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The evolution of taste perception in human populations

The ability to detect bitter and sweet compounds has been largely attributed to genetic variation in the TAS2R and TAS1R genes, respectively. However, few studies have characterized patterns of diversity and signatures of selection at these genes in human populations, particularly in Africa. To overcome this gap in knowledge, we examined sequence variation at 22 of the 25 bitter taste receptor genes in rainforest hunter-gatherers and Bantu-speaking agriculturalists from West Central and Central Africa. Separately, we examined sequence variation at three well-known genes (namely TAS1R1, TAS1R2, and TAS1R3) associated with sweet perception in a larger set of global populations. Based on our analyses, we identified 353 single nucleotide polymorphisms across the TAS2R genes, 35 of which have never been previously described. We also observed striking signatures of positive selection, including unusually long haplotypes around alleles at the TAS2R genes. In addition, some of these signals of selection were shared between rainforest hunter-gatherers and Bantu-speaking agriculturalists. Similarly, we observed extended haplotype structure around ancestral alleles at the TAS1R1 and TAS1R2 sweet perception genes in African populations indicative of a recent selective sweep. In contrast, however, we detected long-range haplotypes around derived alleles at the same sweet-associated genes in non-African populations, indicating a divergent pattern of selection that likely emerged after humans left Africa ~60,000-80,000 years ago. Overall, this research provides new insights into the evolution of biologically relevant taste perception and diet in diverse human populations.

IN PERSON

HEB Seminar
April 29, 2024 | 12:00 PM – 1:00 PM
Allan Hancock Foundation Building - Torrey Webb Room