to capture this information. The rainbow trout genome has undergone a WGD event 100 My ago and offers a unique opportunity to investigate the early evolutionary fate of a duplicated vertebrate genome. We show that the two ancestral subgenomes have remained extremely collinear, despite the loss of half the duplicated protein-coding genes, mostly through pseudogenization. In striking contrast is the fate of miRNA genes that have almost all been retained as duplicated copies. The slow and stepwise rediploidization process characterized here challenges the hypothesis that WGD is followed by massive and rapid genomic reorganizations and gene deletions.</p>