

TABLE 8

probe	signal of PM probe	signal of MM probe		
Mt6s at 653 337	11238	63439	DNA sequence of PM	GAATCAATTAACCTTATGGTTTCTTA
			DNA sequence of tested strain	GAATCAATTAACATATGGTTTCTTA
Sc-21 33-1 _at 59 _283	4725	27825	DNA sequence of PM	CCCCTTAGTGCGAAGATATCTTTT
			DNA sequence of tested strain	GCTCTTGGTGACCAGGATACTTTTT

INDUSTRIAL APPLICABILITY

[16744] A database compiling the data of the whole genome sequences of an industrial yeast or, particularly, of a brewing yeast used for the production of alcoholic beverages such as beer is prepared. Using such a database, genes of brewing yeast are selected, and functions of the genes are analyzed by disruption or overexpression in yeast cells, and find genes participating in the desired brewing character. Furthermore, it is possible to breed yeast strains by controlling the expression of the said genes, and produce an alcohol or an alcoholic beverage where productivity and quality are

improved, such as alcoholic beverages with high concentration of sulfite which shows antioxidant activity in the product, excellent flavor stability and a longer quality preservation period.

[16745] Based on the database compiling the data of the whole genome sequences of an industrial yeast or, particularly, of a brewing yeast, a DNA array is produced. Using the DNA array, it is possible to analyze functions of the genes, classify industrial yeasts and detect nucleotide polymorphism and so on.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20060046253A1>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1. A method for analyzing gene of an industrial yeast comprising

(a) determining nucleotide sequence of the whole genome sequence of the industrial yeast; and

(c-1) selecting a gene of the industrial yeast encoding an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or

(c-2) selecting a gene of the industrial yeast consisting of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*.

2. The analyzing method according to claim 1, comprising,

(b) comparing the genome sequence with the whole genome sequence of *Saccharomyces cerevisiae* after the step (a) and before the step (c-1) or (c-2).

3. The analyzing method according to claim 1, comprising

(d) carrying out functional analysis of the selected gene after the step (c-1) or (c-2).

4. The analyzing method according to claim 3, which comprises screening genes participating in increase in pro-

ductivity and/or improvement in flavor in the production of an alcohol or an alcoholic beverage by the functional analysis of the step (d).

5. The analyzing method according to claim 3, wherein functional analysis is performed by disruption of a gene or overexpression of a gene.

6. The analyzing method according to claim 1, wherein the industrial yeast is a brewing yeast.

7. The analyzing method according to claim 6, wherein the brewing yeast is a beer yeast.

8. The analyzing method according to claim 7, wherein the beer yeast is a bottom fermenting yeast.

9. A gene of the industrial yeast encoding an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or consisting of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, which is obtained by the analyzing method according to any one of claims 1-8.

10. A gene library comprising one or more of genes of the industrial yeast each of which encodes an amino acid sequence having 70 to 97% identity to an amino acid sequence encoded by the gene of *Saccharomyces cerevisiae*, or consists of a nucleotide sequence having 60 to 94% identity to the nucleotide sequence of the gene of *Saccharomyces cerevisiae*, which is obtained by the analyzing method according to any one of claim 1.