proceedings

Abstract

The Genetics of Sweet Taste: Perception, Feeding Behaviours, and Health †

Harry Stevens [1,2,*], Francesco Piluso [1,2], Paolo Gasparini [1,2,3], Yiannis Mavrommatis [4], Leta Pilic [4], Catherine Anna-Marie Graham [2,5] and Maria Pina Concas [3]

1 Department of Medical Sciences, The University of Trieste, 34127 Trieste, Italy; francesco.piluso@phd.units.it (F.P.); paolo.gasparini@burlo.trieste.it (P.G.)
2 Lake Lucerne Institute, 6354 Vitznau, Switzerland; cat.maher@llui.org
3 Institute for Maternal and Child Health, IRCCS "Burlo Garofolo", 34137 Trieste, Italy; mariapina.concas@burlo.trieste.it
4 Faculty of Sport, Allied Health and Performance, St Mary's University Twickenham, London TW1 4SX, UK; yiannis.mavrommatis@stmarys.ac.uk (Y.M.); leta.pilic@stmarys.ac.uk (L.P.)
5 Cereneo Foundation—Center for Interdisciplinary Research, 6353 Vitznau, Switzerland
* Correspondence: harry.stevens@phd.units.it
† Presented at the 14th European Nutrition Conference FENS 2023, Belgrade, Serbia, 14–17 November 2023.

Abstract: Background: Sweet taste is partly modified by genetics. The rs35874116 single-nucleotide polymorphism (SNP) in taste receptor type 1 member 2 (TAS1R2) reduces the availability of a G protein-coupled receptor (GPCR), which binds to 'sweet' molecules. This might alter sweet taste perception, diet choices, and health outcomes. However, these findings, and other genes and pathways involved in sweet taste are yet to be identified. Therefore, a candidate gene study on TAS1R2 and a genome-wide association study (GWAS) exploring these outcomes were performed. Methods: TAS1R2 rs35874116, sweet perception, liking, diet, and health were investigated in two age- and sex-matched European cohorts (UK, $n = 50$/Italy, $n = 235$). Linear models were used to explore associations. The GWAS was performed with 2555 Italian participants. Associations with sweet food liking, food adventurousness (FA), reward dependence (RD), and health were explored. Results: The wildtype of TAS1R2 was associated with increased sweet taste and food liking ($p = 0.049$, $\beta = 0.62$, $p = 0.038$, $\beta = 0.45$), increased fibre consumption ($p = 0.006$, $\beta = 7.95$), and decreased HDL cholesterol ($p = 0.025$, $\beta = -3.56$). The GWAS identified rs58931966 in the regulator of G-protein signalling 9 (RGS9) gene. The minor allele was associated with decreased sweet food liking ($p = 7.05 \times 10 - 9$, $\beta = 0.3$), a higher BMI ($p = 0.007$, $\beta = 0.391$), serum glucose ($p = 0.013$, $\beta = 1.211$), lower FA ($p = 0.049$, $\beta = -0.065$), and RD ($p = 0.011$, $\beta = -3.840$). Discussion: The TAS1R2 results show that taste receptor variations are associated with preference, diet, and health-related outcomes. TAS1R2 not reaching significance in the GWAS shows that sweet food liking is modified by pathways besides taste reception. RSG9 is expressed in the striatum, which is involved in the mesolimbic reward pathway, which is activated by sweet taste. RGS9 rs58931966 may moderate dopaminergic signalling in response to sweet foods via the negative regulation of G-protein signalling. This might explain why the minor allele was associated with reduced RD. The lower FA might decrease preference for bitter-tasting vegetables, which could explain the higher BMI and serum glucose. The FA and RD results provide evidence that food choice depends on psychological/biological interplay. These results show that sweet taste is modified by multiple pathways and genes, and variations can modify taste, diet, and health outcomes.

Keywords: genetics; diet; health; sweet-taste; sweet-liking

check for updates

Citation: Stevens, H.; Piluso, F.; Gasparini, P.; Mavrommatis, Y.; Pilic, L.; Graham, C.A.-M.; Concas, M.P. The Genetics of Sweet Taste: Perception, Feeding Behaviours, and Health. *Proceedings* **2023**, *91*, 342. https://doi.org/10.3390/proceedings2023091342

Academic Editors: Sladjana Sobajic and Philip Calder

Published: 19 February 2024

Author Contributions: Conceptualization, H.S., P.G., Y.M., L.P., C.A.-M.G. and M.P.C.; methodology, H.S., Y.M., L.P., C.A.-M.G. and M.P.C.; software, H.S., F.P. and M.P.C.; validation, F.P., C.A.-M.G.

and M.P.C.; formal analysis, H.S., C.A.-M.G. and M.P.C.; investigation, H.S., Y.M., L.P., C.A.-M.G. and M.P.C.; resources, P.G., Y.M. and L.P.; data curation, P.G., Y.M. and L.P.; writing—original draft preparation, H.S., C.A.-M.G. and M.P.C.; writing—review and editing, H.S., F.P., C.A.-M.G. and M.P.C.; supervision, P.G., C.A.-M.G. and M.P.C.; project administration, P.G., Y.M., C.A.-M.G. and M.P.C.; funding acquisition, P.G., Y.M. and L.P. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the Italian Ministry of Health, through the contribution given to the Institute for Maternal and Child Health IRCCS Burlo Garofolo, Trieste, Italy (5 per mille 2015 senses, genetics of senses and related diseases, CUP: C92F17003560001, to P.G.).

Institutional Review Board Statement: The study was conducted in accordance with the Declaration of Helsinki and approved by the Institutional Review Boards and Ethics Committes San Rafaelle Hospital, IRCCS Burlo Garofolo, and St Mary's University (under the univocal code Prot. CE/V-78, 06/08/2007/SMU_ETHICS_2021-22_217).

Informed Consent Statement: Informed consent was obtained from all subjects involved in the study.

Data Availability Statement: A subset of the data is already available in the European Genome-phenome Archive (EGA) at the following links. FVG cohort: BAM files https://www.ebi.ac.uk/ega/studies/EGAS00001000252 (accessed on 3 November 2023); sample list, vcf files https://www.ebi.ac.uk/ega/studies/EGAS00001001597 (accessed on 3 November 2023); https://www.ebi.ac.uk/ega/datasets/EGAD00001002729 (accessed on 3 November 2023); VBI cohort: BAM files https://www.ebi.ac.uk/ega/studies/EGAS00001000398 (accessed on 3 November 2023); https://www.ebi.ac.uk/ega/studies/EGAS00001000458 (accessed on 3 November 2023). Other data presented in this study are available on request from the corresponding author.

Conflicts of Interest: L.P. is the founder of Optimyse Nutrition LTD, a personalised nutrition company offering genetic testing to clients. Y.M. is an advisor in nutrition genetics for the wellbeing company MyHealthChecked.