METHOD FOR ANALYZING GENES OF INDUSTRIAL YEASTS

SEQUENCE LISTING

[0001] The Sequence Listing is submitted on one compact disc including a duplicate. The material on the compact disc including the duplicate copy is hereby incorporated by reference in its entity. The compact disc including the duplicate copy contains a file named "YCT966 sequence listing", which was created on Aug. 23, 2004 (and stored on the compact disc on Sep. 2, 2004) and is 52,018 kilobytes.

[0002] Summary of the sequence listing is as follows:

[0003] SEQ ID NO: 1 represents the nucleic acid sequence for the nonSc-SSU1 gene.

[0004] SEQ ID NO: 2 represents the nucleic acid sequence for the nonSc-MET14 gene.

[0005] SEQ ID NO: 3 represents the amino acid sequence for the nonSc-SSU1 protein deduced from the nucleic acid sequence.

[0006] SEQ ID NO: 4 represents the amino acid sequence for the nonSc-MET14 protein deduced from the nucleic acid sequence.

[0007] SEQ ID NOs: 5-32 represent oligonucleotide primers for amplification.

[0008] SEQ ID NOs: 33-6236 represent 6204 DNA sequences of non-Sc type ORFs, which can be preferably used as probes of the microarry.

[0009] SEQ ID NOs: 6237-75336 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 33-6236, which can be preferably used as probes of the microarry.

[0010] SEQ ID NOs: 75337-82784 represent 7448 DNA sequences of Sc type ORFs.

[0011] SEQ ID NOs: 82785-166153 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 75337-82784.

[0012] SEQ ID NOs: 166154-166181 represent 28 DNA sequences of mtochondrial ORFs from 34/70 strain, which can be preferably used as probes of the microarry.

[0013] SEQ ID NOs: 166182-166489 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 166154-166181, which can be preferably used as probes of the microarry.

[0014] SEQ ID NOs: 166490-167042 represent 553 DNA sequences which have not been identified as the above non-Sc ORFs but have significant similarity to the proteins of *S. cerevisiae* using NCBI-BlastX homology searching.

[0015] SEQ ID NOs. 167043-173124 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 166490-167042.

[0016] SEQ ID NOs: 173125-174603 represent 1479 DNA sequences ORFs which have not been identified as the above, but have significant similarity to the proteins of *S. cerevisiae* using NCBI-BlastP homology searching.

[0017] SEQ ID NOs. 174604-190810 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 173125-174603.

[0018] SEQ ID NOs: 190811-191213 represent 403 *S. cerevisiae* ORFs from SGD which are not identified as Sc type ORFs in strain 34/70.

[0019] SEQ ID NOs: 191214-195587 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 190811-191213.

[0020] SEQ ID NOs: 195588-195651 represent 64 DNA sequences of genes from *Saccharomyces cerevisiae, Bacillus subtulis, Escherichia coli.,* or *Bacteriophage* P1, used as internal standard.

[0021] SEQ ID NOs: 195652-197021 represent sequences of oligonucleotides based on DNA sequences of SEQ ID NOs: 195588-195651.

[0022] The character "n" in various nucleotides sequences of the Sequence Listing is used in accordance with its well known meaning in the art to mean or represent a or g or c or t/u, unknown, or other.

TECHNICAL FIELD

[0023] The present invention relates to a method analyzing genes of an industrial yeast used for the production of an alcoholic beverage such as beer or sake, a fuel alcohol, etc. and particularly for genes of brewing yeast used for the production of an alcoholic beverage. More particularly, it relates to a method where, in the production of an alcoholic beverage, DNA sequence information of brewing yeast is compiled in a database so that the gene which participates in increase in productivity and/or improvement in flavor such as stabilization, reinforcement, etc. of the flavor is selected; a method for breeding yeast suitable for the brewing in which expression of a gene is controlled, such as yeast in which the selected gene is disrupted or yeast in which the gene is overexpressed; and a method for the production of an alcoholic beverage using the bred yeast.

BACKGROUND ART

[0024] Development of techniques for production of fuel alcohols, alcoholic beverages such as beer or sake, etc. has been carried out using industrial yeast. Especially in the production of an alcoholic beverage using brewing yeast, there has seen a brisk development in the techniques for increasing productivity and improving flavor such as stabilization or enhancement of flavor of an alcoholic beverage.

[0025] The most consumed alcoholic beverage in the world is beer and the amount of beer produced in the world in 2001 was about 140,000,000 kL. Type of beer is roughly classified into three depending upon type of yeast and fermentation method. The three types are, naturally fermented beer where fermentation is carried out utilizing yeast and microorganisms inhabiting in breweries; ale-type beer where fermentation is carried out using a top fermenting yeast belonging to *Saccharomyces cerevisiae* (hereinafter, abbreviated as *S. cerevisiae*) at the temperature of 20 to 25° C. and the following aging period is shortened; and lager-type beer where fermentation is carried out using a bottom fermenting yeast belonging to Saccharomyces pastorianus at the temperature of 6 to 15° C. and then subjected to a