
Coding and non-coding changes drive the repeated evolution of the placenta in live-bearing fish

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During vertebrate evolution, complex organs have evolved several times. Theory predicts that such a change in body plan is accompanied by re-routing of developmental gene regulation. However, these predictions have never been tested in closely related species, as most complex organs evolved hundreds of millions of years ago. In this light, the live-bearing fish family Poeciliidae is an interesting model, as in this family a placenta evolved multiple times independently. It is currently unknown whether convergent genomic changes underlie this repeated evolution. Here we use whole genomes of 26 poeciliid species to show that the evolution of the placenta in the Poeciliidae is accompanied by convergent genomic changes in terms of the evolutionary rate of protein-coding genes, as well as conservation of regulatory elements. Shifts in evolutionary rate that correlate with placentation were mainly observed in transporter- and vesicle-located genes, while shuffling of regulatory elements occurred mainly around developmental genes. This indicates that changes in the regulation of developmental genes can occur within a single family. Based on these observations, we propose a model for the repeated evolution of the placenta in the Poeciliidae that relies on the observed variability of functional simple sequence repeats.