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Abstract

The Palatability Dance—SNPs and Genetic Taste Scores of Umami, Sweet, and Bitter Taste Receptors (TAS1R and TAS2R Genes) †

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Abstract: Background and objectives: Several factors may account for food behavior, including common genetic variation. Robust evidence shows that specific single-nucleotide polymorphisms (SNPs) are involved in palatability phenotypes. Considering the limited knowledge of these associations in the context of admixed groups, like the Brazilian population, we aimed to investigate associations of SNPs in the TAS1R and TAS2R taste receptor gene families with diet quality. Methods: A sample of 901 individuals ≥ 12 years old from the general population, categorized into age groups (adolescents, adults, and elderly), was interviewed in the Health Survey of Sao Paulo (ISA-Capital). Data on socioeconomic, demographic, and health characteristics were collected, including dietary information from two 24 h recalls in two nonconsecutive days and blood samples. The 24 h recalls were analyzed using the Revised Brazilian Healthy Eating Index (BHEI-R), comprising 12 components referring to food groups, nutrients, and calories from saturated fats, alcohol, and added sugar. Blood samples were genotyped for 255 SNPs in the TAS2R gene family (related to bitterness) and 73 SNPs in the TAS1R (related to sweetness and umaminess). BHEI-R was normally inversed transformed (invBHEIR). After data cleaning and quality control procedures, genotype and phenotype data of 637 individuals were made available for association analysis with invBHEI-R using linear models adjusted for age, age2, age × sex, sex, BMI, and the two first principal components of ancestry. Genetic taste scores (GTSs) were derived from the significant SNPs of each gene family and tested for associations. Analysis was performed with the software R version 4.0.2 using a significance level of 0.05. Results: There were 31 SNPs of TAS2R genes and four SNPs of TAS1R genes significantly associated with BHEI-R ($p < 0.05$). GTSs were positively associated, and their use increased the model's performance, especially with TAS2R SNPs (r^2 rose from 0.135 to 0.188). Conversely, the estimated effect of the TAS1R score on BHEI-R was 2.02 higher than the TAS2R one. Discussion: Our results show potential genetic influences on diet quality by applying genetic taste scores. Unraveling associations between SNPs and food intake might help guide public policies towards healthier food behavior considering genetic differences, i.e., personalized nutrition.

Keywords: diet quality; palatability; TAS receptors; SNPs; highly-admixed population

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