

# Development of sensory genomics and basic analysis of taste bioinformatics

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## 【 Outline of survey 】

Taste is a fundamentally important factor for animals to take a proper food-intake action and for humans to make up advanced dietary cultures and to develop sophisticated food industries. With it as a background, this study starts particularly for the purpose of analyzing signal-processing systems involved in taste perception and recognition, and thus understanding how the taste of food as an exogenous chemical signal is converted to the sense of taste as an endogenous physiological signal.

To attain the purpose the study uses the aspect of bioinformatics as well as the “ sensory genomics ” which refers to the genome science applicable to our sensation. Different from conventional taste physiology and biochemistry, the sensory genomics is a unique and up-to-date science. The uniqueness is found in the use of DNA-microarray technology for systematizing a variety of information about gustatory gene expression profiles in connection with molecular features in multi-stage taste sensory systems and individual taste-signaling processes. The study also has an aim to apply the obtained information to objective evaluation of food tastes as in the example of developing new foods by taste synergism and cancellation. The execution of such applications as well as basic analyses is an important target of the study.

## 【 Expected results 】

The study plans to produce transgenic mice and Medaka fish with mutated senses of taste. DNA-microarray analysis of these sensitive models will elucidate their signal-processing mechanisms proceeding in taste cells, at taste cell-taste neuron synapses, and through the pathway from each taste neuron to the central nervous system. In case it is technically impossible to use humans, the use of such model animals is indispensable as a basis of taste research and this approach will no doubt produce fully expected results.

## 【 References by the principal researcher 】

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Matsumoto, I., Emori, Y., Nakamura, S., Shimizu, K., Arai, S., and Abe, K. DNA microarray cluster analysis reveals tissue similarity and potential neuron-specific genes expressed in cranial sensory ganglia. *J. Neurosci. Res.* **74**, 818-828 (2003).

【 Term of project 】 FY 2004 - 2008

【 Budget allocation 】 82,100,000 yen

【 Homepage address 】 <http://park.itc.u-tokyo.ac.jp>