

“Scanning genomes for the footprints of historic selection”

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Abstract

When a selective sweep occurs in the chromosomal region around a target gene in two populations that have recently separated, it produces three dramatic genomic consequences: 1) decreased multi-locus heterozygosity in the region; 2) elevated or diminished genetic divergence (F_{ST}) of multiple polymorphic variants adjacent to the selected locus between the divergent populations, due to the alternative fixation of alleles; and 3) a consequent regional increase in the variance of F_{ST} (S^2F_{ST}) for the same clustered variants due to the increased alternative fixation of alleles in the loci surrounding the selection target. In the first part of our study, to search for potential targets of directional selection, we developed and validated a resampling based computational approach, we then scanned an array of 30 different-sized moving windows of SNP variants (5 to 65 SNPs) across the human genome in a set of European and African American population samples with 183,997 SNP loci after correcting for the recombination rate variation. The analysis revealed 180 regions of recent selection with very strong evidence in either population or both. In the second part of our study, we compared the newly discovered putative regions to those sites previously postulated in the literature, using methods based on inspecting patterns of linkage disequilibrium, population divergence and other methodologies. The newly found regions were cross-validated with those found in nine other studies that have searched for selection signals. Our study was replicated especially well in those regions confirmed by three or more studies. These validated regions were independently verified using a combination of different methods and different databases in other studies, and should include fewer false positives. The main strength of our analysis method compared to others is that it does not require dense genotyping and therefore can be used with data from population based genome SNP scans from smaller studies of humans or other species.

About the speaker: Taras Oleksyk studies human genetics, epidemiology and genomics as a Scientist II at the Laboratory of Genomic Diversity, and teaches as Adjunct Professor, at the Johns Hopkins University, Zanvyl Krieger School of Arts and Sciences, Advanced Academic Programs, Rockville, MD. His main research interests are population genetics and genomics, and can be directly applied to the field of animal biology. Dr. Oleksyk received a Ph.D. in Toxicology from the Institute of Ecology, University of Georgia, Athens, GA in 2001. His doctoral research was in population genetics of vertebrate populations exposed to environmental radioactivity in Chernobyl. He received his MS in Biology from Bowling Green State University, Bowling Green, OH, and his Undergraduate Diploma from the Uzhgorod National University, Uzhgorod, Ukraine in 1992.