

Proteome-Wide Convergent Evolution on Vocal Learning Birds Reveals Insight into cAMP-Based Learning Pathway

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Abstract : Vocal learning, the ability to imitate vocalizations based on auditory experience, is a homoplastic character state observed in different independent lineages of animals such as songbirds, parrots, hummingbirds and human. It has now become possible to perform genome-wide molecular analyses across vocal learners and vocal non-learners with the recent expansion of avian genome data. It was analyzed the whole genomes of human and 48 avian species including those belonging to the three avian vocal learning lineages, to determine if behavior and neural convergence are associated with molecular convergence in divergent species of vocal learners. Analyses of 8295 orthologous genes across bird species revealed 141 genes with amino acid substitutions specific to vocal learners. Out of these, 25 genes have vocal learner specific genetic homoplasies, and their functions were enriched for learning. Several sites in these genes are estimated under convergent evolution and positive selection. A potential role for a subset of these genes in vocal learning was supported by associations with gene expression profiles in vocal learning brain regions of songbirds and human disease that cause language dysfunctions. The key candidate gene with multiple independent lines of the evidences specific to vocal learners was DRD5. Our findings suggest cAMP-based learning pathway in avian vocal learners, indicating molecular homoplastic changes associated with a complex behavioral trait, vocal learning.

Keywords : amino acid substitutions, convergent evolution, positive selection, vocal learning

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