"Languages and Genes" Can typological differences between languages be related to genetic differences between their speakers?

Natalia Rakhlin, Communication Sciences and Disorders, Associate Professor, Feng Tao, Biological Sciences, Ph.D. candidate, Chuanzhu Fan, Biological Sciences, Assistant Professor and the members of the WSU interdisciplinary working group “Languages and Genes”

Wednesday, November 8, 2017 12:30PM-1:30PM Rm. 2339 F/A Bldg

Although the role of the human genome in language evolution and language acquisition is no longer controversial, the precise contribution of “nature” in the phylogeny and ontogeny of language is still debated.

We have pursued a novel avenue for discovering genetic underpinnings of the capacity for human language, focusing on the broad variation in sound systems and grammatical organization found in world languages. We hypothesized that some of this diversity has genetic bases, as it plausibly arose from subtle but detectable differences between members of human populations with respect to the functioning of the perceptual/articulatory and cognitive systems rooted in the human genome. We characterized 416 languages in relation to 20 features of phonological, morphological, and syntactic structure. For each respective population, we retrieved allele frequency information from a public web-based database and compared populations with positive and negative values for each feature on the frequency of the ancestral versus derived alleles of informative SNPs (single nucleotide polymorphisms) in candidate “language genes” identified in previous research. We found significant differences between languages that morphologically mark verbs for past tense and those that do not. The differences involve SNPs located in genes DCDC2 and KIAA0319, involved in neuronal migration during development of the cerebral cortex and previously found to be associated with language-related phenotypes. We will discuss implications of our findings for the relationship between biological factors and linguistic diversity.

Dr. Natalia Rakhlin is an Associate Professor in the Department of Communication Sciences and Disorders. She is a clinically oriented linguist specializing in child language acquisition and developmental language disorders.

Dr. Chuanzhu Fan is an Assistant Professor in Department of Biological Sciences. His research is integrating computational and high-throughput experiments addressing genetics and genomics underlying the evolution and functionalization of genes and genomes and defined new direction of the contribution of heritable DNA mutation and DNA methylation epimutation to divergence of genes and genomes in plant species.

Feng Tao is a Ph.D. candidate in Department of Biological Sciences under Dr. Chuanzhu Fan’s supervision. He is 2017-2018 Thomas C. Rumble University Graduate Fellow.

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