

EVOLUTIONARY MECHANISMS IN THE BENGALESE FINCH'S SONG: PARALLELS AND IMPLICATIONS FOR THE STUDY OF HUMAN SPEECH

MADZA FARIAS-VIRGENS^{*1}, TERRENCE DEACON², KAZUO OKANOYA³,
STEPHANIE WHITE⁴, EMILIA HUERTA-SANCHEZ⁵

*Corresponding Author: madzayasodara@ucla.edu

¹Interdepartmental Graduate Program in Molecular, Cellular and Integrative Physiology,
University of California Los Angeles, Los Angeles, United States of America

²Department of Anthropology, University of California Berkeley, Berkeley,
United States of America

³Graduate School of Arts and Sciences, The University of Tokyo & RIKEN-
Brain Science Institute, Tokyo, Japan

⁴Department of Integrative Biology and Physiology, University of California
Los Angeles, Los Angeles, United States of America

⁵Department of Ecology and Evolutionary Biology, Brown University,
Providence, United States of America

A robust body of evidence accrued over >100 years of research in birdsong demonstrates striking analogies between this exquisite behavior practiced by a much evolutionarily distant animal group and speech in our species. Both birdsong and speech depend upon vocal production learning, that is the ability to learn how to produce vocal sounds via imitation - in addition to vocal usage learning, the ability to associate innate sounds with specific elements and events. Like a child learning to speak, a young bird must first hear the vocal sounds of adults and then imitate those sounds on its own. Initially, the bird will sing a faint, unstructured song, akin to babbling in human infants. By adulthood, this immature chirping progresses to a more consistent birdsong, just as babbling progresses to speaking. These parallel developmental trajectories are accompanied by striking similarities in the way brains and their underlying molecular apparatus functions to produce speech and birdsong. All this resemblance has motivated the additional search for similar evolutionary pressures leading to vocal learning in songbirds and humans. Our research uses a

songbird system to identify evolutionary processes leading to increased complexity of learned vocal behavior, a key aspect also in speech evolution. The Bengalese finch (BF) has a remarkably complex song, in which transitions between vocal units are less firmly fixed, introducing variability in song sequencing. This vocal complexity evolved during BF's domestication from the white-backed munia (WBM). Our study investigates genetic signatures left by evolutionary forces shaping BF's song complexity. For this, we have sequenced whole genomes of individuals within the two bird strains (11 BFs and 11 WBMs). Using analytical tools from comparative and population genomics, we have been able to access the relative contributions of selection processes, such as female choice for more complex songs, and relaxation of sources of evolutionary constraints to song complexity that are commonly found in the wild but absent in the domesticated scenario, such as stress related to finding food or defending from predators or pressures to avoid confusion with cohabitating finch species. We have identified a group of about 300 out of 14.000 genes highly differentiated between the two bird strains, as evidenced by a higher fixation index (F_{ST}), which indicates greater variability between relative to within populations. This list includes genes with a known role in bird song, such as DRD3, which encodes the dopamine D3 receptor and has also been linked to schizophrenia, as well as genes causally related to important motor and sensory neuropathies, such as HK1 which codifies the brain form hexokinase and when mutated leads to Charcot-MarieTooth disease. We also introduce sets of genes for which observed variability deviates from the expected in each bird strain, as evidenced by Tajima's D. We report overall reduced levels of genetic variability in the BF. However, genes showing increased variability in the BF relative to its ancestor strains also exist. We have inferred a demographic model shaping BF's genetic variation, which corroborates historical reports, and have estimated the impact of the population bottleneck during domestication. Our results have the potential to guide further comparative efforts toward identifying similar patterns of evolutionary change between humans and other primates or hominid lineages (e.g. Denisovans and Neanderthals).