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Articles Highlighted

Molecular Determinants of Monellin's Sweetness

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Monellin is an intensely sweet-tasting protein consisting of 2 subunits that could offer a potential alternative to sugar and synthetic high-intensity sweeteners. It activates the human sweet taste receptor, but little is known about the structural basis of this interaction. To elucidate the basis of monellin's sweetness, Templeton et al. now crystallized less sweet tasting mutants of a monellin variant in which the 2 subunits are connected by a dipeptide linker. The crystal structures, however, revealed that the mutant polypeptides essentially adopted wild-type structures with only slight alterations to amino acid positions within the protein core, which are unlikely to account for the reduced sweetness of the mutant proteins. Biophysical analysis also demonstrated that the residual sweetness of the mutants did not well correlate with their thermal stability. Finally, solution spectroscopic measurements uncovered changes in protein flexibility and carboxy-terminal structures that correlated with protein function. The data allowed the authors to propose that altered protein core affects a critical C-terminal helix and that interaction of monellin with the sweet taste receptor is sensitive to the relative positions of key residues across its protein surface.

Sweet Taste Receptor Gene Variation and the Taste of Aspartame

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Unlike sugars which are perceived as sweet by humans and elicit attraction in numerous mammals, the artificial high-intensity sweetener aspartame is only sweet to humans, apes, and Old World monkeys, whereas most other mammals are indifferent to it. The behavioral deficit to respond to aspartame by the latter is paralleled by the absence of gustatory neural responses. Moreover, data from cell-based receptor assays suggest that the species differences are due to the peculiarity of aspartame to activate the sweet taste receptor dimer, Tas1r2-Tas1r3, in a species-specific fashion. Li et al. now established and compared the sequences the *Tas1R2* and *Tas1r3* genes in a number of aspartame taster and non-taster species. This led them identify variant sites in Tas1r2 and Tas1R3 that distinguished aspartame tasting from non-tasting species. Molecular docking of aspartame to computational models of the sweet taste receptors then suggested that alterations in a previously unknown allosteric binding site in Tas1R2 likely accounts for the differences in aspartame's sweet taste across species.

Discriminating Citric Acid from Quinine

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Various lines of evidence from sensory studies in humans and rodents point to some degree of difficulty in discriminating bitter from acidic stimuli. Moreover, some gustatory neurons respond to both, bitter compounds and acids. In the present study, Treesukosol et al. investigated in mice, a preferred model system, to what extent the taste perception evoked by acids or bitter compounds are distinct from one another. Using a 2-response operant discrimination task, they demonstrated that C57BL/6J mice had severe problems to distinguish citric acid from the model bitter compounds quinine and propylthiouracil, whereas they easily discriminated these chemicals and NaCl from sucrose. In addition, mice which learned to avoid quinine also avoided citric acid but not salty or sweet stimuli in brief access tests. However, the opposite did not apply. Mice conditioned to avoid citric acid did not generalize the sour stimulus with quinine. Based on these findings, the authors propose that, even though citric acid and quinine are not perceptually identical, they possess common chemosensory properties making their discrimination difficult.

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