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(54) **PROMOTER DERIVED FROM ORGANIC ACID-RESISTANT YEAST AND METHOD FOR EXPRESSION OF TARGET GENE BY USING SAME**

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(58) **Field of Classification Search**

CPC C12N 15/75; C12N 15/62; C12N 15/81

See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to a novel promoter for regulating ADH gene expression in an organic acid-resistant yeast, and a method of producing an organic acid by expressing an organic acid production-related gene using the same. When an organic acid production-related target gene is expressed in the organic acid-resistant yeast using the novel promoter according to the present invention, there is an advantage in that the yeast can produce the organic acid with high efficiency while having resistance to the organic acid without inhibiting the growth ability of the yeast.

9 Claims, 9 Drawing Sheets

Specification includes a Sequence Listing.

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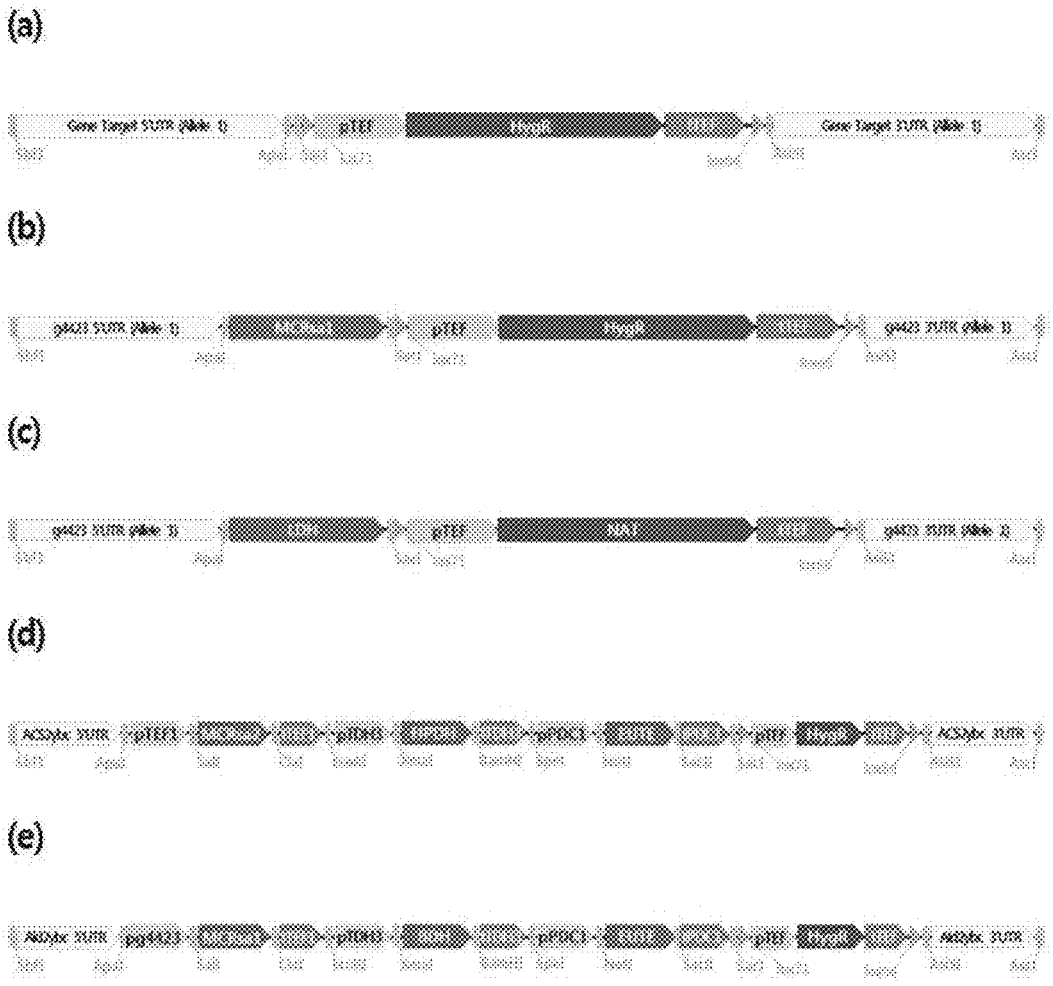
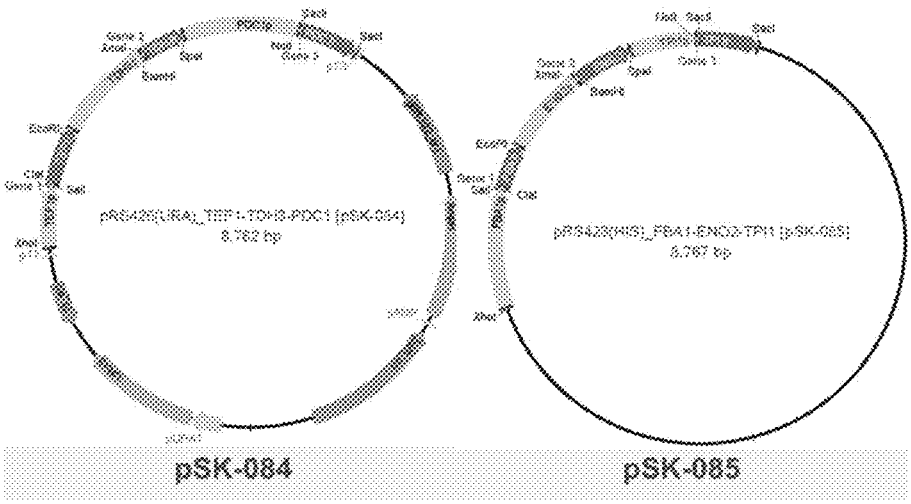
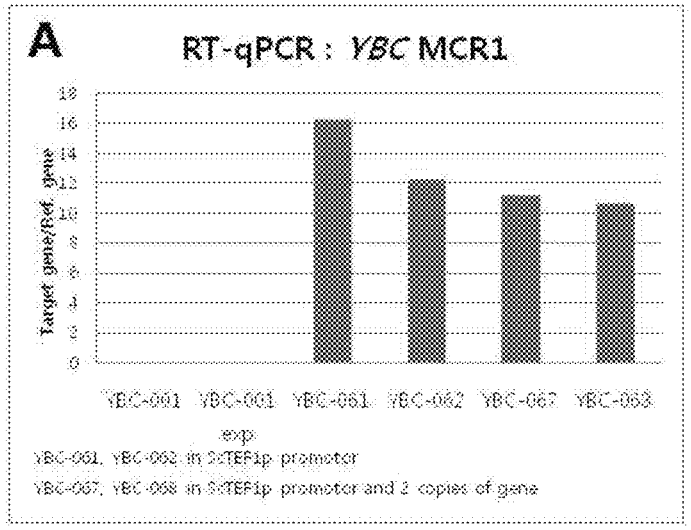
【Fig. 1】

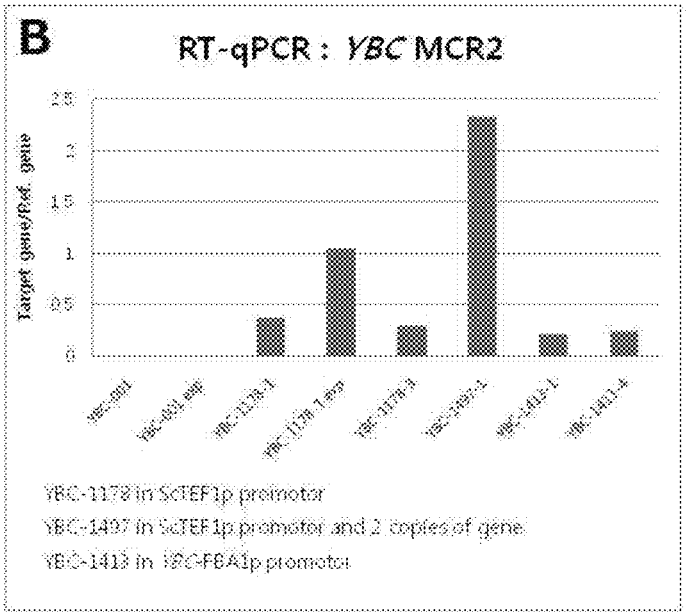


【Fig. 2】

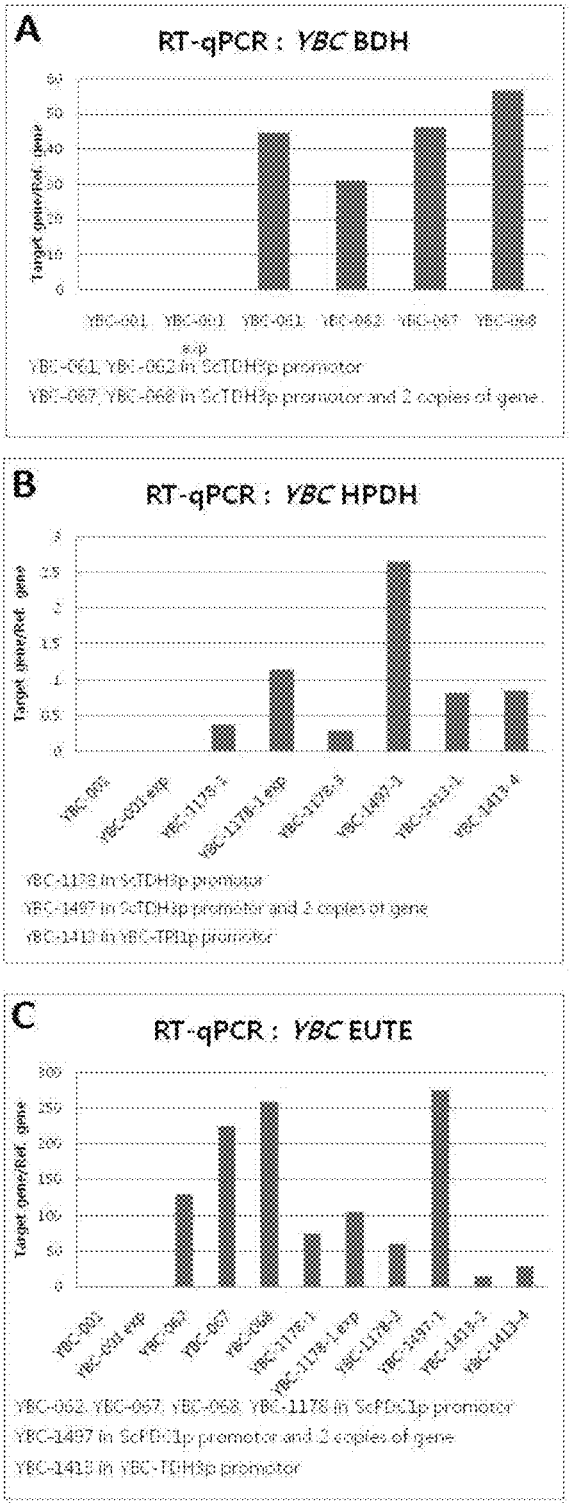


【Fig. 3】

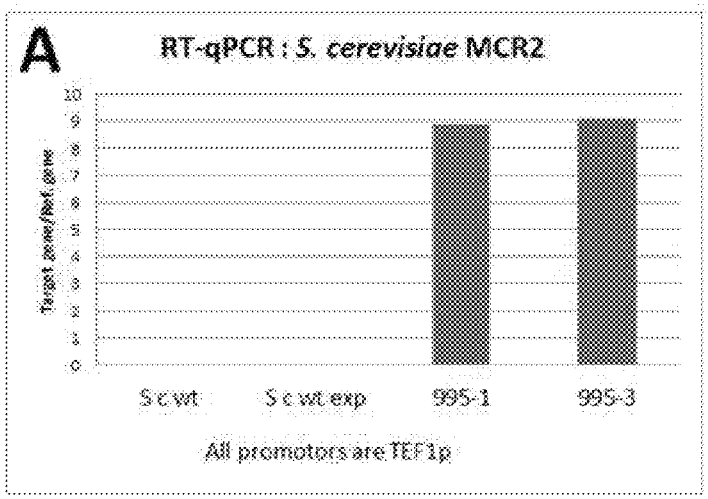

A
RT-qPCR : YBC MCR1
Target gene/Ref. gene
18
16
14
12
10
8
6
4
2
0
YBC-001
YBC-061
YBC-062
YBC-067
YBC-068
exp
YBC-061, YBC-062 in ScTEF1p promotor
YBC-067, YBC-068 in ScTEF1p promotor and 2 copies of gene

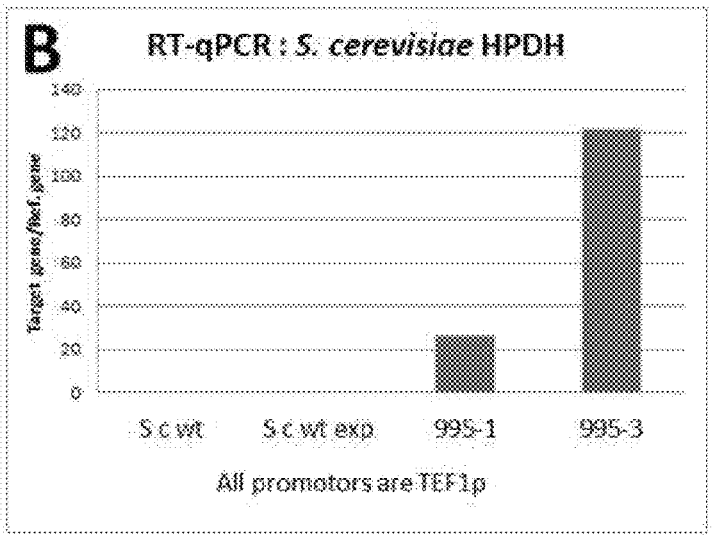

B
RT-qPCR : YBC MCR2
Target gene/Ref. gene
2.5
2
1.5
1
0.5
0
YBC-1178 in ScTEF1p promotor
YBC-1497 in ScTEF1p promotor and 2 copies of gene
YBC-1413 in YBC-FBA1p promotor

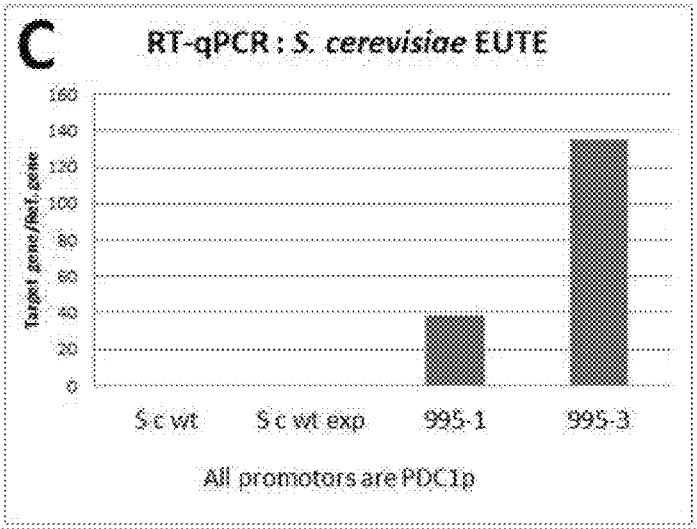
【Fig. 4】


A
RT-qPCR : YBC BDH
Target gene/Ref. gene
YBC-061
YBC-062
YBC-067
YBC-068
YBC-061, YBC-062 in ScTDH3p promotor
YBC-067, YBC-068 in ScTDH3p promotor and 2 copies of gene
B
RT-qPCR : YBC HPDH
Target gene/Ref. gene
YBC-1178 in ScTDH3p promotor
YBC-1497 in ScTDH3p promotor and 2 copies of gene
YBC-1413 in YBC-TPI1p promotor
C
RT-qPCR : YBC EUTE
Target gene/Ref. gene
YBC-062, YBC-067, YBC-068, YBC-1178 in ScFDC1p promotor
YBC-1497 in ScFDC1p promotor and 2 copies of gene
YBC-1413 in YBC-TDH3p promotor

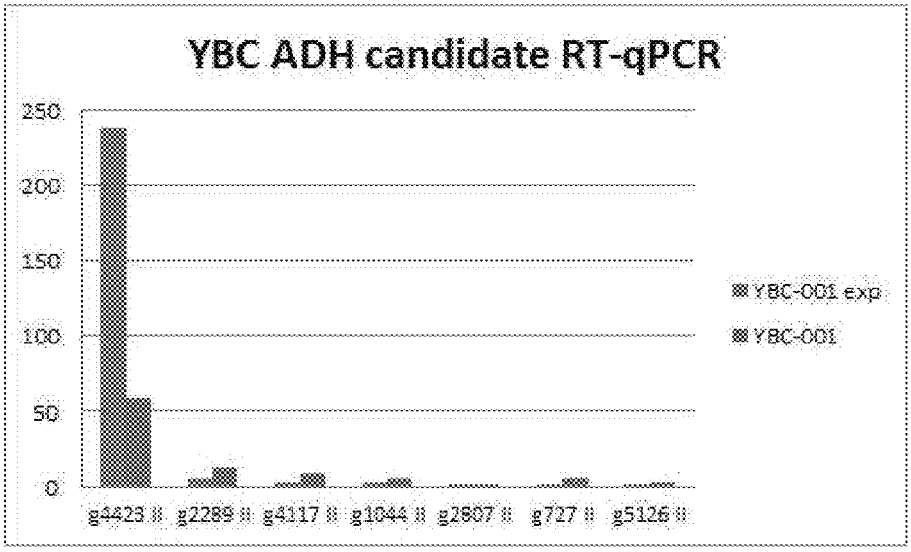
【Fig. 5】


A
RT-qPCR : S. cerevisiae MCR2
Target gene/Ref. gene
0
1
2
3
4
5
6
7
8
9
10
S c wt
S c wt exp
995-1
995-3
All promotors are TEF1p

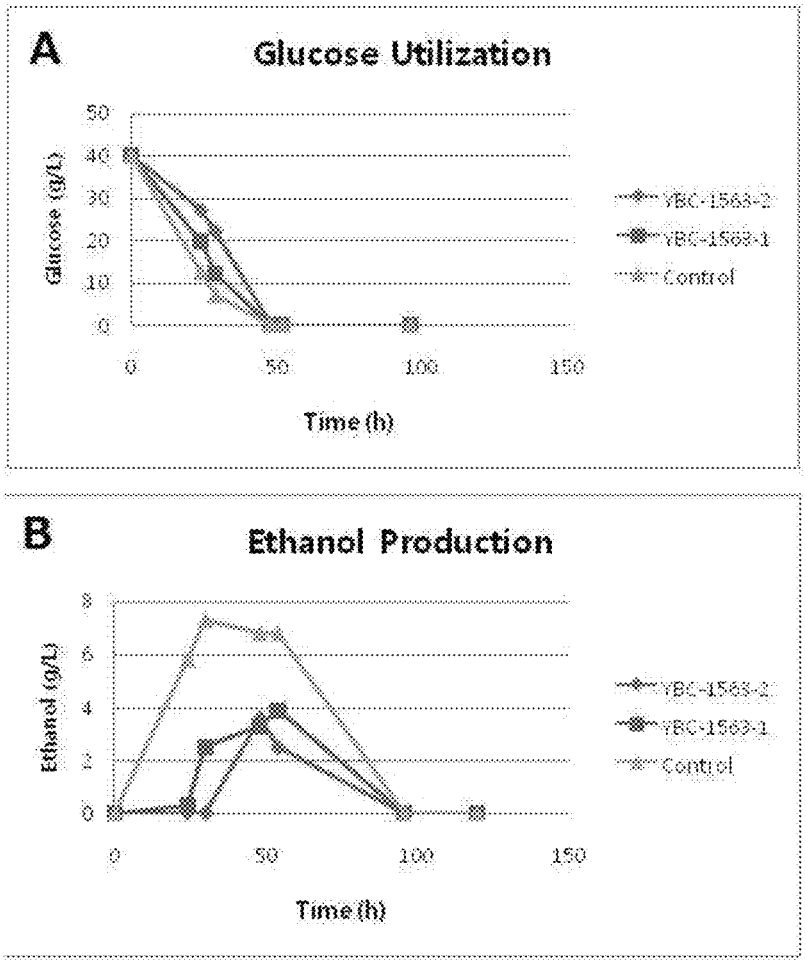

B
RT-qPCR : S. cerevisiae HPDH
Target gene/Ref. gene
0
20
40
60
80
100
120
140
S c wt
S c wt exp
995-1
995-3
All promotors are TEF1p


C
RT-qPCR : S. cerevisiae EUTE
Target gene/Ref. gene
0
20
40
60
80
100
120
140
160
S c wt
S c wt exp
995-1
995-3
All promotors are PDC1p

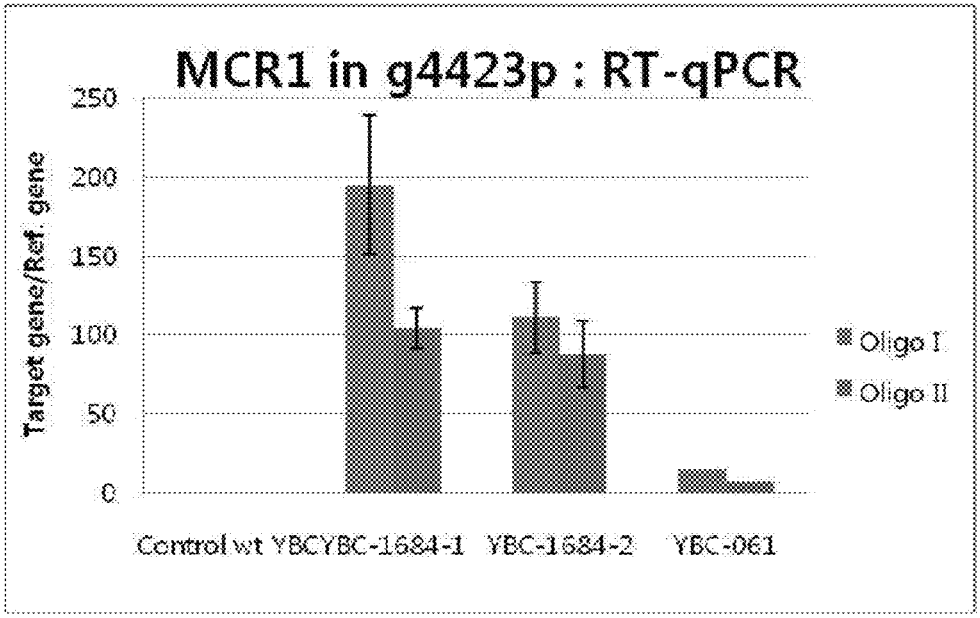
【Fig. 6】


YBC ADH candidate RT-qPCR
250
200
150
100
50
0
g4423
g2289
g4117
g1044
g2807
g727
g5126
YBC-001 exp
YBC-001

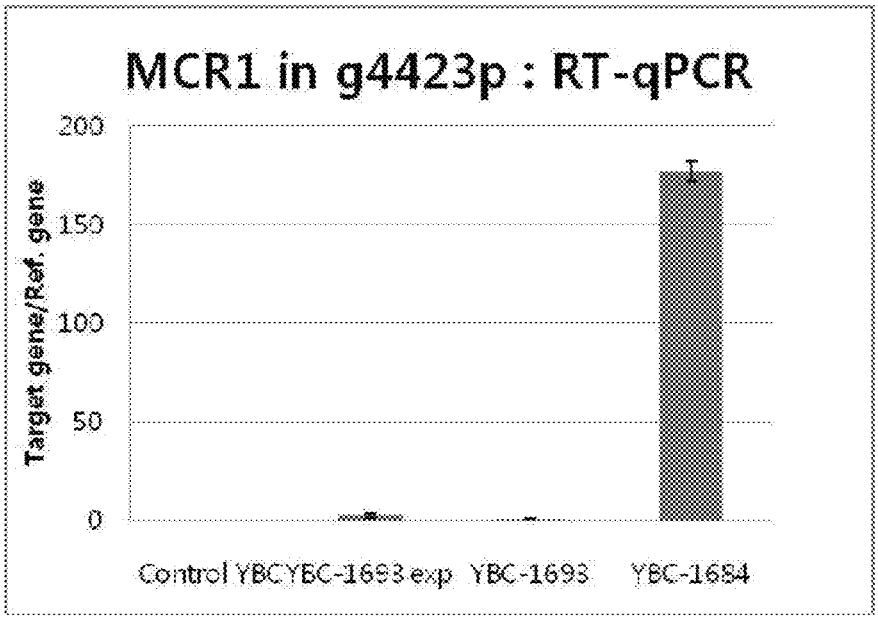
【Fig. 7】


A
Glucose Utilization
Glucose (g/L)
50
40
30
20
10
0
0
50
100
150
Time (h)
YBC-1568-2
YBC-1568-1
Control
B
Ethanol Production
Ethanol (g/L)
8
6
4
2
0
0
50
100
150
Time (h)
YBC-1568-2
YBC-1568-1
Control

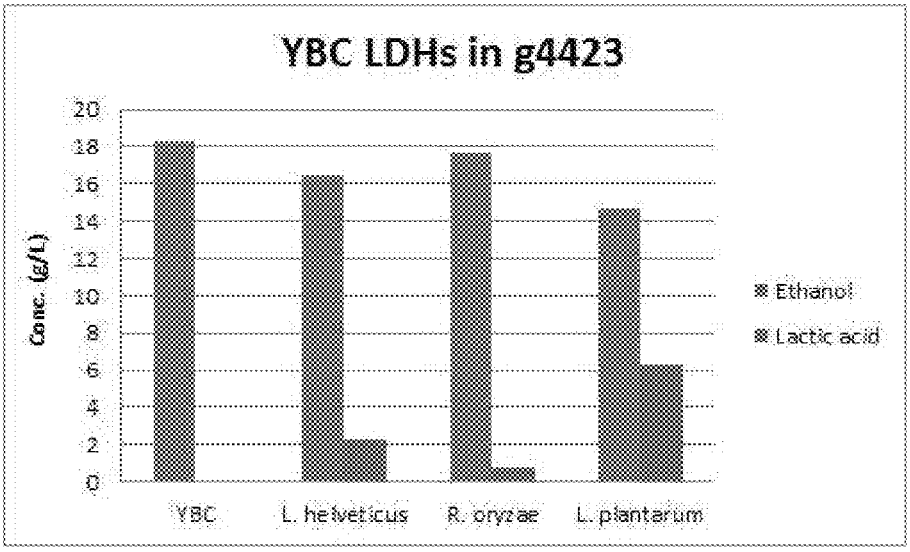
【Fig. 8】


MCR1 in g4423p : RT-qPCR
Target gene/Ref. gene
250
200
150
100
50
0
Control wt YBCYBC-1684-1
YBC-1684-2
YBC-061
Oligo I
Oligo II

【Fig. 9】


MCR1 in g4423p : RT-qPCR
Target gene/Ref. gene
200
150
100
50
0
Control YBCYBC-1693 exp
YBC-1693
YBC-1684

【Fig. 10】


YBC LDHs in g4423
Conc. (g/L)
20
18
16
14
12
10
8
6
4
2
0
YBC
L. helveticus
R. oryzae
L. plantarum
Ethanol
Lactic acid

PROMOTER DERIVED FROM ORGANIC ACID-RESISTANT YEAST AND METHOD FOR EXPRESSION OF TARGET GENE BY USING SAME

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a national phase of PCT application No. PCT/KR2019/002432, filed Feb. 28, 2019, which claims priority to KR patent application No. 1020180044508 filed Apr. 17, 2018, all of which are incorporated herein by reference thereto.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 15, 2020, is named 216870_PFB2478_ST25_Seq.txt and is 61,228 bytes in size.

TECHNICAL FIELD

The present invention relates to a novel promoter derived from an organic acid-resistant yeast, and more particularly, to a novel promoter for regulating ADH gene expression in an organic acid-resistant yeast, and a method of producing an organic acid by expressing an organic acid production-related gene using the same.

BACKGROUND ART

Bioconversion of various raw materials into chemicals, such as organic acids, alcohols and amines, through bioprocesses, has attracted attention in terms of environmental friendliness, carbon dioxide reduction, sustainability, and supply of new platform chemicals. Through this bioconversion, foods, cosmetics, nutraceuticals and drug-related chemical products have been provided.

However, in general, products that are produced through bioconversion need to undergo a purification process of removing impurities. In the production of organic acids, fermentation is often performed at a neutral pH adjusted by a base in order to prevent the growth of strains from being inhibited by the produced organic acids, and acidification is then performed to separate and purify these organic acids. Due to this purification process, large amounts of neutralized salts are generated as by-products, and production costs increase as the production process becomes complicated. The high-cost burden of this purification processes acts as a factor that hinders the entry of fermented products into the chemicals market.

When microorganisms that shows high fermentation ability while being capable of growing even at low pH are used for the production of acidic substances such as organic acids in order to solve the above-described problems, processes of neutralizing the pH of media and performing acidification may be omitted, and thus it is possible to reduce costs through process simplification and reduction in the use of additives.

In many cases, however, the growth rate of microorganisms that survive at low pH is very low, and hence it is not possible to obtain a sufficient amount of cells required for the production of substances. Therefore, these microorganisms show a low consumption rate of raw materials, and thus

are difficult to apply to industrial fermentation processes. Therefore, it is very important to select microorganisms that have the property of maintaining a high consumption rate of raw materials while growing rapidly at a pH lower than the pKa of the product.

These microorganisms can be selected from various strain libraries through various selection pressures. Examples of the selection pressures include resistance at the target product concentration, resistance to the raw material concentration, the consumption rates of raw materials, pH conditions, and the growth ability in minimal media. The selection of microorganisms can be performed manually, but when automated screening is performed, strains having excellent characteristics can be quickly selected from a larger number of subjects.

The selected microorganisms possess excellent properties of withstanding the selection pressures, but in most cases, they produce other products without producing a target product. Therefore, in order to impart the ability to produce the target product to the selected microorganisms, studies have been conducted to genetically introduce genes for conversion into the target product and to eliminate the ability to produce the products that are originally produced.

In order to impart the ability to produce the target product to the selected microorganisms, genes enabling conversion into the target product are introduced or a method of enhancing the genes originally contained in the microorganisms is used. However, in general, since the activities of the contained genes and the enzymes produced therefrom are often low, highly active exogenous genes are introduced in most cases. In addition, in this process, it is essential to introduce a promoter capable of strongly expressing exogenous DNA.

As to usable promoters, when a target microorganism is yeast, the promoter of *Saccharomyces cerevisiae*, a well-known yeast, may generally be used, and various genetic engineering techniques developed for *S. cerevisiae* may also be applied. In addition, strong promoters may be selected from promoters that are involved in the major carbon flux of selected microorganisms, and it is necessary to apply a method that can most effectively express the target gene through various techniques. In particular, for selected acid-resistant yeasts, when genetic engineering studies related to the yeasts have not been conducted, it is a common approach to use the promoter of *S. cerevisiae* or use the endogenous promoter of the selected microorganisms.

In general, promoters have various regulatory regions including a core promoter region in eukaryotic bacteria, and the regulatory genes are different between microorganisms. Therefore, it is possible to find an optimal region while confirming the role of the promoter by selecting a sequence having a sufficient length at the 5' end of the ORF, but a separate study is needed for remote control mechanisms (enhancer, silencer, etc.) or control mechanisms that work in combination.

Accordingly, the present inventors have made extensive efforts to find a promoter suitable for exogenous gene expression in order to select a yeast having resistance to an organic acid and impart the ability to produce useful substances to the yeast. As a result, the present inventors have found that, when a target gene is expressed using a promoter derived from an ethanol-producing metabolic pathway, expression of the target gene significantly increases, so that the production of the target product increases, thereby completing the present invention.

SUMMARY OF THE INVENTION

An object of the present invention is to provide a novel promoter derived from an organic acid-resistant yeast.

Another object of the present invention is to provide a recombinant vector containing the promoter, and a recombinant microorganism having the recombinant vector introduced therein.

Still another object of the present invention is to provide a gene construct in which the novel promoter and a gene encoding a target protein are operably linked to each other.

Yet another object of the present invention is to provide a method of producing an organic acid using a recombinant microorganism having introduced therein a recombinant vector containing the novel promoter and an organic acid production-related gene.

To achieve the above objects, the present invention provides a promoter comprising the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

The present invention also provides a recombinant vector containing the promoter.

The present invention also provides a recombinant microorganism having the recombinant vector introduced therein.

The present invention also provides a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism having the recombinant vector introduced therein; and (b) collecting the produced organic acid.

The present invention also provides a gene construct in which a promoter comprising the nucleotide sequence comprising SEQ ID NO: 1 and a gene encoding a target gene are operably linked to each other.

The present invention also provides a recombinant microorganism having the gene construct introduced into the chromosome thereof.

The present invention also provides a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism having the gene construct introduced therein; and (b) collecting the produced organic acid.

The present invention also provides a recombinant strain obtained by deleting or inactivating g4423 gene in an acid-resistant yeast YBC strain (KCTC13508BP) and having reduced ethanol productivity.

The present invention also provides a recombinant microorganism for target gene overexpression in which a target gene is inserted downstream of the promoter of g4423 in the genome of a YBC strain (KCTC13508BP) and expression of the target gene is regulated by the promoter of g4423.

The present invention also provides a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism; and (b) collecting the produced organic acid.

The present invention also provides a method of overexpressing a target gene by culturing the recombinant microorganism.

BRIEF DESCRIPTION OF DRAWINGS

FIG. **1** shows examples of gene cassettes for expressing one, two or three 3-HP pathway enzymes. (a) is a general cassette for expressing one enzyme, (b) is a cassette for introducing MCRsa1 enzyme while using the g4423 promoter, (c) is a cassette for introducing LDH while using the g4423 promoter, (d) is a cassette for introducing three 3-HP producing enzymes (MCR, HPDH, and EUTE), and (e) a cassette for using a 1-kb g4423 promoter which is the promoter of MCR enzyme.

FIG. **2** shows examples of yeast expression plasmids for expressing one, two or three 3-HP pathway enzymes.

FIG. **3** shows the results of analyzing the expression levels of MCR genes (MCRsa1 and MCRsa2) in constructed recombinant strains containing the promoter of *S. cerevisiae* and the promoter (1 kb) of a YBC strain.

FIG. **4** shows the results of analyzing the expression levels of BDHcm gene, HPDHec gene and EUTEdz gene, which are other genes involved in 3-HP production, in recombinant strains containing an ScTEF1p promoter.

FIG. **5** shows the results of comparing the expression levels of MCR gene and 3-HP production-related genes in *S. cerevisiae* strains. In FIGS. **5**, **995-1** and **995-3** show different phenotypes of the same genotype.

FIG. **6** shows the results of RT-qPCR performed to analyze the expression levels of seven ADH gene candidates selected through genetic information on *S. cerevisiae*.

FIG. **7** shows the results of analyzing glucose utilization (A) and ethanol production (B) in recombinant strains YBC-1563 from which g4423 gene was removed.

FIG. **8** shows the results of analyzing the expression levels of MCRsa1 in recombinant YBC strains in which g4423 gene is replaced with MCRsa1 gene.

FIG. **9** shows the results of analyzing expression of MCRsa1 gene in which g4423 promoter and terminator regions are located in a 1-kb truncated region.

FIG. **10** shows the results of analyzing the production of lactate in recombinant YBC strains in which three LDH genes are replaced with g4423.

DETAILED DESCRIPTION AND PREFERRED EMBODIMENTS OF THE INVENTION

Unless otherwise defined, all technical and scientific terms used in the present specification have the same meanings as commonly understood by those skilled in the art to which the present invention pertains. In general, the nomenclature used in the present specification is well known and commonly used in the art.

For a bioconversion process for the production of products, such as organic acids, which create an acidic environment, among various products, acid-resistant microorganisms, particularly microorganisms that show rapid growth even in an acidic environment and may maintain a high raw material absorption rate, are selected in order to reduce the complexity of the downstream process and the accompanying compound and facility investment costs. The selected microorganisms inherently have the ability to produce the target product in many cases, and thus it is necessary to develop a variety of genetic engineering tools in order to effectively impart the ability to produce the target product to the target microorganism.

A promoter is a regulatory region capable of strongly expressing an exogenous target gene or expressing the exogenous target gene according to conditions, and basically, it is necessary to select a promoter that can strongly express the target gene. Under glucose conditions, this strong promoter is generally selected from promoters involved in glycolysis or in the production of a major fermentation product by the microorganism.

Known strong promoters include, but are not necessarily limited to, TEF1, TPI1, HXT7, TDH3, PGK1, ADH1, and PYK1, and may differ between strains.

Common Crabtree-positive yeasts, including the microorganisms selected in the present invention, produce ethanol as a major fermentation product in many cases, and the promoters thereof are also strongly expressed and mostly work under favorable conditions for fermentation, that is, under conditions of high sugar concentration.

In particular, for promoters involved in ethanol metabolism, technology is often developed with the aim of blocking ethanol production while expressing exogenous genes. Thus, when the endogenous promoter of a strain is used, there is an advantage in that the effect of blocking ethanol production and the effect of strongly expressing exogenous genes can be simultaneously achieved.

In the present invention, to introduce an organic acid production-related gene with high efficiency in order to impart organic acid productivity to the acid-resistant yeast YBC (KCTC13508BP), a promoter suitable for this introduction was selected. In one example of the present invention, it was confirmed that, when MCR gene, which is a gene related to 3-hydroxypropionic acid (3-HP) production, was introduced using a promoter derived from *Saccharomyces cerevisiae* or the endogenous promoter of YBC, which has been used in a conventional art, the expression efficiency of the gene was significantly low. In another example of the present invention, it was confirmed that, when MCR gene was expressed using the promoter of g4423 that is the gene of the enzyme ADH involved in ethanol production, a high expression level of the gene and excellent 3-HP productivity were obtained.

Therefore, in one aspect, the present invention is directed to a promoter comprising the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

The promoter of the present invention is strongly expressed in glucose culture and the logarithmic growth phase, and shows a good expression level even when cultured in an acidic medium. In addition, the promoter works well on yeast expression of heterologous genes, including yeast-derived genes, particularly Archaeal-derived genes and bacteria-derived genes. In particular, the promoter of the present invention is an essential promoter for producing various compounds in acid-resistant strains, and is a promoter capable of enhancing the expression of protein-encoding DNA influenced by the promoter, especially when the DNA is an organic acid-producing DNA. In addition, the promoter is a promoter that can be strongly expressed even in the presence of organic acids inside and outside cells.

In another aspect, the present invention is directed to a recombinant vector containing the promoter, and a recombinant microorganism having the recombinant vector introduced therein.

In the present invention, the recombinant vector may further contain a terminator comprising the sequence of SEQ ID NO: 3 or SEQ ID NO: 4.

In the present invention, the recombinant vector may further contain a gene encoding a target protein, and the target protein may be a protein that is involved in organic acid production.

In the present invention, it has been found that it is possible to produce 3-hydroxypropionic acid and lactic acid as the organic acids, but the present invention is not necessarily limited thereto.

Examples of organic acid production-related genes that are expressed using this promoter include genes encoding fumarate reductase, succinyl coA synthetase and phosphoenolpyruvate carboxylase in the succinic acid pathway (Progress of succinic acid production from renewable resources: Metabolic and fermentative strategies, Bioresource Technology 245(B); 1710-1717, 2017); genes encoding butyryl kinase, enoate reductase, adipyl coA transferase and adipate semialdehyde dehydrogenase in the adipic acid pathway (Development of a Platform Strain for Production of Adipic Acid Yields Insights into the Localized Redox Metabolism of *S. cerevisiae*, Patrick Hyland. A thesis of Master of Applied Science, Graduate Department of Chemical Engineering and Applied Chemistry, University of Toronto, 2013); a gene encoding methylmalonyl CoA reductase in the 3-hydroxyisobutyric acid pathway (Korean Patent Application No. 2016-0075640); genes encoding alpha-ketoisovalerate decarboxylase and potentially phenylacetaldehyde dehydrogenase in the isobutyric acid pathway (ChemSusChem 2011, 4, 1068-1070); a gene encoding malate dehydrogenase in the malic acid pathway (Malic Acid Production by *Saccharomyces cerevisiae*: Engineering of Pyruvate Carboxylation, Oxaloacetate Reduction, and Malate Export, Appl. Environ. Microbiol., 74: 2766-2777, 2008); and a gene encoding cis-aconitic acid decarboxylase in the itaconic acid pathway (Biochemistry of microbial itaconic acid production, Front Microbiol. 2013; 4: 23.). The promoter may be used for overexpression of the gene in the last step of each of the pathways, and this is also specified in the related prior art document (JP4700395B2). In addition, the promoter may also be applied to other genes of the same pathway, in addition to the genes exemplified above.

The promoter of the present invention is a polynucleotide that comprises the nucleotide sequence set forth in SEQ ID NO: 1 and has strong activity even under organic acid production conditions. In addition, sequences with mutations such as deletion or insertion in the nucleotide sequence of SEQ ID NO: 1 may exist due to the diploid nature of the YBC strain, and sequences including these mutated sequences can also exhibit the same characteristics (The Baker's Yeast Diploid Genome Is Remarkably Stable in Vegetative Growth and Meiosis, PLoS Genet 6(9):2010. Ploidy changes and genome stability in yeast, Yeast 31: 421-430, 2014).

In addition, the terminator, which acts together with the promoter of the present invention, comprises the nucleotide sequence set forth in SEQ ID NO: 3 or 4.

In the present invention, examples of the target protein include, but are not limited to, malonyl-CoA-reductase, lactate dehydrogenase, fumarate reductase, succinyl coA synthetase, phosphoenolpyruvate carboxylase, butyryl kinase, enoate reductase, adipyl coA transferase, adipate semialdehyde dehydrogenase, methylmalonyl CoA reductase, alpha-ketoisovalerate decarboxylase, potentially phenylacetaldehyde dehydrogenase, malate dehydrogenase, and cis-aconitic acid decarboxylase.

In the present invention, the recombinant is preferably yeast, more preferably the acid-resistance yeast YBC (KCTC13508BP).

In still another aspect, the present invention is also directed to a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism having the recombinant vector introduced therein; and (b) collecting the produced organic acid.

In yet another aspect, the present invention is directed to a gene construct in which a promoter comprising the nucleotide sequence comprising SEQ ID NO: 1 or SEQ ID NO: 2, and a gene encoding a target gene are operably linked to each other, and a recombinant microorganism having the gene construct introduced into the chromosome thereof.

In the present invention, the target protein may be a protein that is involved in organic acid production. The target protein may be selected from among malonyl-CoA-reductase, lactate dehydrogenase, and the like, but is not limited thereto, and any protein that is involved in organic acid production may be used without limitation.

In the present invention, the recombinant is preferably yeast, more preferably the acid-resistance yeast YBC (KCTC13508BP).

In yet another aspect, the present invention is directed to a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism having the gene construct introduced therein; and (b) collecting the produced organic acid.

The promoter of the present invention constitutes a DNA construct to be introduced into yeast together with a gene encoding the target protein. These DNA constructs include constructs suitable for various yeast transformation methods known to those skilled in the art, and examples of DNA constructs for homologous recombination are shown in SEQ ID NOs: 5 and 6. The DNA construct is a two-allele deletion cassette for deletion of the g4423 gene. In addition, when the target DNA is inserted into this cassette, a gene insertion cassette for each allele is produced, which is well known to researchers skilled in the art.

In the present invention, the cassette may be comprising the nucleotide sequence of SEQ ID NO: 5 or SEQ ID NO: 6, and the cassette may contain a target gene.

In a further aspect, the present invention is directed to a method for overexpressing a target gene, the method comprising replacing the g4423 gene in the genome of the YBC strain (KCTC13508BP) with the target gene.

In another aspect, the present invention is directed to a recombinant microorganism for target gene overexpression in which a target gene is inserted downstream of the promoter of g4423 in the genome of the YBC strain (KCTC13508BP) and expression of the target gene is regulated by the promoter of g4423.

In yet another aspect, the present invention is directed to a method for producing an organic acid, the method comprising steps of: (a) producing the organic acid by culturing the recombinant microorganism; and (b) collecting the produced organic acid.

In yet another aspect, the present invention is directed to a method of overexpressing a target gene by culturing the recombinant microorganism.

In yet another aspect, the present invention is directed to a recombinant strain obtained by deleting or inactivating the g4423 gene in the acid-resistant yeast YBC strain (KCTC13508BP) and having reduced ethanol productivity.

As used herein, "homology" refers to the percent identity between two amino acid or polynucleotide moieties for comparison. The term "similarity" refers to the degree to which two amino acid or polynucleotide sequences are functionally or structurally identical to each other as determined by the comparison window. The sequence homology or similarity can be determined by comparing sequences using the standard software, for example, a program called BLASTN or BLASTX, developed based on BLAST (Proc. Natl. Acad. Sci. USA, 90, 5873-5877, 1993).

The g4423 promoter may preferably have a sequence showing a sequence homology of 90% or more, 92% or more, 93% or more, 95% or more, 97% or more, 98% or more, 99% or more, or 100% to the sequence of SEQ ID NO: 1.

If any promotor exhibits an equivalent level of expression efficiency while having a homology of 90% or more to the g4423 promoter of the present invention, it can be considered a substantially equivalent promoter.

In some cases, the g4423 promoter according to the present invention may be mutated using techniques known in the art in order to increase the expression efficiency of the target gene.

In the present invention, the recombinant yeast may have acid resistance. In order to produce an acid-resistant recombinant yeast suitable for the present invention, a host yeast having resistance to organic acids is preferably used.

The acid-resistant yeast may be an acid-resistant yeast selected from the group consisting of the genus *Saccharomyces, Kazachstania saccharomyces* and the genus *Candida*. For example, the acid-resistant yeast may be selected from the group consisting of *Saccharomyces cerevisiae, Kazachstania exigua, Kazachstania bulderi*, and *Candida humilis*, but is not limited thereto.

"Acid-resistant yeast" refers to a yeast having resistance to an organic acid such as 3-HP or lactic acid, and acid resistance can be determined by evaluating growth in media containing various concentrations of organic acid. In other words, "acid-resistant yeast" refers to yeast that has a higher growth rate and biomass consumption rate compared to general yeast in media containing a high concentration of organic acid.

In the present invention, the term "acid-resistant yeast" is defined as a yeast that can maintain a biomass consumption rate (sugar consumption rate, etc.) of at least 10% or a specific growth rate of at least 10% at a pH lower than the pKa value of the organic acid in a medium containing 1 M or more of organic acid compared to a medium containing no organic acid. More specifically, in the present invention, the term "acid-resistant yeast" is defined as a yeast that can maintain a biomass consumption rate (sugar consumption rate, etc.) of at least 10% or a specific growth rate of at least 10% at a pH of 2 to 4 compared to a pH of 7.

The recombinant yeast according to the present invention may be produced according to a conventional method by inserting the gene into the chromosome of the host yeast or by introducing a vector containing the gene into the host yeast.

As the host yeast, a host cell into which DNA is introduced with high efficiency and in which the introduced DNA is expressed with high efficiency is commonly used. Although an acid-resistant yeast was used in one example of the present invention, but the present invention is not limited thereto, any type of yeast may be used as long as a target DNA may be sufficiently expressed therein.

The recombinant yeast may be produced according to any transformation method. "Transformation" refers to a process of introducing DNA into a host cell and making the DNA replicable therein as a chromosomal factor or by completion of chromosomal integration, which is a phenomenon of artificially causing a genetic change by introducing exogenous DNA into a cell. Typical transformation methods include electroporation, a lithium acetate-PEG method, and the like.

In addition, in the present invention, any commonly known genetic engineering method may be used as a method of inserting a gene into the chromosome of a host microorganism. Examples of the method include methods that use a retroviral vector, an adenovirus vector, an adeno-associated virus vector, a herpes simplex virus vector, a poxvirus vector, a lentiviral vector, a non-viral vector, or the like. "Vector" refers to a DNA construct containing a DNA sequence operably linked to a suitable control sequence capable of expressing the DNA in a suitable host. The vector may be a plasmid, a phage particle, or simply a potential genomic insert. Once transformed into a suitable host, the

vector may replicate and function independently of the host genome, or may, in some cases, integrate into the genome itself. Plasmid is currently the most commonly used form of vector, and linearized DNA is also a form that is commonly used for integration into the genome of yeast.

A typical plasmid vector has a structure comprising: (a) a replication origin that allows replication to occur efficiently such that plasmid vectors per host cell are created; (b) an antibiotic-resistance gene or an auxotrophic marker gene that allows a host cell transformed with a plasmid vector to be selected; and (c) restriction enzyme digestion sites into which foreign DNA fragments may be inserted. Even if there is no suitable restriction site of a restriction enzyme, a vector and foreign DNA may be easily ligated when using the linker or the synthetic oligonucleotide adaptor according to a general method. Even if suitable restriction enzyme digestion sites are not present in the vector, the use of a synthetic oligonucleotide adaptor or linker according to a conventional method enables foreign DNA fragments to be easily ligated with the vector.

In addition, the gene is "operably linked" when placed in a functional relationship with another nucleic acid sequence. This can be a gene and regulatory sequence(s) which are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences(s). For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it affects transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation.

Generally, "operably linked" means that the DNA sequences being linked are contiguous and, in the case of a secretory leader, are contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction enzyme sites. If such sites do not exist, a synthetic oligonucleotide adaptor or linker is used in accordance with a conventional method.

It is well understood that not all vectors function equally in expressing the DNA sequence of the present invention, likewise, not all hosts are equally suitable for hosting an identical expression vector. However, those skilled in the art are able to make a suitable selection from other various vectors, expression regulatory sequences and hosts without undue experimentation without departing from the scope of the present invention. For example, a vector may be selected taking into consideration the host cell since the vector should be replicated in the host cell. In addition, the copy number of a vector, the ability to control the copy number, expression of another protein (e.g., an antibiotic marker) encoded by the gene in the vector should also be considered.

A carbon source that is used in the present invention may be one or more selected from the group consisting of glucose, xylose, arabinose, sucrose, fructose, cellulose, galactose, glucose oligomers and glycerol, but is limited thereto.

In the present invention, culture may be performed under conditions in which microorganisms, such as *E. coli*, no longer act (e.g., cannot produce metabolites). For example, the culture may be performed at a pH of 1.0 to 6.5, preferably 1.0 to 6.0, more preferably 2.6 to 4.0, but is not limited thereto.

Hereinafter, the present invention will be described in more detail with reference to examples. These examples are only to illustrate the present invention, and it will be apparent to those of ordinary skill in the art that the scope of the present invention is not construed as being limited by these examples.

Example 1: Analysis of Expression Pattern of Malonyl-CoA Reductase (MCR) Using Conventional Promoter in YBC Strain

Selection of Acid-Resistant Strain

The present inventors selected a group of strains having acid resistance through a test for various yeast strains (Korean Patent Application Publication No. 2017-0025315). For the selected yeast strains, lactic acid was added to the medium at the beginning of culture, and the strain having the best acid resistance was selected while checking the growth and sugar consumption rates of the microorganisms. At this time, an inoculum OD value of 4 and a YP medium (20 g/L peptone and 10 g/L yeast extract) supplemented with 3.5% glucose were used, and the experiment was performed with a 50-ml flask culture under conditions of 30° C. and 100 rpm. The lactic acid concentration at the beginning of culture varied from 0 to 80 g/L. The results were compared and analyzed, and a YBC strain having the best acid resistance was selected.

The YBC strain (*Kazachstania exigua* sB-018c) was deposited in the Korea Research Institute of Bioscience and Biotechnology Biological Resource Center, a depository institution, on Apr. 11, 2018 under accession number KCTC13508BP.

MCR Expression Using Conventional Promoter in Acid-Resistant Strain YBC

In this Example, a gene encoding MCR (malonyl-CoA reductase), an enzyme involved in 3-HP (3-hydroxypropionic acid) production, was expressed in the YBC strain.

The malonyl-CoA pathway that produces 3-HP is a metabolic pathway in which acetyl-CoA is converted to malonyl-CoA through carboxylation and then converted to 3-HP through a reduction reaction (acetyl-CoA→malonyl-CoA→3-HP). The malonyl-CoA pathway has been studied the most as a 3-HP production pathway, because intermediates commonly produced by microorganisms including *E. coli* pass through this pathway (US Patent Application Publication No. US 2013/0071893 A1). Malonyl-CoA can be converted into 3-HP by the action of malonate reductase and 3-HP dehydrogenase, and thus a method of converting malonyl-CoA to 3-HP using recombinant *E. coli* in the presence of glucose or glycerol is well known.

In this Example, the experiment was conducted on MCRsa1 and MCRsa2, which are highly efficient genes among known MCR genes. The MCRsa1 and MCRsa2 used were synthesized using yeast codon usage based on data from Genbank, and the information on the MCR genes used in this Example is shown in Table 1 below.

TABLE 1

Gene	GenBank Accession No.	GI No.	Organism	Abbreviation
	WP_020198954.1	519043079	*Sulfolobales archaeon* AcdI	MCRsa1
SacRon12I_11780	AGE74568.1	449039143	*Sulfolobus acidocaldarius* Ron12/I	MCRsa2

In order to introduce the gene into the YBC strain, a cassette shown in FIG. **1**(*a*) was constructed.

The cassette was constructed to have an antibiotic resistance gene. For targeting the target gene, the 5' UTR and 3' UTR regions of the target gene were designed to have the restriction enzyme sites shown in FIG. **1** on the basis of the full genome sequence or the partial genome sequence, and then subjected to PCR. The promoter and terminator derived from *S. cerevisiae* were constructed based on known genetic information (for example, *Saccharomyces* Genome Database). As the antibiotic resistance gene, HygR was used as an example in FIG. **1**(*a*). However, other antibiotic resistance genes for eukaryotes may be used for the strain, and these genes may be easily constructed by any person skilled in the art. Since the antibiotic resistance gene needs to be removed after use so that genetic manipulation in the next step can be performed, sites (lox71 and lox66) for Cre-loxp at both ends were introduced. In addition, the promoter and terminator derived from the YBC strain were constructed using the same method as the method of extracting the UTR region. When a plurality of target genes is to be expressed, a cassette capable of expressing the plurality of genes as shown in FIG. **1**(*d*) was constructed, and the UTR, the ORF gene and antibiotic resistance gene were constructed by exchange using the restriction enzyme located at the end of each region so as to suit the purpose.

For Donor DNA, a plasmid containing a cassette was cleaved using restriction enzymes or amplified by PCR, and regions of each gene can be exchanged using a restriction enzyme located at each end. In addition to the method that uses the restriction enzymes, a cassette was also constructed using Gibson assembly. For how to use this Gibson assembly, a number of products and usages are well known. In this Example, the cassette was constructed using NEB Gibson assembly master mix and cloning kit. Thereamong, oligomers related to MCR and G4423 are shown in Table 2 below.

TABLE 2

Name	SEQ ID NO	Sequence	Description
oSK-1125	9	CTTCAAAGTTCTTCTCATTTTGTTGTCGACTT TTGTTTATAATTTATCAAATATGTTGATT	keFBA1p MCRsa1 GA
oSK-1126	10	GTCGACAACAAAATGAGAAGAAC	MCRsa1 GA
oSK-1127	11	CTTTCAAGACTCTTCTCATTTTGTTGTCGACT TTTGTTTATAATTTATCAAATATGTTGATT	keFBA1p MCRsa2 GA
oSK-1130	12	GTCGACAACAAAATGAGAAGAGTC	MCRsa2 GA
oSK-1220	13	TACGACTCACTATAGGGCGAATTGCCTGCA GGGTTAACTCAGTTTTCTCTCTTTCCC	ADH1ke (g4423) GA
oSK-1221	14	ACTAGAGCTCCCTCGGACGTGGGCCCTTTTA AATGATTTTTATTTGTATTGATATATGG	ADH1ke (g4423) GA
oSK-1222	15	GGGCCCACGTCCGAGGGAGCTCTAGTACCT CGGCGATCGCTTTGTCTTTATTTTTGAAATG TTAATAGTC	ADH1ke (g4423) GA
oSK-1223	16	TAACCCTCACTAAAGGGAACAAAAGCTGGG CGCGCCCTTTTGCAGTTGCGGATTTC	ADH1ke (g4423) GA
oSK-1358	17	GGTTACATCCCTAAGTGAATCGATGGAGAT TGATAAGACTTTTC	MCRsa1 - TEF1t GA fwd
oSK-1359	18	CAAAAGTCGACAACAAAATGAGAAGAACTT TGAAGGCTGC	keFBAp-MCRsa1 GA fwd
oSK-1360	19	CTTCAAAGTTCTTCTCATTTTGTTGTCGACTT TTGTTTATAATTTATTGAAATATGTTG	keFBAp-MCRsa1 GA rev
oSK-1412	20	CTGTAGCACCTAAAATGGCAGCCTTCAAAG TTCTTCTCATTTTTAAATGATTTTTATTTGTA TTGATATATGGATATATATGTGTACGG	g4423 promoter rev + MCRsa1 flank
oSK-1413	21	GGTTACATCCCTAAGTGAGTCATTTAATTTA TTCTTTTAGAATATAATTATTTTGTCTTTATT TTTGAAATGTTAATAGTCTTTTTTTT	g4423 terminator forw + MCRsa1 flank

TABLE 2-continued

Name	SEQ ID NO	Sequence	Description
oSK-1414	22	CCGTACACATATATATCCATATATCAATACA AATAAAAATCATTTAAAAATGAGAAGAACT TTGAAGGCTGCCATTTTAGG	MCRsa1 forw + g4423 flank
oSK-1415	23	ATTTCAAAAATAAAGACAAAATAATTATAT TCTAAAAGAATAAATTAAATGACTCACTTA GGGATGTAACCCTTTTCGATCAAATATTC	MCRsa1 rev + g4423 flank
oSK-1416	24	AAATTCGGGCCCGTTAACTCAGTTTTCTCTC TTTCCCTCCACC	g4423 promoter forw + ApaI restriction site
oSK-1417	25	TTTGTTGTCGACTTTTAAATGATTTTTATTTG TATTGATATATGGATATATATGTGTACGG	g4423 promoter rev + SalI restriction site
oSK-1418	26	TGCTACCTTAATTTCTCATGGAAAGTGGCA	g4423 promoter forw
oSK-1419	27	GTTAACGAGTTTAATGTTTAAAAGCGTATAT AAG	g4423 terminator rev
oSK-1621	28	TAATCTCACCGTACACATATATATCCATATA TCAATACAAATAAAAATCATTTAAAAATGA GAAGAGTCTTGAAAGCAGCAATCTTGG	MCRsa2 + g4423p flank
oSK-1622	29	GTGGAACCCAAGATTGCTGCTTTCAAGACT CTTCTCATTTTTAAATGATTTTTATTTGTATT GATATATGGATATATATGTGTACGG	g4423p + MCRsa2 flank
oSK-1623	30	TGGTATTTTGGCAACAGAATTTTTGGTTGAA AAGGGTTACATGGATTGATTTGTCTTTATTT TTGAAATGTTAATAGTCTTTTTTTT	g4423t + MCRsa2 flank
oSK-1624	31	TTTGTTCAAAGTAAAAAAAAAAAGACTATTA ACATTTCAAAAATAAAGACAAATCAATCCA TGTAACCCTTTTCAACCAAAAATTCTG	MCRsa2 + g4423t flank

In the case of the acid-resistant *S. cerevisiae* strain, expression was performed using the cassette or the expression plasmid shown in FIG. **2** (pSK-084 and/or pSK-085) (FIG. **2**).

To introduce the constructed cassette into the YBC strain, a linearized donor DNA was constructed by PCR or a restriction enzyme method and then introduced using an electroporation method or a lithium acetate method, as in general yeast transformation. Next, selection was performed using a medium according to the auxotroph marker or antibiotic marker used. Through the colonies selected from the selection medium, whether the gene was introduced into the correct locus of the chromosome was confirmed by colony PCR either using the gene ORF primers into which the target is to be introduced and using the primers of the introduced gene. Subsequently, genomic DNA was extracted from the cultured cells, and the correct genotype was determined.

These constructed strains were each cultured (30° C. and 250 rpm) in a 250-mL flask using 20-mL selective SC-based medium (20 g/L of glucose) or YPD medium, and culture was continued until glucose and ethanol were completely consumed.

Table 3 below shows recombinant strains which were constructed by the above-described method and into which the MCR gene was introduced together with a *Saccharomyces cerevisiae*-derived promoter (TEFL) and a YBC strain-derived promoter (FBA1p).

TABLE 3

Strain	Description
S.c wt	*S. cerevisiae* wt (acid tolerant)
S-995	*S. cerevisiae* Acs2Δ-HygR::TEF1p-MCRsa2-TEF1t: TDH3p-HPDH-TDH3t: PDC1p-EutE-PDC1t
YBC-001	YBC wt
YBC -061	acs2Δ-TEF1p-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t-(NatR)
YBC -062	ald2Δ-TEF1p-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t
YBC -067	ald2Δ-TEF1p-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t
YBC -068	ald2Δ-TEF1p-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t
YBC -1178	ald2Δ-NAT::TEF1p-MCRsa2-TEF1t: TDH3p-HPDH-TDH3t: PDC1p-EutE-PDC1t
YBC -1413	ald2Δ-NAT::YBC-FBA1p-MCRsa2-TEF1t: YBC-TPI1p-HPDH-TDH3t: YBC-TDH3p-EutE-PDC1t
YBC -1497	ald2Δ-TEF1p-MCRsa2-TEF1t: TDH3p-HPDH-TDH3t: PDC1p-EutE-PDC1t

The recombinant strains were each cultured (30° C. and 250 rpm) in a 250-mL flask using 20-mL YPD medium (20 g/L peptone, 10 g/L yeast extract, and 20 g/L dextrose). The cells were collected at the time of ethanol production and the time of ethanol consumption, and then RT-qPCR was performed on the MCR gene.

The RT-qPCR method used in this Example was as follows. After extracting RNA during exponential growth of the target strain, cDNA was produced using the RNA as a template. An oligomer specific to each of the target gene and the housekeeping gene (used as the Ref gene) was synthesized, and qPCR was performed using the oligomer. The

gene used in this Experiment was ALG9, and the size of the fragment amplified with the primers used was 147±3 bp.

Table 4 below shows the qPCR primers used in the experiment and the primers used in the following Examples.

TABLE 4

Primers for qPCR

Name	SEQ ID NO	Sequence	Description
oSK-1318	32	CGGACTTTAGAGCCTTGTAGAC	g4423 qPCR fwd
oSK-1319	33	ATCTGGTTACACTCACGATGG	g4423 qPCR rev
oSK-1320	34	CCAAGTACGTTAGAGCTAACGG	g4423 qPCR 2 fwd
oSK-1321	35	GAGCTTCTCTGGTATCAGCT	g4423 qPCR 2 rev
oSK-1322	36	AGCTTTAGCAAACATTAGACCC	g1044 qPCR fwd
oSK-1323	37	ATTCCATCCGAATATGCTGGT	g1044 qPCR rev
oSK-1324	38	GGAACCTAAATGACTGTTGGCA	g1044 qPCR 2 fwd
oSK-1325	39	AGGATGTTGATTTCGACTCGT	g1044 qPCR 2 rev
oSK-1326	40	TTCCAAAGGGTACCAATTTAGCTG	g2289 qPCR fwd
oSK-1327	41	GTACCGCTAATGAACCTAAACCA	g2289 qPCR rev
oSK-1328	42	AGAGCTGACACTAGAGAAGCC	g2289 qPCR 2 fwd
oSK-1329	43	GATGTGTCTACGACGTATCTACC	g2289 qPCR 2 rev
oSK-1330	44	GTACTGGTAACGTCCAAGTC	g4117 qPCR fwd
oSK-1331	45	GAACCCTTCCATACTCTACCA	g4117 qPCR rev
oSK-1332	46	TTCAGTTCGTGCTACTCAAGG	g4117 qPCR 2 fwd
oSK-1333	47	TCAATTGCAACGACAGAGAC	g4117 qPCR 2 rev
oSK-1334	48	CCGTACCCTGAAGAGTTTACTG	g2807 qPCR fwd
oSK-1335	49	CAACCATAGATTCACGAATTGCTC	g2807 qPCR rev
oSK-1336	50	AGTGGATTTGGATTAATGGGTG	g2807 qPCR 2 fwd
oSK-1337	51	GCTTCTGTAACACCTTTAACAC	g2807 qPCR 2 rev
oSK-1338	52	AAATTGGTGACCGTGTTGGT	g727 qPCR fwd
oSK-1339	53	AACCACCTTTACTACGGTAACCA	g727 qPCR rev
oSK-1340	54	TTTAGTCGTCATCTGTTCAGGT	g727 qPCR 2 fwd
oSK-1341	55	GAGACACCTAACAAACCAAATGG	g727 qPCR 2 rev
oSK-1342	56	GATTCAAGCTTCTTCTCGTATCGG	g3610 qPCR fwd (ALG9 homolog)
oSK-1343	57	GGAAATGATACCATTCACGACCT	g3610 qPCR rev (ALG9-homolog)
oSK-1350	58	GTTCCGTCAAAGAAATCAAGCA	g5126 qPCR fwd
oSK-1351	59	TGGTAAACCTGTATCTGACATCAC	g5126 qPCR rev
oSK-1352	60	TTTAGTTGTCATTTGTGCCGGT	g5126 qPCR 2 fwd
oSK-1353	61	GACACCTAACAAACCAAACGGA	g5126 qPCR 2 rev
oSK-1362	62	GCTAACTTCAAAGGTGAACCTC	MCRsa1 qPCR fwd
oSK-1363	63	AATCTACCAACTACGACGGAC	MCRsa1 qPCR rev
oSK-1364	64	CAGATTCGAACCAGATATCCCT	MCRsa2 qPCR fwd
oSK-1365	65	CCAATGGTAACAATACACCTTGAG	MCRsa2 qPCR rev
oSK-1382	66	GGTAAAGCTTACTCAGAAGTTGTC	MCRsa1 qPCR 2 fwd

TABLE 4-continued

Primers for qPCR

Name	SEQ ID NO	Sequence	Description
oSK-1383	67	CAGCACCTTGAGGTAATGGA	MCRsa1 qPCR 2 rev
oSK-1384	68	CTATGCAAGCTGTTTCCGGT	MCRsa2 qPCR 2 fwd
oSK-1385	69	CGTTGACGTTTCTCTTAGTTTCAG	MCRsa2 qPCR 2 rev
oSK-1386	70	CTTTGAGTGCAAGTATCGCC	ALG9 qPCR fwd
oSK-1387	71	TGTGTAATTGTTCACCAAAGCC	ALG9 qPCR rev

As a result, as shown in FIG. **3**, it was confirmed that the MCR genes (MCRsa1 and MCRsa2) were expressed in the recombinant strains constructed using the acid-resistant strain YBC. The levels of the genes expressed using the promoter of *Saccharomyces cerevisiae* and the promoter (1 kb) of the YBC strain were analyzed, and as a result, it was shown that the expression levels of the genes were not high or rather low compared to that of the Ref gene in qPCR. In addition, it was confirmed that the level of MCRsa2 expressed using the 1-kb FBA promoter (YBC FBA1p) derived from the YBC strain was lower than the level of MCRsa2 expressed using the ScTEF1p promoter (YBC-1413 in FIG. **3**B).

In addition, the analysis of expression was also performed on BDHcm gene, HPDHec gene and EUTEdz gene, which are other genes involved in 3-HP production, in the recombinant strains YBC-061, YBC-062, YBC-067 and YBC-068 containing the ScTEF1p promoter.

As a result, as shown in FIG. **4**, it was confirmed that, similarly to the MCR gene, the expression levels of these genes expressed using the ScTEF1p promoter were lower than the expression levels of the genes expressed using the endogenous promoter FBA1p of the YBC strain and the *Saccharomyces cerevisiae*-derived promoter (TEF1).

In addition, the production of 3-HP by the recombinant strain was also very low, and the production of 3-HP by the recombinant strain (in which the expression levels of three genes (MCRsa2, HPDH and EUTE) all increased) containing two copies of the gene was rather lower than the production of 3-HP by the YBC-1178 strain.

Example 2: Analysis of 3-HP Productivities by MCR Gene and Related Genes Expressed by Conventional Promoter

The 3-HP productivities of the recombinant strains constructed in Example 1 were analyzed.

First, each of the recombinant strains was cultured with 25 mL of a YPD medium (20 g/L peptone, 10 g/L yeast extract, and 20 g/L dextrose) in a shake flask at 250 rpm and 30° C., and 15 μM of cerulenin (Sigma-Aldrich, USA) was added. Cerulenin functions to facilitate the production of 3-HP by inhibiting lipid synthesis from the carboxylation of cytosolic acetyl-CoA to malonyl-CoA. After each recombinant strain was cultured under the above culture conditions until the glucose was completely consumed, the cell density was measured and the production amounts of main metabolites including 3-HP in the culture medium were analyzed. In addition, culture was also performed under changed concentration, medium and culture conditions for specific conditions, but was not specifically described.

For analysis of 3-HP in the cell culture supernatant, a culture supernatant sample was analyzed using a Waters Alliance e2695 HPLC system (Waters, Milford, USA) with an injection volume of 10 μl. In HPLC, an Aminex HPX-87H organic acid column (300 mm×7.8 mm) (Bio-Rad, USA) connected to a fast acid analysis column (100 mm×7.8 mm) (Bio-Rad, USA) was used in the stationary phase. The column was maintained at +55° C., and 5.0 mM H_2SO_4 (Merck KgaA, Germany) was used as an eluent at a flow rate of 0.3 or 0.5 ml/min.

For detection of 3-hydroxypropionic acid, glucose, acetate, succinate, pyruvate, glycerol and ethanol, a Waters 2489 dual wavelength UV (210 nm) detector (Waters, Milford, USA) and a Waters 2414 differential refractometer (Waters, Milford, USA) were used.

As a result, as shown in Table 5 below, it was confirmed that all the recombinant strains showed low 3-HP productivity. From this low productivity, it was determined that the expression efficiency of major genes, particularly MCR, had a great influence on the production of 3-HP.

TABLE 5

Production of 3-HP in recombinant YBC strains

Strain name	YBC-1178-1	YBC-1178-3	YBC1497-1	YBC-1413-1	YBC-1413-4
3-HP concentration (mg/L)	16.4	8.5	8.1	1.8	1.6

Example 3: Analysis of Expression Efficiency of MCR Gene in *S. cerevisiae*

In order to compare the expression efficiency of MCR gene and related genes in the *S. cerevisiae* strain in which genetic information and gene tools are well set-up, the expression levels of 3-HP-producing genes, especially the MCR gene with low expression efficiency, were analyzed by the RT-qPCR method described in Example 1.

As a result, as shown in FIG. **5**, it was confirmed that the expression level of the MCRsa2 gene was low even in the recombinant strains containing the endogenous promoter of

S. cerevisiae. Thus, it was confirmed that it was necessary to select a novel promoter capable of increasing expression of the MCR gene.

Example 4: Analysis of Expression of Alcohol-Producing Gene in YBC Strain

In this Example, in order to select a promoter capable of increasing the expression of an exogenous gene in the YBC strain, a promoter that regulates the expression of a gene having high expression efficiency in the YBC strain itself was used, and the gene was replaced with an exogenous gene to be expressed.

From glycolysis- and ethanol production-related genes which are strongly expressed in the presence of glucose, genes which are highly efficient without influencing growth when replaced with other genes were selected, and a promoter that regulates expression of ADH (alcohol dehydrogenase) gene was targeted.

In particular, in order not to directly affect microbial growth, glycolysis-related genes should be eliminated. If the glycolysis-related genes are deleted or inactivated, the production of pyruvate, which is important for microbial growth, is inhibited or a problem occurs in the balance of the chain reaction, and thus the growth properties of microorganisms are adversely affected, resulting in a decrease in the fermentation ability. For this reason, when the target strain is an ethanol-producing strain, the PDC (pyruvate dehydrogenase complex) gene or the ADH gene is selected as the endogenous gene to be replaced, and PDC is used as an important pathway to produce a target compound in the target strain. For this reason, the ADH gene was selected as the gene to be deleted.

Strains with strong ethanol fermentation ability, such as yeast, have ADHs having a wide variety of strengths and functions. In order to identify major ethanol-producing ADHs among yeast ADHs and to select and use the corresponding promoter, several candidate genes were identified by comparing genome information on the YBC strain with known information on the ADH gene of *S. cerevisiae* and subjected to qPCR.

Seven ADH gene candidates were selected using bioinformatics information from the genome-wide sequence data of *S. cerevisiae* (see Table 6), and oligomers specific to the selected genes were designed and subjected to RT-qPCR (See Table 4 for primer sequences).

TABLE 6

S. cerevisiae gene	Homolog in YBC	Identity-% (protein)	Genomic location*	Targeting signal
ADH1	g4423	89.1%	ADH5	no
ADH2	g4423	77.2%	ADH5	no
ADH3	g2289	80.4%	ADH3	mitochondrial
ADH4	No homologs			
ADH5	g4423	74.4%	ADH5	no
SFA1	g4117	79.5%	SFA1	
ADH6	g5126	63.4%	—	no
	g1044	64.1%	—	no
	g4395	64.0%	—	no
	g727	63.7%	—	no
	g2807	60.4%	—	no
ADH7	g5126	63.0%	—	no
	g1044	60.0%	—	no
	g4395	61.8%	—	no
	g727	62.1%	—	no
	g2807	58.0%	—	no

*Genes having similar gene sequences in YBC compared to *S. cerevisiae* genome

As a result, as shown in FIG. **6**, it was confirmed that the expression level of the g4423 gene was significantly high.

A strain (YBC-1563) from which the g4423 gene was removed was constructed. Based on information on g4423 and UTR, a gene cassette similar to FIG. **1**(*a*) was constructed, from which the g4423 ORF was removed and which had 5' and 3' UTRs and an antibiotic marker. The constructed gene cassette was used as donor DNA. For construction of the donor DNA, the cloning method using restriction enzymes as described above and the method using Gibson assembly were used. The constructed donor DNA was introduced, and the colonies grown in the plate corresponding to the marker gene were analyzed using ORF primers (forward primer (SEQ ID NO: 72): GAGATAGCACACCATTCACCA, and reverse primer (SEQ ID NO: 73): CAACGTT72AAGTACTCTGGTGTTTG) for identifying g4423. As a result, it was confirmed that the ORF was removed.

The strain was cultured with 50 ml of a medium (containing 40 g/L glucose) in a 250 ml flask at 30° C. and 250 rpm with a starting OD value of 0.7 until sugar and ethanol were completely consumed. Then, glucose consumption and ethanol production were analyzed. As a result, it was confirmed that ethanol production was reduced by 50% or more (FIG. **7**).

Example 5: Analysis of Expression Level of YBC Recombinant Constructed by Replacing g4423 Gene with MCR Gene

In order to use the strong expression ability of the g4423 gene identified in Example 4, the recombinant strain YBC-1684 was constructed by replacing the g4423 gene in the genome of the YBC strain with the MCRsa1 gene, and the expression level of the MCRsa1 gene was analyzed. Based on information on g4423 and UTR, the gene cassette of FIG. **1**(*b*) was constructed, from which the g4423 ORF was removed and which had 5' and 3' UTRs and an antibiotic marker. In addition, an MCRsa1 sequence optimized for yeast codon usage was introduced into the ORF site of g4423. The constructed gene cassette was used as donor DNA. For construction of the donor DNA, the cloning method using restriction enzymes as described above and the method using Gibson assembly were used. The plasmid (pSK863) used in the donor DNA is set forth in SEQ ID NO: 7.

The donor DNA in the constructed cassette was amplified and introduced into the YBC strain. The grown colonies were analyzed using the following primers for identifying the g4423 ORF. As a result, it was confirmed that the g4423 ORF was removed and the MCRsa1 ORF existed, suggesting that MCRsa1 was introduced.

```
Forward primer (SEQ ID NO: 74) for analysis:
ATGAGAAGAACTTTGAAGGCTG,

Reverse primer (SEQ ID NO: 75):
TTACTTAGGGATGTAACCCTTTTCGA)
```

The strain was cultured with 50 ml of a medium (containing 40 g/L glucose) in a 250 ml flask at 30° C. and 250 rpm with a starting OD value of 0.7 until sugar and ethanol were completely consumed. Then, the amount of 3-HP and the amounts of sugar and ethanol produced were analyzed. RT-qPCR for analyzing the gene expression level was performed under the same conditions as those in Example 1, and the culture medium was sampled during the logarithmic

growth phase. Table 7 below shows the specific genotypes of the constructed recombinant YBC strains.

TABLE 7

Recombinant YBC strains constructed by replacing g4423 gene with MCRsa1 gene

Strain	Description
YBC-061	acs2Δ(1/2)-TEF1p-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t-(NatR)
YBC-1684	g4423::MCRsa1
YBC-Trans	g4423::MCRsa1, ald2Δ-FBA1p-MCRsa1-FBA1t: Eno2p-HiBADH-Eno2t: TPI1p-EUTE-TPI1t
YBC-1693	ald2Δ-g4423p(1kb)-MCRsa1-TEF1t: TDH3p-BDH-TDH3t: PDC1p-EutE-PDC1t

As a result, as shown in FIG. **8**, it was confirmed that the expression level of the MCRsa1 gene in the constructed recombinant strain was similar to that of the g4423 gene, and was much higher than that in the strain (control YBC-061) containing the TEFL promoter that is a strong promoter derived from *S. cerevisiae*.

The promoter of G4423 was compared with the promoters of various ADH isozymes derived from *S. cerevisiae* used in the past, and as a result of comparing homology, it was found that the homology was very low (Table 8). The comparison of homology between the promoter of G4423 and the promoters of various conventional ADH isozymes derived from *S. cerevisiae* was performed, and as a result, it could be seen that the homology was very low (Table 8).

TABLE 8

Comparison of homology between g4423 promoter region and *S. cerevisiae* ADH promoter regions

Target gene	Adh1p	Adh2p	Adh3p	Adh4p	Adh5p	Adh6p	Adh7p	SFA1p
Percent identity	28.06	29.71	24.48	27.63	31.44	29.02	28.05	29.47

Example 6: Production of 3-HP in Recombinant Strain Constructed by Replacing g4423 Gene with MCRsa1 Gene

Analysis was performed as to the production amount of 3-HP in the recombinant YBC-1684 confirmed to have an increased expression level of the MCR gene in Example 5.

Comparison with the results in Table 3 of Example was performed. As shown in Table 3 above, when the three core genes related to 3-HP production were expressed using the scTEF promoter or the FBA promoter, about 1 to 16 mg/L of 3-HP was produced in flask culture.

In addition, analysis was performed as to the production amounts of 3-HP in the recombinant strain YBC-1684 and a strain constructed by inserting 3-HP production-related genes into the YBC-1684 strain in which the g4423 site was replaced with MCRsa1 which was expressed.

Each of the strains was cultured with a YP medium (20 g/L peptone, and 10 g/L yeast extract) supplemented with 4% glucose and 15 μM cerulenin in a flask at 30° C., and on day 5 when sugar was completely consumed, the culture medium was sampled and the production of 3-HP was analyzed.

As a result, as shown in Table 9 below, the YBC-1684 strain in which only the MCRsa1 gene was inserted into the g4423 site produced 200 mg/L of 3-HP, and the strain in which the 3-HP production-related genes (HiBADH gene and EUTE gene) were additionally inserted into the g4423 site produced 146 to 710 mg/L of 3-HP, which was different between colonies. Thus, it could be confirmed that production of 3-HP in this strain was significantly higher than production of 3-HP in the recombinant strain in which the corresponding gene was expressed by the scTEF promoter or the FBA promoter.

TABLE 9

	Control	YBC-1684	YBC-trans (multiple colonies)
3-HP concentration at 5 days (mg/L)	0	200	342 46 to 710)

From these results, it was confirmed that the increased expression of the MCRsa1 gene by the g4423 promoter could have a great influence on the increased production of 3-HP. Thereby, it could be seen that, if the expression of genes involved in a target compound is increased by the g4423 promoter, the production of the target compound can increase.

Example 7: Analysis of Mobility of g4423 Promoter

The G4423 promoter and the terminator region in the genomic DNA of the YBC strain were cut into a length of 1 kb, and the expression level of the MCRsa1 gene for 3-HP production was analyzed. Based on information on g4423 and UTR in the genome of the YBC strain, the 1 kb region of the 5'UTR region of g4423 was amplified using primers and extracted, and then amplified using the oSK-1412 to oSK1419 primers of Table 2 above, thus obtaining an MCRsa1 fragment optimized for yeast codon usage with the promoter of g4423. The obtained fragment was introduced into the cassette of FIG. **1**(*e*) capable of expressing a plurality of genes, and the plasmid (pSK-865) used is set forth in SEQ ID NO: 8. The donor DNA cassette was amplified, purified and introduced into YBC, and the genotype of the grown colonies was analyzed.

It was confirmed that the expression level of MCRsa1 in the recombinant strain YBC-1693 conducted by the above method was lowered, like when the promoter (FBA) of YBC or the TEF1p promoter of *S. cerevisiae* was used (FIG. **9**). Thus, it is presumed that the promoter action of the YBC acid-resistant strain requires a longer fragment or has mechanisms that act even at a long distance (enhancer or silencer) or mechanisms that work in combination by multiple factors. Additional research is needed to accurately elucidate these mechanisms.

When the g4423 gene is replaced with a target gene, two effects can be obtained: the target gene can be strongly expressed, and the g4423 gene that is involved in ethanol production is removed. Thus, it is possible to effectively accomplish the purpose of research to produce various compounds using the strain.

Example 8: Expression of LDH Gene by g4423 Promoter

In this Example, a recombinant YBC strain was constructed, in which the LDH (lactate dehydrogenase) gene involved in lactate production in addition to the MCR gene was replaced with the g4423 gene. The lactate productivity of the constructed strain was analyzed.

The recombinant strain was constructed so that three representative genes (*L. helveticus*-derived LDH, *R. oryzae*-derived LDH, and *L. plantarum*-derived LDH) would be expressed by the g4423 promoter.

Based on information on g4423 and UTR, a gene cassette similar to that shown in FIG. **1**(*e*) was constructed, in which the g4423 ORF was removed and which had 5' and 3' UTRs and an antibiotic marker. Based on information on three genes from the NCBI, sequences optimized for yeast codon usage were synthesized, and then introduced into the cassette using restriction enzymes (ApaI and SacI). The donor DNA in the completed cassette was amplified and introduced into the YBC strain. The grown colonies were analyzed using the following primers for identifying the g4423 ORF, and as a result, it was confirmed that one allele of the g4423 ORF was removed and each of the LDH genes was introduced.

L. helveticus forward primer (SEQ ID NO: 76):
ATGAAAATTTTTGCTTATGG;

L. helveticus reverse primer (SEQ ID NO: 77):
TTAATATTCAACAGCAATAG;

R. oryzae forward primer (SEQ ID NO: 78):
ATGGTTTTGCATTCTAAAGT;

R. oryzae reverse primer (SEQ ID NO: 79):
TTAACAAGAAGATTTAGAAA;

L. plantarum forward primer (SEQ ID NO: 80):
ATGTCTTCTATGCCAAATCA;

L. plantarum reverse primer (SEQ ID NO: 81):
TTATTTATTTTCCAATTCAG

The constructed recombinant strain was shake-cultured with YP (20 g/L peptone, and 10 g/L yeast extract) medium supplemented with 4% glucose and 150 mg/L uracil at 30° C. and 100 rpm for 24 hours.

Lactate and ethanol in the culture medium were analyzed by HPLC. The concentrations of glucose, ethanol and L-lactate in the culture medium were analyzed using a Bio-Rad Aminex 87-H column with a Waters 1525 Binary HPLC pump. Glucose and ethanol were analyzed using a Waters 2414 refractive index detector, and L-lactate was analyzed using a Waters 2489 UV/visible detector (210 nm). The concentration of each component was calculated using a peak area standard curve plotted according to the concentration of each component, and specific conditions for analysis are as follows.

1. Mobile phase condition: 0.005M H_2SO_4 solution
2. Flow rate: 0.6 mL/min
3. Run time: 40 min
4. Column oven temperature: 60° C.
5. Detector temperature: 40° C.
6. Injection volume: 10 μL
7. Auto sampler tray temperature: 4° C.

As a result, as shown in FIG. **10**, it was confirmed that the replaced target genes exhibited LDH activity, so that lactate was produced.

[Depository Information]

Name of Depositary Authority: Korea Research Institute of Bioscience and Biotechnology

Accession Number: KCTC13508BP

Deposit Date: Apr. 11, 2018

INDUSTRIAL APPLICABILITY

When an organic acid production-related target gene is expressed in an organic acid-resistant yeast using the novel promoter according to the present invention, there is an advantage in that the yeast can produce the organic acid with high efficiency while having resistance to organic acids without inhibiting the growth ability of the yeast.

Although the present invention has been described in detail with reference to specific features, it will be apparent to those skilled in the art that this description is only of a preferred embodiment thereof, and does not limit the scope of the present invention. Thus, the substantial scope of the present invention will be defined by the appended claims and equivalents thereto.

Sequence List Free Text

Electronic file is attached

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tctaactgct accttaattt ctcatggaaa gtggcaaata cagaaattat atattcttat 780

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aataaattct caataattta tttggaacca aataatgcaa taactagcaa actaagtggt 300

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caacacacca tcatctttcg tgattatttt tatcatttct atcatgtaat taaattaaca 660

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agtggcaaat actgaaatta tttaattcta ctttcatttt cttataattt ttatcaatta 780

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acctttattc tttatccatt taatttattt cttgtatctt tcttttctat ttctcttttc 900

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<210> SEQ ID NO 3
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: g4423 terminator region Allele 1

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<220> FEATURE:
<223> OTHER INFORMATION: g4423 terminator region Allele 2

<400> SEQUENCE: 4

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acagggacaa atatatcaga aggtccacta agaattattc cacaattaca aactttctat 600

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gatccaacaa aattattaca atcacaaaat tcttcacgtc ctttatggtt atcattcaag 780

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<210> SEQ ID NO 5

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<211> LENGTH: 6402
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: g4423 deletion cassette containing plasmid
Allele 1

<400> SEQUENCE: 5

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: g4423 deletion cassette containing plasmid
Allele 2

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<210> SEQ ID NO 10
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 10

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<210> SEQ ID NO 11
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 11

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<210> SEQ ID NO 12
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

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<400> SEQUENCE: 12

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<210> SEQ ID NO 13
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 13

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<210> SEQ ID NO 14
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

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gttaatagtc 70

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 16

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<210> SEQ ID NO 17
<211> LENGTH: 44
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 17

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<210> SEQ ID NO 18
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 18

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<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 19

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 21

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atttttgaaa tgttaatagt cttttttttt 89

<210> SEQ ID NO 22
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 22

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tttgaaggct gccattttag g 81

<210> SEQ ID NO 23
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 23

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gggatgtaac ccttttcgat caaatattc 89

<210> SEQ ID NO 24
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 24

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<210> SEQ ID NO 25
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 25

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<210> SEQ ID NO 26
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 26

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<210> SEQ ID NO 27
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 27

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<210> SEQ ID NO 28
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 28

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gaagagtctt gaaagcagca atcttgg 87

<210> SEQ ID NO 29
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 29

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ttgatatatg gatatatatg tgtacgg 87

<210> SEQ ID NO 30
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 30

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ttttgaaatg ttaatagtct ttttttt 87

<210> SEQ ID NO 31
<211> LENGTH: 87
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: oligomer for Gibson assembly

<400> SEQUENCE: 31

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tgtaaccctt ttcaaccaaa aattctg 87

<210> SEQ ID NO 32
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 32

cggactttag agccttgtag ac 22

<210> SEQ ID NO 33
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 33

atctggttac actcacgatg g 21

<210> SEQ ID NO 34
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 34

ccaagtacgt tagagctaac gg 22

<210> SEQ ID NO 35
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 35

gagcttctct ggtatcagct 20

<210> SEQ ID NO 36
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 36

agctttagca aacattagac cc 22

<210> SEQ ID NO 37
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 37

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<210> SEQ ID NO 38
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 38

ggaacctaaa tgactgttgg ca 22

<210> SEQ ID NO 39
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 39

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<210> SEQ ID NO 40
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 40

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<210> SEQ ID NO 41
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 41

gtaccgctaa tgaacctaaa cca 23

<210> SEQ ID NO 42
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 42

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<210> SEQ ID NO 43
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 43

gatgtgtcta cgacgtatct acc 23

<210> SEQ ID NO 44
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 44

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<210> SEQ ID NO 45
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 45

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<210> SEQ ID NO 46
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 46

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<210> SEQ ID NO 47
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<212> TYPE: DNA
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<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 47

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<210> SEQ ID NO 48
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 48

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<210> SEQ ID NO 49
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 49

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<210> SEQ ID NO 50
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<212> TYPE: DNA
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<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 50

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<210> SEQ ID NO 51
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 51

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<210> SEQ ID NO 52
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 52

aaattggtga ccgtgttggt 20

<210> SEQ ID NO 53
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aaccaccttt actacggtaa cca 23

<210> SEQ ID NO 54
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 54

tttagtcgtc atctgttcag gt 22

<210> SEQ ID NO 55
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 55

gagacaccta acaaaccaaa tgg 23

<210> SEQ ID NO 56
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 56

gattcaagct tcttctcgta tcgg 24

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<210> SEQ ID NO 57
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 57

ggaaatgata ccattcacga cct 23

<210> SEQ ID NO 58
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURE:
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gttccgtcaa agaaatcaag ca 22

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<211> LENGTH: 24
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<213> ORGANISM: Artificial Sequence
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<210> SEQ ID NO 60
<211> LENGTH: 22
<212> TYPE: DNA
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<400> SEQUENCE: 60

tttagttgtc atttgtgccg gt 22

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gacacctaac aaaccaaacg ga 22

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<211> LENGTH: 22
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gctaacttca aaggtgaacc tc 22

<210> SEQ ID NO 63
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aatctaccaa ctacgacgga c 21

<210> SEQ ID NO 64
<211> LENGTH: 22
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<400> SEQUENCE: 64

cagattcgaa ccagatatcc ct 22

<210> SEQ ID NO 65
<211> LENGTH: 24
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

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ccaatggtaa caatacacct tgag 24

<210> SEQ ID NO 66
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ggtaaagctt actcagaagt tgtc 24

<210> SEQ ID NO 67
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cagcaccttg aggtaatgga 20

<210> SEQ ID NO 68
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ctatgcaagc tgtttccggt 20

<210> SEQ ID NO 69
<211> LENGTH: 24
<212> TYPE: DNA
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<400> SEQUENCE: 69

cgttgacgtt tctcttagtt tcag 24

<210> SEQ ID NO 70
<211> LENGTH: 20

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 70

ctttgagtgc aagtatcgcc 20

<210> SEQ ID NO 71
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURE:
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<400> SEQUENCE: 71

tgtgtaattg ttcaccaaag cc 22

<210> SEQ ID NO 72
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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer for qPCR

<400> SEQUENCE: 72

gagatagcac accattcacc a 21

<210> SEQ ID NO 73
<211> LENGTH: 24
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<223> OTHER INFORMATION: primer

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caacgttaag tactctggtg tttg 24

<210> SEQ ID NO 74
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<400> SEQUENCE: 74

atgagaagaa ctttgaaggc tg 22

<210> SEQ ID NO 75
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ttacttaggg atgtaaccct tttcga 26

<210> SEQ ID NO 76
<211> LENGTH: 20
<212> TYPE: DNA
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<400> SEQUENCE: 76

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atgaaaattt ttgcttatgg 20

<210> SEQ ID NO 77
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 77

ttaatattca acagcaatag 20

<210> SEQ ID NO 78
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 78

atggttttgc attctaaagt 20

<210> SEQ ID NO 79
<211> LENGTH: 20
<212> TYPE: DNA
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<400> SEQUENCE: 79

ttaacaagaa gatttagaaa 20

<210> SEQ ID NO 80
<211> LENGTH: 20
<212> TYPE: DNA
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<400> SEQUENCE: 80

atgtcttcta tgccaaatca 20

<210> SEQ ID NO 81
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 81

ttatttattt tccaattcag 20

The invention claimed is:

1. A recombinant microorganism having an isolated promoter comprising the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

2. The recombinant microorganism of claim **1**, further containing an isolated terminator comprising the sequence of SEQ ID NO: 3 or SEQ ID NO: 4.

3. The recombinant microorganism of claim **1**, which is yeast.

4. The recombinant microorganism of claim **3**, wherein the yeast is YBC, deposited under Accession No. KCTC13508BP.

5. A method for producing an organic acid, the method comprising steps of:

(a) producing the organic acid by culturing the recombinant microorganism of claim **1** introduced therein; and

(b) collecting the produced organic acid.

6. A recombinant microorganism having a gene construct in which an isolated promoter comprising the nucleotide sequence comprising SEQ ID NO: 1 or SEQ ID NO: 2 and a gene encoding a target gene are operably linked to each other in an acid-resistant yeast YBC strain deposited under Accession No. KCTC13508BP.

7. The recombinant microorganism of claim **6**, further containing an isolated terminator comprising the sequence of SEQ ID NO: 3 or SEQ ID NO: 4.

8. The recombinant microorganism of claim 6, further containing a malonyl-CoA-reductase coding gene or lactate dehydrogenase coding gene involved in organic acid production.

9. A method for producing an organic acid, the method comprising steps of:

(a) producing the organic acid by culturing the recombinant microorganism of claim 6 introduced therein; and

(b) collecting the produced organic acid.

* * * * *