additional amino acid chemoreceptor(s). None of the other MLPs with tandem PAS-like domains appeared to mediate amino acid taxis. We then turned our attention to MLPs with a single PAS-like domain. The overproduction of two members of this family, Mlp2 and Mlp3, in the Δmip2 Δmip3 strain enhanced taxis to serine in capillary assays, suggesting that these MLPs mediate attractant responses to serine. Interestingly, the expression of Mlp3, but not Mlp2, enhanced taxis to alanine, cysteine, glycine and threonine, implying the difference in specificity between these MLPs. However, we failed to detect direct binding of serine to these MLPs in isothermal titration calorimetry measurements with periplasmic fragments of Mlp2 and Mlp3, as well as membrane vesicles of an otherwise receptor-less strain of Escherichia coli expressing Mlp2 or Mlp3. This raises the possibility that these MLPs sense serine via periplasmic serine-binding protein(s).

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**Functional diversity of bitter taste receptor TAS2R16 by amino acid substitution**

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In mammals, bitter taste is mediated by TAS2Rs, which belong to the large family of seven transmembrane G protein-coupled receptors. Since TAS2Rs are directly involved in the interaction between mammals and their dietary sources, it is likely that these genes evolved to reflect species-specific diets during mammalian evolution (1, 2). Here, we investigated the sensitivities of TAS2R16s of various primate by using a cultured cell expression system in combination with behavioral tests (3). We found that the sensitivity of each primate species varied according to the ligand. Especially, the sensitivity of TAS2R16 of Japanese macaques to salicin, a bitter compound contained in the bark of Salicaceae (willow) plants, was much lower than that of human TAS2R16, which was supported by behavioral tests. The replacement of amino acid residue at position 86 caused dynamic changes in the sensitivities of TAS2R16. These results suggest the possibility that bitter taste sensitivities evolved independently by replacing specific amino acid residues of TAS2Rs in different primate species to adapt to accessible food items they use. The amino acid residues responsible for the specificities of each ligand would be discussed in the presentation.

References


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**Ensemble Docking Simulation for β2 Adrenergic Receptor Using Elastic Network Models**

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G protein-coupled receptors (GPCRs) are membrane proteins involved in signal transduction and participate in many diseases. Therefore, the receptors are important targets in the field of drug discovery. Protein structural information is useful to understand their function and enable us to develop new therapeutic molecules. However, these membrane proteins are not easy to crystallize. And it sometimes happens that rigid-body protein docking simulation for GPCR based on one ligand-receptor complex structure to discovery new drugs lead to inefficient results with own flexible conformation. In this study, GPCR’s conformational polymorphism into the virtual screening of β2 adrenergic receptor (ADRβ2) using elastic network model (ENM) and normal mode analyses (NMA). First, we build the ENM of ADRB2 and performed NMA. Next, we make virtual models based on ADRB2’s elastic network normal mode analysis data and we do docking simulation for the virtual model group to make up for the above shortcoming. According to the results, the screening efficiency of virtual model group is improved by over 20% against of that of the initial model.