

The gain and loss of genes during 600 million years of vertebrate evolution

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Abstract

Background: Gene duplication is assumed to have played a crucial role in the evolution of vertebrate organisms. Apart from a continuous mode of duplication, two or three whole genome duplication events have been proposed during the evolution of vertebrates, one or two at the dawn of vertebrate evolution, and an additional one in the fish lineage, not shared with land vertebrates. Here, we have studied gene gain and loss in seven different vertebrate genomes, spanning an evolutionary period of about 600 million years.

Results: We show that: first, the majority of duplicated genes in extant vertebrate genomes are ancient and were created at times that coincide with proposed whole genome duplication events; second, there exist significant differences in gene retention for different functional categories of genes between fishes and land vertebrates; third, there seems to be a considerable bias in gene retention of regulatory genes towards the mode of gene duplication (whole genome duplication events compared to smaller-scale events), which is in accordance with the so-called gene balance hypothesis; and fourth, that ancient duplicates that have survived for many hundreds of millions of years can still be lost.

Conclusion: Based on phylogenetic analyses, we show that both the mode of duplication and the functional class the duplicated genes belong to have been of major importance for the evolution of the vertebrates. In particular, we provide evidence that massive gene duplication (probably as a consequence of entire genome duplications) at the dawn of vertebrate evolution might have been particularly important for the evolution of complex vertebrates.

Background

The sequencing of vertebrate genomes occurs at an ever-increasing pace. Currently, the genome sequences, or at least first drafts thereof, are available for more than 14 different vertebrate species, while many more are underway. These

vertebrate genome sequences cover a phylogenetic distance of more than 450 million years of evolution, dating back as far as the split between fishes and land vertebrates. Unfortunately, genome sequences of cartilaginous fish such as sharks, rays or skates, or of jawless vertebrates such as lampreys and