

Genome-wide identification of genes for anorexia and their cascade analysis on disease development by functional study

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【Outline of survey】

Eating disorder is now quite prevalent, especially in young generations, the percentage of its contraction amounting to as many as 0.2%~2%. However, there is no effective treatment so far available, resulting in poor prognosis with the death rate of about 6%. Therefore, identification of genetic basis followed by clarification of pathogenesis of eating disorder is an important subject for curing the disease. We have so far identified 11 candidate gene regions and 4 candidate genes for anorexia using our original genome-wide association technique with 30,000 microsatellites. It must be noted that most of the gene regions and genes represent genome segments implicated to be involved in control and/or regulation of neural cells. In this project, our objectives are to elucidate the detailed cascade and molecular mechanism for disease development by function analysis on these susceptible genes by network analysis, proteomics, construction of disease model mouse and chemical genomics with design of low molecule ligand to suitable targets, contributing to establishment of the molecular basis on the treatment and prevention of eating disorder.

【Expected results】

Our aim in this project lies in functional analysis on several susceptible genes for anorexia we have first identified and also development of medical treatment based on their information. Therefore, outcomes from our project can be expected to contribute to acceleration of research for drug design and prevention of eating disease. Taking it into consideration that anorexia sometimes develops into bulimia, these two eating disorder may share the same genetic basis on disease development. This means that our project can also provide us with an important clue to tackle with fat problem most developed countries have now seriously encountered as health medical care.

【References by the principal investigator】

1. Tamiya G, Shinya M, Imanish T, Ikuta T, Kamatani N, Gojobori T, Bahram S, Hidetoshi Inoko H: Whole genome association study of rheumatoid arthritis Using 27,039 microsatellites. *Hum Mol Genetics* **14**: 2305-2321, 2005
2. Abi-Rached L, Gilles A, Shiina T, Pontarotti P, Inoko H: Evidence of en bloc duplication in vertebrate genomes. *Nature Genetics* **31**: 100-105, 2002.

【Term of project】 FY2007—2011

【Budget allocation】 18,000,000 yen

(2007 direct cost)

【Homepage address】

<http://mls.med.u-tokai.ac.jp/mlsRes.htm>