

Progress in Japan on the genomic analysis of molds

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The effort in Japan to analyze the genome of molds is currently focused on *Aspergillus oryzae*, which has been utilized to brew traditional Japanese fermented foods, such as sake, miso and soy sauce, for more than a thousand years*.

The genome of *A. oryzae* is currently being mapped by Expressed Sequence Tag (EST) analysis; the total number of ESTs has reached about 17,000, with 6,700 clusters determined by the end of year 2000. It is estimated that at least 5,000 independent EST clones have been isolated. The number of genes represented by the EST clones is believed to be about 40% of the total genes in the *A. oryzae* genome.

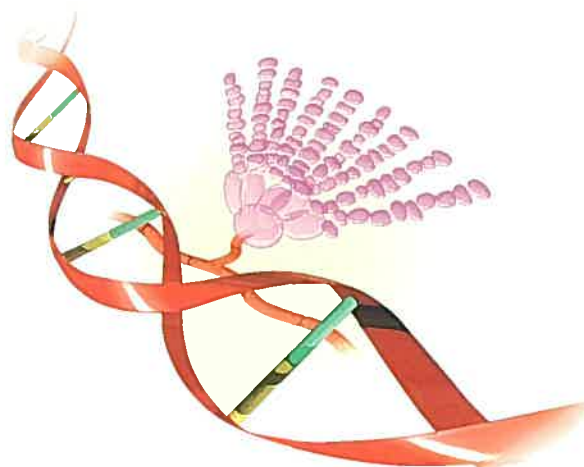
Whole-genome sequence analysis of *A. oryzae* was initiated in August 2001. Whole-genome shotgun sequencing procedures have resulted in the accumulation of sequence data representing about 6 times the length of the entire genome of *A. oryzae*. Analysis of the data revealed a unique sequence of 37 million base pairs, which indicates that at least 95% of the whole genome sequence has been determined. Based on this data, together with the results of EST analysis (5,000 clones) as described above, and prediction of gene identification, we estimate that the total number of genes in the genome of *A. oryzae* to be about 13,000.

Since April 1998, an international consortium has performed whole-genome analysis of *A. nidulans*, followed by analysis of other molds, including *A. fumigatus*, *A. niger*, *Neurospora crassa*, etc. in the U.S. and Europe. The

Japanese group and the American and European groups have exchanged their genetic data to allow more accurate prediction of the individual gene functions studied by each group, as well as more efficient and unified annotation of individual genes.

The total number of known genes in the *A. oryzae* genome exceeds the earlier estimate by about 40%, which indicates that *A. oryzae* is a very valuable genetic resource. We anticipate that *A. oryzae* will make more contributions to industry when the functions of the genes of *A. oryzae* are revealed by post-genome sequencing techniques such as gene expression analyses by DNA microarrays and proteomic analyses.

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