

Fastly evolving genes in parrots (Aves, Psittacidae) are associated with developmental processes

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Abstract

During the course of evolution of protein-coding genes, most non-synonymous mutations (dN) are removed from gene pools due to negative selection, leaving a footprint of synonymous mutations (dS). However, some homologous genes have an excess of dN substitutions when compared to dS, indicating a selective advantage for sequence variation over conservation. Such genes are referred as adaptive genes and have been demonstrated to be involved in major adaptive processes in vertebrates, such as reproduction and immunity. Therefore, the detection of genes evolving under positive Darwinian evolution is a prevailing strategy in comparative genomics studies to identify genes potentially involved in adaptation processes. Birds are subject to unique selective pressures due their diverse lifestyles, and previous studies found the genes with evidence of positive selection in this taxon to be associated with developmental processes, such as spinal cord and bone development. Among birds, Psittaciformes (parrots and relatives) are known by their unusual longevity and cognitive capabilities. In this work, we investigated candidate genes for traits relevant to Psittaciformes ecological and functional diversity using POTION2, a software developed by our group to search for genes evolving under evidence of positive selection. We used the complete genomes from 16 avian species representing major extant clades to search for fastly-evolving genes in Psittaciformes when compared to other Psittacopasseria. In a group of 16 high-quality complete genomes (10 Passeriformes, 4 Psittaciformes, 2 Falconiformes birds with BUSCO completeness greater than 0.89). We used MUSCLE for protein alignment, trimAL to remove poorly aligned columns (> 50% gaps), newick utilities for newick tree file manipulation and FastCodeML to infer positive selection. POTION2 requires a phylogenetic species tree to be executed in branch mode, which was obtained from TimeTree of Life website, and ML phylogenetic reconstructions conducted by us. Preliminary analysis of 7036 high-quality 1-1 orthologs found 230 genes (3%) with evidence of positive selection in Psittaciformes. In addition to the processes described in previous studies, we have also found genes related to the regulation of reproductive processes, embryological and cellular processes of development, stimulation and response to beta growth transforming factor, and oxygen depletion. Besides that, many of the positively targeted genes still represent uncharacterized proteins, and comprise interesting targets for functional characterization. Thus, these genes could have been important in the evolution of morphological, physiological and behavioral adaptive traits peculiar to each bird order.

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