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Estimating Alzheimer's disease causative genes by an evolutionary medicine approach

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Alzheimer's disease patients are increasing with the aging of the world's population, becoming a huge health care and social burden. To find the cause of various diseases, in recent years, scientists have focused within the human genome on copy number variations (CNVs), which are changes in the number of genes within a population.

Likewise, a group of genes responsible for a gene number change has also been reported for Alzheimer's disease, but to date, it has not been easy to identify a causative gene from multiple genes within the pathogenic CNV region.

Now, a new approach to finding Alzheimer's disease (AD) causative genes was estimated by paying attention to special duplicated genes called "ohnologs" included in the genomic region specific to AD patients. Human ohnologs, which are vulnerable to change in number, were generated by whole genome duplications 500 million years ago.

In a new study published in the advanced online edition of *Molecular Biology and Evolution*, Mizuka Sekine and Takashi Makino investigated the gene expression and knockout mouse phenotype for ohnologs, and succeeded in narrowing down the genetic culprits. The narrowed gene group had a function related to the nervous system and a high expression level in the brain which were similar to characteristics of known AD causative genes.

Their findings suggest that the identification of causative genes using

ohnologs is a promising and effective approach in diseases caused by dosage change.

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