

Sensory acuity for alarming oral sensations associates with specific networks of salivary bacteria and dietary intakes

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TOPIC: Fundamentals of sensory perception; Sensory science and diversity; Emerging sensory and consumer science methodologies; Sensometrics; Challenges and opportunities in a digital sensory world; Effective use of sensory science in product development; User experience of food and non-food products; Culinary arts, Hospitality and Sensory and Consumer Science; Global resource challenges, sustainability & food waste; Collecting and communicating sensory properties in the global village; Education and training in Sensory and Consumer science

Abstract (Max 300 words):

Oral microbiota-host interactions are increasingly regarded as relevant in explaining interpersonal variations in taste perception and food intake. Nonetheless, whether such links may be fostered by specific patterns of bacterial co-habitation has yet to be empirically proven.

To this end, we used 16s rRNA gene sequencing to profile the salivary microbiota of 100 healthy individuals (52% women; 18-30 y/o), who provided both hedonic and psychophysical responses to 5 liquid and 5 solid commercial foods, each selected to evoke a clearly recognizable target taste (sweet, sour, bitter, salty) or sensation (pungent). The same cohort also filled out a series of food-related psychological measures and a 4-day dietary record.

Unsupervised data-driven clustering of the genus-level Aitchison distances supported the existence of two salivary microbial clusters (CL-1, CL-2). Compared to CL-1 (n = 57; 49.1 % women), CL-2 (n = 43; 55.8 % women) showed greater acuity for a range of alarming oral sensations (astringent, bitter, sour) in both liquid and solid foods, as well as pronounced tendencies to crave sweet foods and to endorse prosocial behaviors. Relatedly, CL-2 reported habitually consuming more simple carbohydrates and fewer beneficial nutrients (e.g., vegetable proteins).

Intriguingly, CL-2 harbored greater amounts of cariogenic bacterial taxa (e.g., genus *Lactobacillus*), whilst the salivary specimens of CL-1 were enriched in microbes allocated to *Clostridia* class commonly linked to healthful diets (e.g., genus *Lachnospiraceae* [*G-3*]). Moreover, CL-1 was assigned to a spectrum of inferred microbial functional pathways related to the biosynthesis of a sour-eliciting compound (acetate), whose putative involvement in sensory adaptation phenomena might further explain the hyporesponsiveness to alarming oral sensations distinguishing this cluster.

To conclude, this contribution suggests that dietary habits may also be affected by microbe-microbe and microbe-taste interactions, and encourages further research to unveil a potential “core” taste-related salivary microbiota.