

Research opportunity: Evolutionary Forces in the Bengalese Finch Song: Parallels and Implications for the Study of Human Language Evolution

Songbirds have provided a highly successful animal model for the study of certain aspects of human speech, including its production, perception and evolution. Among existing songbird models, the Bengalese Finch (BF) (*Lonchura striata domestica*) is becoming a popular one, due to its remarkably flexible vocal behavior, which evolved during BF's domestication from the white-backed munia (WBM) (*Lonchura striata*). Different hypotheses have been proposed to explain how BF evolved a more flexible vocal behavior than its wild ancestor: one such hypothesis argues for the major role of positive selection (PS) (i.e. female choice for more complex songs); while an alternative hypothesis argues for the major role of relaxation of purifying selection (RS) (i.e. on-going relaxation of sources of purifying selection commonly found in the wild, but absent in the domesticated setting, such as pressures to avoid confusion with other cohabiting finch species). A more flexible vocal behavior is also assumed to distinguish the current human vocal behavior from its ancestral state, and the roles of PS and RS in human language evolution have also been intensely debated. Given the parallels between the changes in vocal behavior in BF relative to WBM and the proposed changes in the current human vocal behavior relative to its ancestral state; along with the existence of striking analogies between birdsong and human speech, we consider the WBM/BF songbird system to be a suitable model for providing insight into the evolution of human speech. We have begun an investigation of the evolutionary forces underlying the changes in vocal behavior in BF relative to WBM. This study involves whole-genome sequencing of individuals within the two bird strains, and subsequent scans for signatures of PS or RS, which will allow us to identify genes that have undergone PS or RS in BF relative to WBM. The final steps of this study involve the search for evolutionary convergence between analogous genes or biological pathways in BF relative to WBM and in humans relative to other primates.

This work will empirically identify evolutionary and genetic processes that correlate with increased social learning and flexibility of vocal behavior in an animal model that parallels key aspects of human language evolution. Furthermore, because BF and WBM are strains of the same species, comparisons between them present less phylogenetic confounds relative to comparisons of different songbird species. Birdsong is a paradigmatic model for the study of speech disorders in translational medicine. We expect this work to provide insights into understanding such disorders.

Expected time commitment – Min of 8h/week or 30h/month. This can be spread throughout the week days and includes attending lab meeting. Availability to work at later times (5-9pm), and possibly on the weekends.

Lab responsibilities – Work on the processing and analysis of next generation whole-genome sequencing data of two songbird strains. Even though, close mentoring will be provided by Professor White, Madza Farias-Virgens and collaborators at the White Lab, the student is expected to take on these responsibilities in the most autonomous way possible; to have initiative to develop skills in an autonomous way. The student will be accessing unique, unpublished data, it is therefore expected for any sort of data manipulation or sharing to be explicitly communicated to both direct mentors, Professor White and Madza Farias-Virgens. Other responsibilities include participating in lab and other meetings TBD, and engage in common lab practices in place at the White Lab.

Qualifications - Experience with running programs from the command line, shell scripting, using a cluster, writing programs/scripts in C/C++, Perl, or Python to parse large files, and using R. Some background on genetic variation and interest in population genetics are major plus. Specific fitting Majors are Computational and Systems Biology (B.S.), Ecology, Behavior, and Evolution (B.S.), Microbiology, Immunology, and Molecular Genetics (B.S.), Molecular, Cell, and Developmental Biology (B.S.), Neuroscience (B.S.), Physiological Science (B.S.), Psychobiology (B.S.), Psychology (B.A.), and Statistics (B.S.), but it could also include Biochemistry (B.S.), Biology (B.S.), Biophysics (B.S.), Chemistry (B.S.), Chemistry/Materials Science (B.S.), Cognitive Science (B.S.), Human Biology and Society (B.A.), Linguistics (B.A.), Linguistics and Computer Science (B.A.), Linguistics and Psychology (B.A.), Marine Biology (B.S.), Mathematics (B.S.), Mathematics, Applied (B.S.), Mathematics/Applied Science (B.S.) Mathematics of Computation (B.S.).

Number of positions – 1 Contact – Madza at madzayasodara@ucla.edu

Position available for Spring and Summer 2017 and beyond

