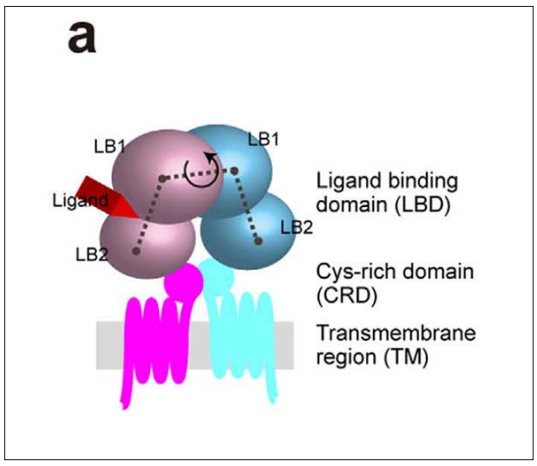
Research Highlights

Fishy approach reveals how things taste sweet or umami

Okayama University have identified the protein conformational changes associated with sweet and umami taste recognition.



Yamashita and colleagues identified the structure and conformational changes in type 1 taste receptor proteins during the recognition of sweet and umami tastes

Taste recognition occurs as specific protein receptors in the mouth interact with molecules in eaten food. The proteins responsible for tasting sweet and umami molecules are described as taste receptor type 1 (T1r) and are common to vertebrates in general, including fish, birds and mammals. It is known that the T1r family of variants interact with food molecules in paired up structures - "heterodimers" – to allow the distinction between umami, sweet, and other tastes. However, difficulties in producing and purifying these proteins have inhibited attempts to directly investigate what interactions occur during sweet and umami taste recognition.

Atsuko Yamashita and a team of researchers at RIKEN SPring-8 Center, the National Institute of Natural Science, the Graduate University for Advanced Studies (SOKENDAI), the Food Research Institute, Osaka University, Okazaki Institute for Integrative Biosciences, and Okayama University have now successfully demonstrated a way around these difficulties. They identified a fish known as medaka or "Japanese rice fish" as a suitable vertebrate model for investigating umami and sweet tastes.

The researchers found they could produce – "express" – the ligand binding domain of the T1r2 and T1r3 proteins in medaka fish as functional heterodimeric proteins. They express the proteins in a glycosylated form, which is closer to the physiological state.

The study identifies the conformational changes the proteins undergo during sweet and umami taste recognition for the first time. The results suggest that venus-flytrap structures in the protein dimers are keys to their ability to transmit the sweet and umami information to our bodies through conformational changes.

Publication and Affiliation

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Koji Yonekura[1], Madoka Shimizu[4], Nanako Atsumi[7], Norihisa Yasui[7], Takaaki Hikima[1], Masaki Yamamoto[1], Yuji Kobayashi[5] & Atsuko Yamashita[1,7] Taste substance binding elicits conformational change of taste receptor T1r heterodimer extracellular domains. *Scientific Reports*, 6, 25745 (2016).

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