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Genome-wide association study of food liking in 162,000 people uncovers the genetic bases of food liking.

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ABSTRACT:

Variable preferences for different foods are among the main determinants of their intake and are influenced by many factors including genetics. Despite ~50% heritability, studies aimed at uncovering food liking genetics have focused mostly on taste receptors. Here we present the first results of a large-scale genome-wide association study of food liking conducted on 161,625 participants from UK-biobank. Liking was assessed over 142 specific foods using a 9-point Likert scale. After performing GWAS we used genetic correlation coupled with structural equation modelling to create a multi-level hierarchical map of food liking which identified 3 main dimensions: high caloric foods defined as “innate”, strong tasting foods ranging from alcohol to strong tasting vegetables defined as “learned” and finally “low caloric” foods such as fruit and vegetables. The “innate” dimension was genetically completely independent from the other two suggesting that two independent processes underlie to liking high reward foods from the learned/low caloric ones. Genetic correlation analysis with corresponding food consumption traits evidenced a high correlation (~0.75) while showing twice the heritability. GWAS analysis identified 1401 food liking-SNP associations located in 173 genomic loci several of which close to taste or olfactory receptors. Genetic correlation with morphological and functional brain data (33,224 participants) results in associations of the three liking dimensions with non-overlapping, distinct brain areas and networks, suggestive of separate neural mechanisms underlying the liking determinants. In conclusion, we created a comprehensive and data-driven map of genetic determinants and associated neurophysiological factors of food liking beyond taste receptor genes.