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(54) **POLYPEPTIDE AND YEAST CELL COMPOSITIONS AND METHODS OF USING THE SAME**

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(51) **Int. Cl.**

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C12N 15/00	(2006.01)
C12N 15/81	(2006.01)
C07K 14/395	(2006.01)
C12N 1/16	(2006.01)
C12G 1/022	(2006.01)
C12G 3/02	(2019.01)
C12C 11/00	(2006.01)

(52) **U.S. Cl.**

CPC ***C12N 15/81*** (2013.01); ***C07K 14/395*** (2013.01); ***C12C 11/00*** (2013.01); ***C12G 1/0203*** (2013.01); ***C12G 3/02*** (2013.01); ***C12N 1/16*** (2013.01); *C12N 2500/34* (2013.01)

(58) **Field of Classification Search**

CPC C12N 15/81; C12N 1/16

See application file for complete search history.

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(57) **ABSTRACT**

Polypeptides comprising maltose/maltotriose transporters are provided. Additionally, polynucleotides, DNA constructs, and vectors encoding a maltose/maltotriose transporter, or yeast cells harboring such polynucleotides are provided. The yeast cell may be a *Saccharomyces eubayanus* cell modified to increase the expression or transport activity of a maltose/maltotriose transporter at the plasma membrane of the cell. Further, methods are provided for making a fermentation product by culturing any one of the yeast cells described herein with a fermentable substrate. Finally, methods are provided to select for and isolate maltotriose-utilizing strains of *Saccharomyces eubayanus*.

12 Claims, 9 Drawing Sheets

Specification includes a Sequence Listing.

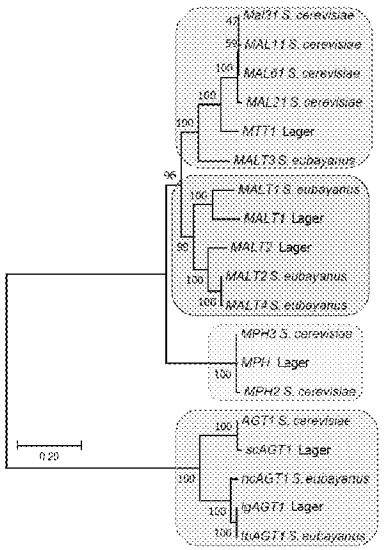

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FIG. 1A

nuc	*lgAGT1*	*ncAGT1*	*scAGT1*	*AGT1*
tbAGT1	99.59	95.74	79.26	80.16
lgAGT1		95.63	79.15	80.05
ncAGT1			79.75	80.66
scAGT1				98.64

aa	lgAgt1	ncAgt1	scAgt1	Agt1
tbAgt1	99.74	95.57	83.74	86.07
lgAgt1		95.41	83.58	85.90
ncAgt1			83.25	85.41
scAgt1				97.24

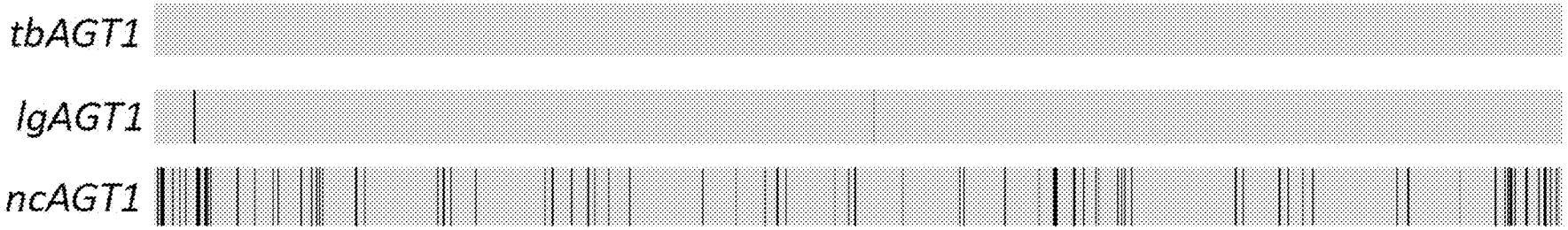


FIG. 1B

FIG. 2

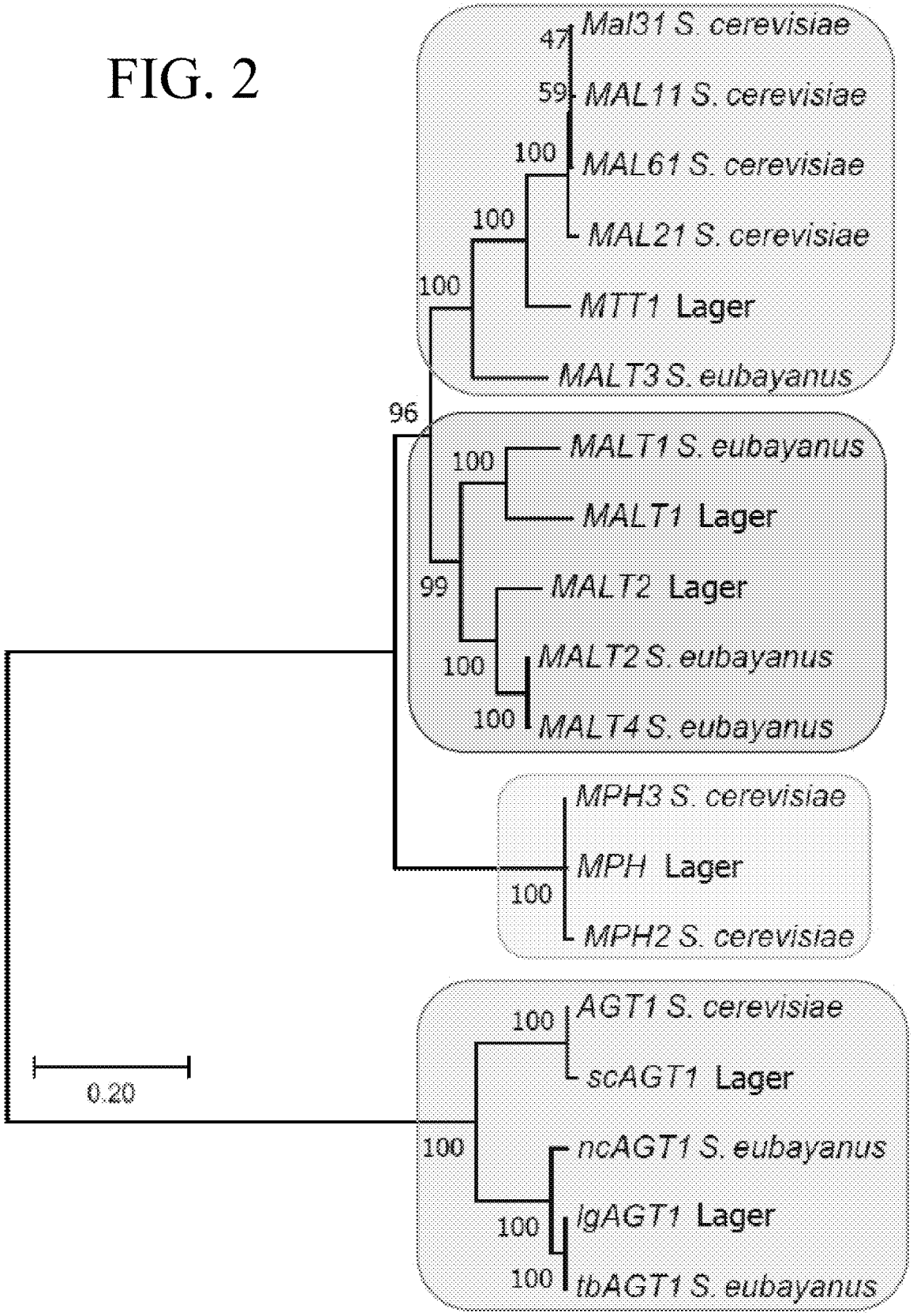

Mal31 S. cerevisiae
MAL11 S. cerevisiae
MAL61 S. cerevisiae
MAL21 S. cerevisiae
MTT1 Lager
MALT3 S. eubayanus
MALT1 S. eubayanus
MALT1 Lager
MALT2 Lager
MALT2 S. eubayanus
MALT4 S. eubayanus
MPH3 S. cerevisiae
MPH Lager
MPH2 S. cerevisiae
AGT1 S. cerevisiae
scAGT1 Lager
ncAGT1 S. eubayanus
lgAGT1 Lager
tbAGT1 S. eubayanus
47
59
100
100
100
96
100
99
100
100
100
100
100
100
0.20

FIG. 3A

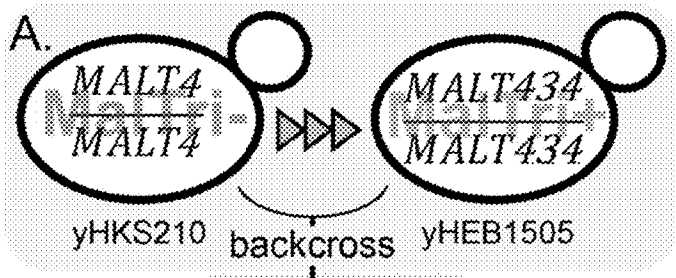


FIG. 3B

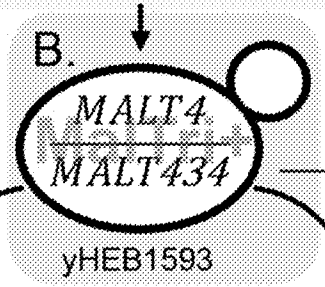


FIG. 3D

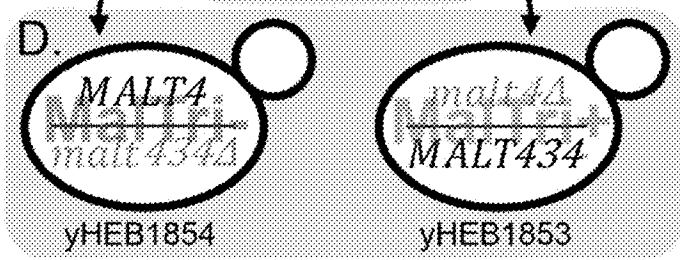


FIG. 3C

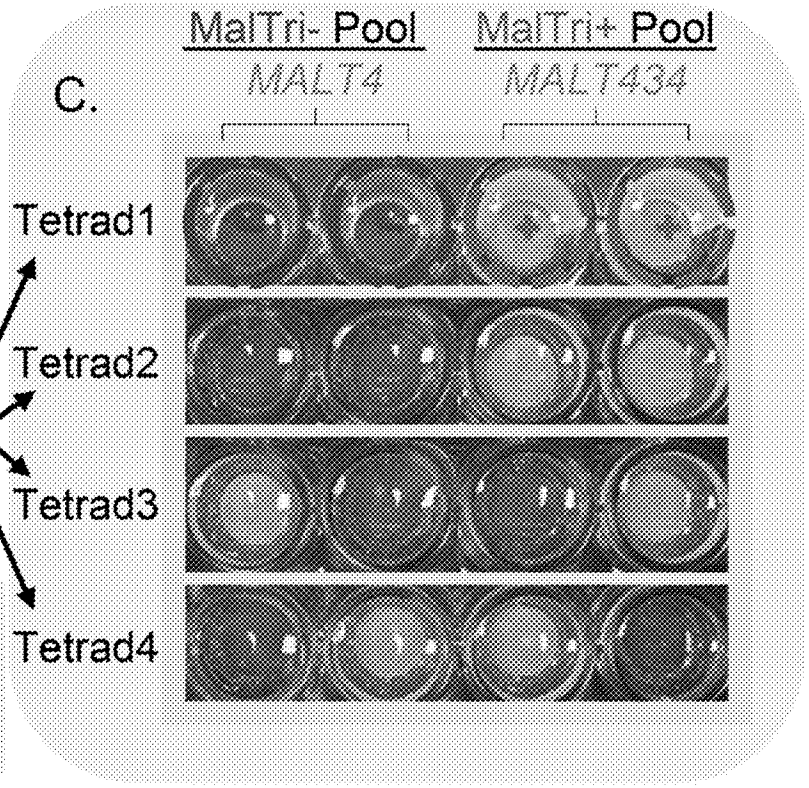


FIG. 3E

Strain	Description	Initial OD	Day 3
yHKS210*	Wild admixture strain	0.22 (+/-0.01)	0.68 (+/-0.06)
yHKS210	Wild admixture strain	0.14 (+/-0.02)	0.39 (+/- 0.01)
yHEB1505	Single-colony isolate of yHKS210 evolved in maltotriose	0.16 (+/-0.02)	1.46 (+/- 0.01)
yHEB1593	yHKS210 x yHEB1505	0.12 (+/-0.01)	1.24 (+/- 0.02)
yHEB1854	yHEB1593 *MALT4/malt434Δ*	0.13 (+/-0.01)	0.39 (+/- 0.01)
yHEB1853	yHEB1593 *malt4Δ/MALT434*	0.11 (+/-0.01)	1.33 (+/- 0.04)

FIG. 3F

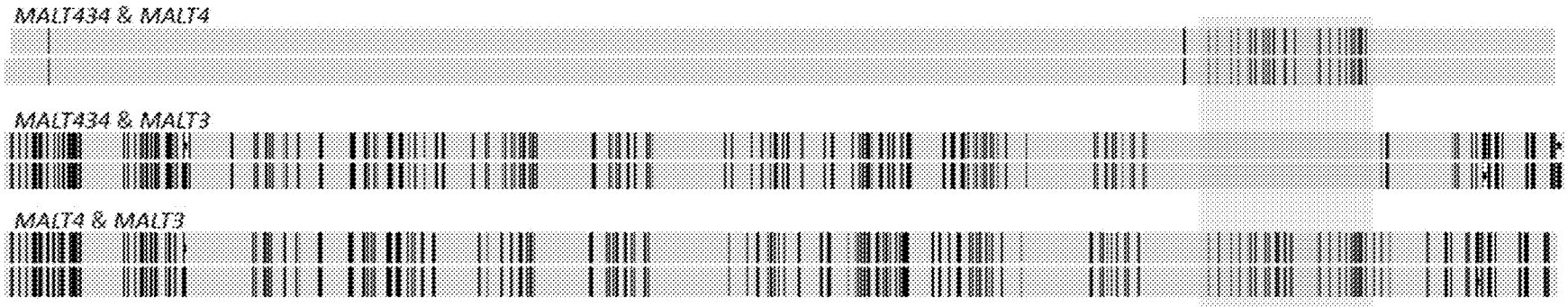


FIG. 3H

Percent identity

Nucleotide

Whole protein

	MAL73	MAL74
MAL7434	82.11	97.07
MAL73		79.50

Amino acid

	Mal3p	Mal4p
Mal434p	82.52	98.31
Mal3p		80.72

Chimeric region (bp 1392-1620)

	MAL73	MAL74
MAL7434		78.17
MAL73		78.17

	Mal3p	Mal4p
Mal434p		85.53
Mal3p		85.53

Excluding chimeric region

	MAL73	MAL74
MAL7434	79.57	
MAL73		79.69

	Mal3p	Mal4p
Mal434p	80.34	
Mal3p		80.04

FIG. 3G

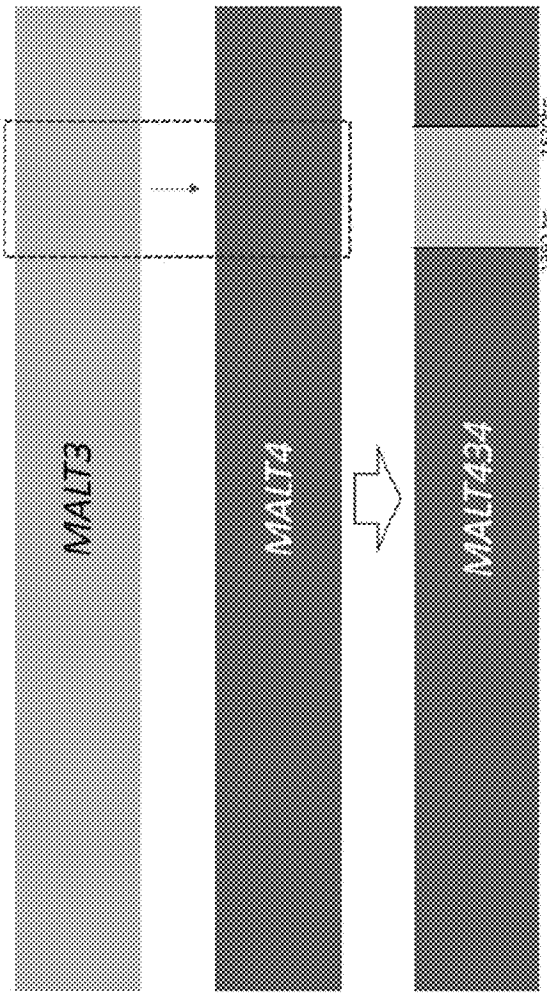


FIG. 3I

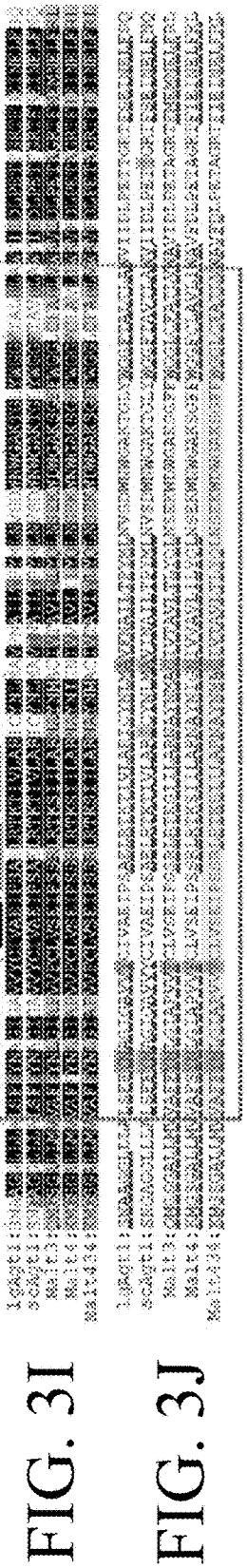
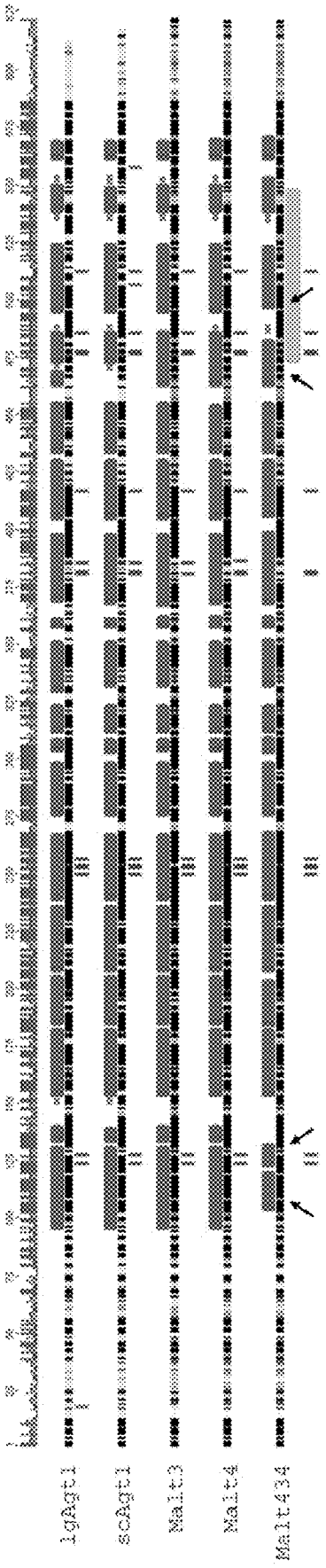


FIG. 3J

FIG. 4



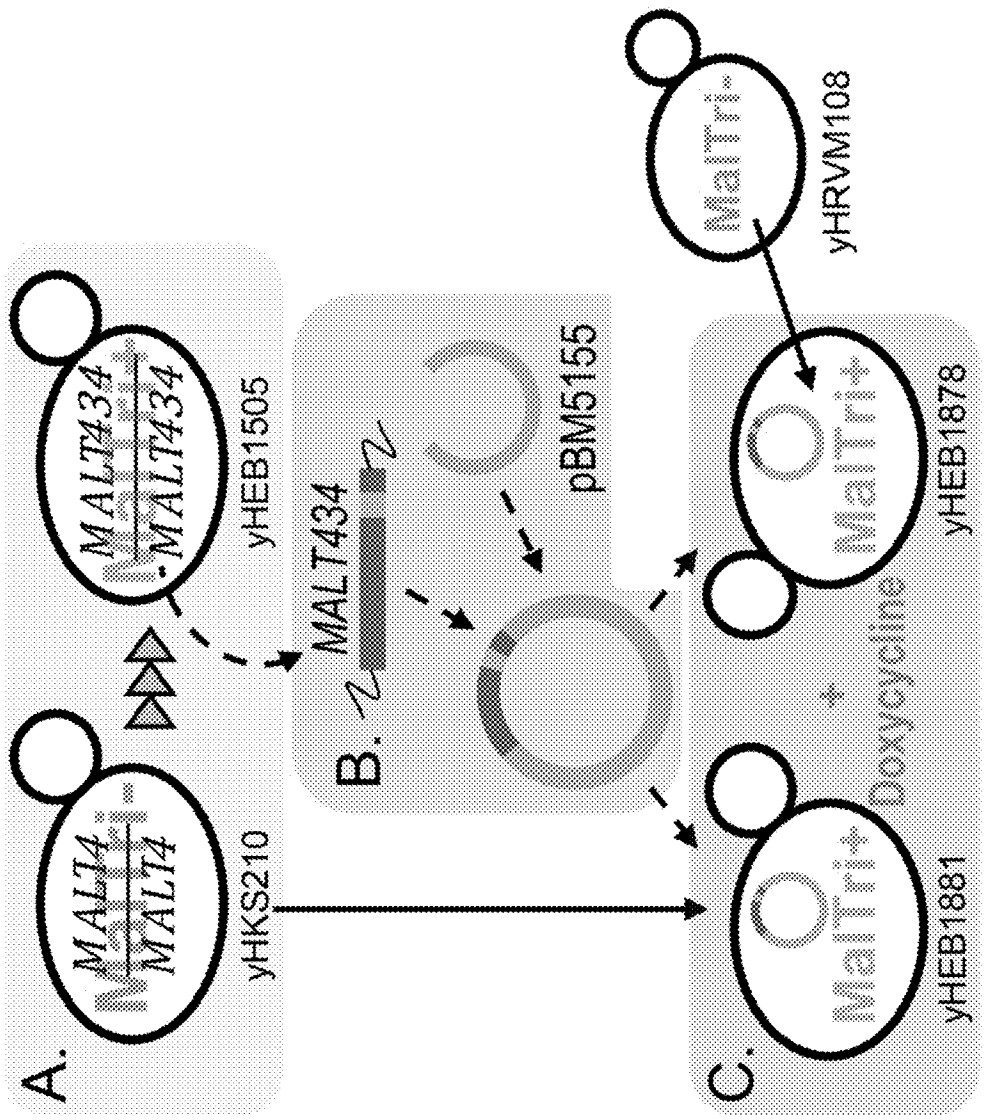


FIG. 5A

FIG. 5B

FIG. 5C

FIG. 5D

Strain	Plasmid	Initial OD	Day 6
yHKS210*	-	0.19 (+/-0.04)	0.52 (+/-0.03)
yHKS210	-	0.14 (+/-0.02)	0.39 (+/-0.05)
yHEB1881	*MALT434*	0.11 (+/- 0.01)	1.31 (+/- 0.05)
yHRVM108*	-	0.16 (+/-0.05)	0.48 (+/-0.01)
yHRVM108	-	0.12 (+/-0.03)	0.46 (+/-0.03)
yHEB1878	*MALT434*	0.12 (+/-0.01)	1.46 (+/-0.04)

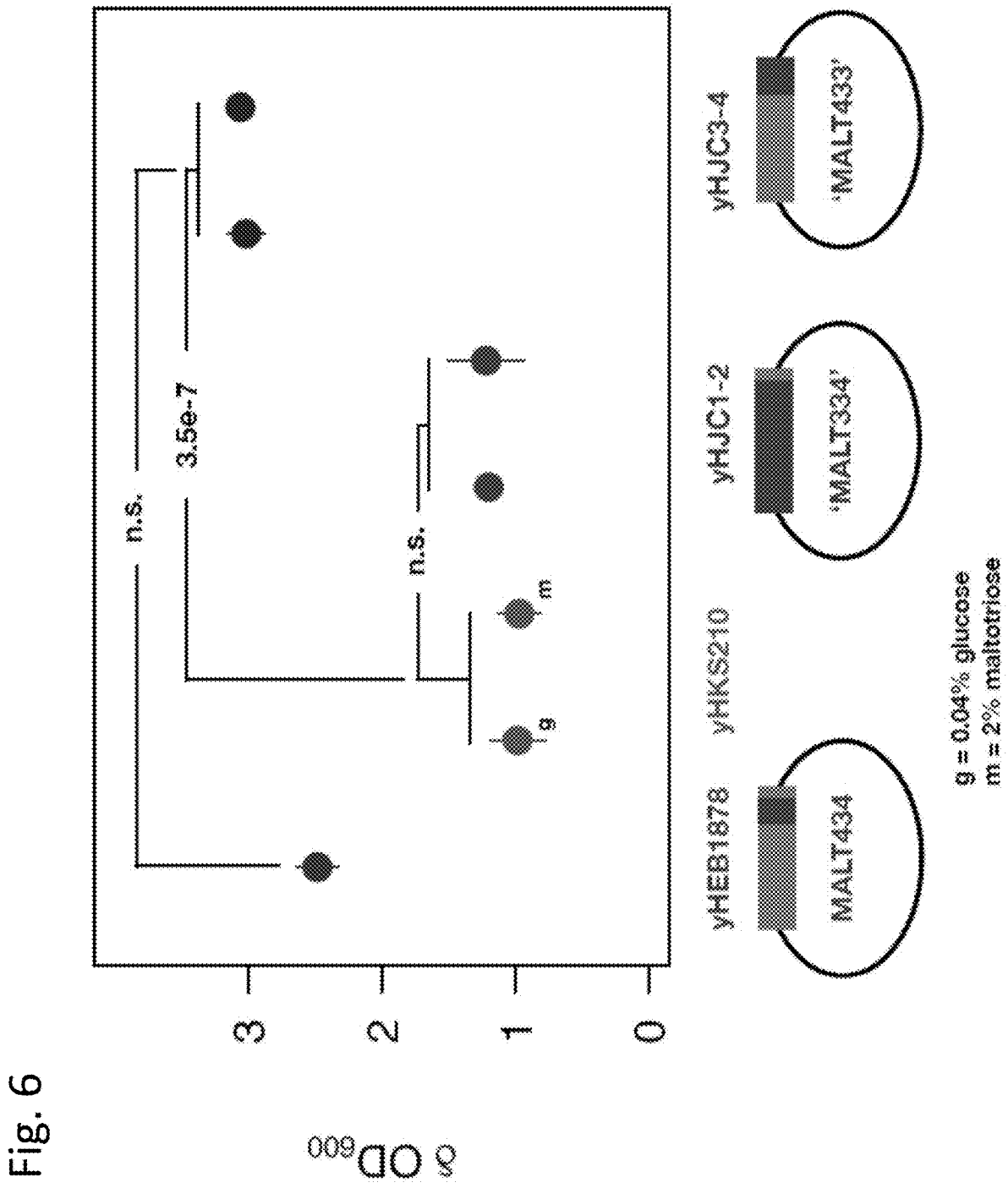

δ OD600
3
2
1
0
n.s.
3.5e-7
n.s.
m
g
yHEB1678
yHKS210
yHJC1-2
yHJC3-4
MALT434
'MALT334'
'MALT433'
g = 0.04% glucose
m = 2% maltotriose

Fig. 6

POLYPEPTIDE AND YEAST CELL COMPOSITIONS AND METHODS OF USING THE SAME

CROSS-REFERENCE TO RELATED APPLICATIONS

This patent application claims the benefit of priority of U.S. Provisional Patent Application No. 62/654,021, filed Apr. 6, 2018, which is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with government support under 17-CRHF-0-6055 awarded by the USDA/NIFA, DEB1253634 awarded by the National Science Foundation and DE-FC02-07ER64494 awarded by the US Department of Energy. The government has certain rights in the invention.

SEQUENCE LISTING

This application includes an electronically submitted Sequence Listing in .txt format. The .txt file contains a sequence listing entitled "2019-06-19_960296-02391_SEQ-_Listing.txt" and was created on Jun. 19, 2019 and is 73,337 bytes in size. The Sequence Listing contained in this .txt file is part of the specification and is hereby incorporated herein in its entirety.

INTRODUCTION

Polypeptides capable of acting as maltotiose transporters and yeast cells comprising such polypeptides are provided. The resultant yeast cells are capable of growing on maltose and/or maltotriose which has wide-ranging applications.

Brewing yeasts operate at the nexus of science and industry, and there is considerable interest in the discovery and/or development of new strains of *Saccharomyces* (both pure species and hybrids) for commercial brewing and biofuel production (Gibson and Liti 2015; Krogerus et al. 2017a; Gibson et al. 2017; Peris et al. 2017; Hittinger et al. 2018; Denby et al. 2018). Special interest has been given to the development of *Saccharomyces eubayanus* for commercial brewing (Hebly et al. 2015; Krogerus et al. 2015, 2017a; Hittinger et al. 2018). As a hybrid with *S. cerevisiae, S. eubayanus* forms lager-brewing yeasts (Libkind et al. 2011), accounting for more than 90% of the total market and the emphasis on commercial development of this newly discovered addition to the genus *Saccharomyces* (Libkind et al. 2011). Most work in this area has focused on producing synthetic lager-brewing hybrids by mating *S. eubayanus* with *S. cerevisiae* (Hebly et al. 2015; Krogerus et al. 2015, 2016, 2017b; Mertens et al. 2015; Alexander et al. 2016; Nikulin et al. 2018), but there is considerable interest in developing brewing strains of pure *S. eubayanus* as well (Gibson et al. 2017; Hittinger et al. 2018).

A key consideration for any new brewing strain is its ability to rapidly and completely use brewing-related sugars, the most important being maltose, followed by maltotriose and glucose. Of these sugars, maltotriose is by far the most difficult to ferment (Briggs D. E., Brookes P. A., Stevens R. 2004; Eβlinger 2009), even though is comprises around 20% of fermentable sugars in wort (Meussdoerffer and Zarnkow 2009). Maltotriose is poorly utilized or completely unutilized by some brewing strains (Stambuk et al. 2006; Wang et al. 2010; Gibson et al. 2013; Magalhães et al. 2016), leading to large amounts of unconsumed sugar, lower amounts of ethanol, and a cloying flavor that is regarded as undesirable in most beer styles. So far, no strain of *S. eubayanus* isolated from nature has been reported to consume maltotriose (Gibson et al. 2013, 2017; Bing et al. 2014; Hebly et al. 2015; Peris and Langdon et al. 2016; Peris et al. 2014). Accordingly, there is a need in the art for new molecular tools that confer maltotriose utilization in, for example, yeast cells. Additionally, there is a need for new yeast strains, such as in *S. eubayanus,* which are capable of consuming maltotriose as the sole carbon source in a growth media.

SUMMARY

In one aspect, the present invention relates to polypeptides. The polypeptides may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 4 (MALT4) and include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid substitution(s) to SEQ ID NO: 4 (MALT4) at position(s) S468, I503, G504, N505, V508, I512, N522, F534, L536, V538, or I540; or a functional fragment of the polypeptide thereof. Suitably, the polypeptide may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to either SEQ ID NO: 1 (MALT434) or SEQ ID NO: 2 (MALT433 Chimeric Protein), or a functional fragment of the polypeptide thereof.

In another aspect, polynucleotides encoding any of the polypeptides disclosed herein are provided.

In still another aspect, DNA constructs are provided. The DNA constructs may include a promoter operably linked to any one of the polynucleotides described herein. Alternatively, the DNA constructs may include a heterologous promoter operably linked to a polypeptide having at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 6 (lgAGT1), SEQ ID NO: 7 (ncAGT1), SEQ ID NO: 8 (AGT1), or SEQ ID NO: 15 (scAGT1), or a functional fragment of the polypeptide thereof.

In a further aspect, vectors, including any one of the DNA constructs or polynucleotides described herein, are provided. The vectors may include vectors for YACs, plasmids, or vectors for homologous recombination.

In another aspect, yeast cells are provided. The yeast cells may include any one of the polypeptides described herein, any one of the polynucleotides described herein, any one of the DNA constructs described herein, or any one of the vectors described herein. Additionally, yeast cells of the present invention may include yeast cells modified to increase, as compared to a control yeast cell, the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter polypeptide. In some embodiments, the yeast cell may be a *Saccharomyces eubayanus* cell modified to increase, as compared to a control *Saccharomyces eubayanus* cell, the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter polypeptide at the plasma membrane of the *Saccharomyces eubayanus* cell.

In still another aspect, the present invention relates to methods for making a fermentation product. The methods may include culturing any one of the yeast cells described herein with a fermentable substrate to produce the fermentation product.

In yet another aspect, methods are provided to select for and isolate maltotriose-utilizing strains of *Saccharomyces eubayanus*.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1**A shows tables highlighting the nucleotide (nuc) and amino acid (aa) percent identities between members of the AGT1 family. Darker colors indicate greater sequence similarity. FIG. **1**B shows multiple sequence alignment between tbAGT1, lgAGT1, and ncAGT1. Black lines indicate nucleotide differences.

FIG. **2** shows a ML phylogenetic tree of MALT genes described in *S. cerevisiae, S. eubayanus,* and lager-brewing hybrids. The scale bar equals the number of nucleotide substitutions per site.

FIG. **3**A is a schematic of the directed evolution of yHKS210, which was originally unable to use maltotriose (MalTri−). After continuous culturing on maltotriose with a small amount of added glucose, yHKS210 evolved the ability to consume maltotriose (MalTri+). FIG. **3**B is a schematic depicting the origins of strain yHEB1593, which is a backcross between yHKS210 and yHEB1505, was also MalTri+. FIG. **3**C shows how yHEB1593 was sporulated to test the inheritance of maltotriose utilization. The panel shows a subset of tetrads screened growing on SC+2% maltotriose. Examples of MalTri− spores in Tetrad 1 are circled in red (Left top row), and MalTri+ examples are circled in green (right top row). Whole genome sequencing of MalTri+ and MalTri− pools showed that maltotriose utilization perfectly correlated with the presence/absence of MALT434. FIG. **3**D is a schematic of the reciprocal hemizygosity test of the MALT4/MALT434 locus in the backcross strain yHEB1593. FIG. **3**E is a table of initial and day-three OD600 (OD) readings of yHKS210, yHEB1505, yHEB1593, yHEB1853, and yHEB1854 on SC+2% maltotriose as the sole carbon source. N=3, standard deviation in parentheses. The control was grown in SC+0.04% glucose to reflect the approximate amount of growth expected from contamination with other carbon sources when using 98% pure maltotriose. FIG. **3**F shows pairwise alignments between MALT3, MALT4, and MALT434. The highlighted region indicates the sequence that was exchanged in MALT4. MALT3 and MALT4 sequences are from strain FM1318, while MALT434 sequences are from strain yHEB1505, an evolved MalTri$^+$ descendent of yHKS210; differences outside of the chimeric region existed in the yHKS210 parent strain. FIG. **3**G shows a schematic of the origin of MALT434. FIG. **3**H shows tables highlighting the percent nucleotide and amino acid identities between the whole protein-coding sequences of MALT3, MALT4, and MALT434, only the chimeric region, and the non-chimeric part of the protein. FIGS. **3**I-**3**J show segments of the alignment of the chimeric region between Malt3 (SEQ ID NO: 5), Malt4 (SEQ ID NO: 4), Malt434 (SEQ ID NO: 1), scAgt1 (SEQ ID NO: 15), and lgAgt1 (SEQ ID NO: 6). The region highlighted in yellow in the Malt434 sequence indicates the chimeric region. The regions underlined with a red dashed line are predicted transmembrane domains. The amino acids highlighted in red are predicted maltose binding residues. The residues highlighted in blue were experimentally found to be important for maltotriose transport by Smit et al. 2008.

FIG. **4** shows a protein structural alignment between Malt3, Malt4, Malt434, scAgt1, and lgAgt1. The purple blocks represent predicted alpha helices, and the orange lines represent predicted beta strands. Red ticks mark predicted maltose binding sites. Blue ticks mark residues found to be important for maltotriose transport by Smit et al. 2008. Green ticks mark the location of the single non-synonymous substitution between lgAGT1 and tbAGT1. Arrows point to alpha helices in Malt434, whose predicted sizes are reduced compared to other transporters in the alignment.

FIG. **5**A is a schematic of the directed evolution of non-maltotriose utilizing strain (MalTri−), yHKS210, to maltotriose utilizing (MalTri+) strain, yHEB1505, by serial passing on maltotriose containing media (same as FIG. **3**A). FIG. **5**B is a schematic of the insertion of MALT434 into vector pBM5155 for doxycycline-inducible heterologous expression in MalTri− strains. FIG. **5**C is a schematic of the transformation of MALT434 expression plasmid in MalTri− *S. eubayanus* strains yHKS210 and yHRVM108. FIG. **5**D is a table of initial and day-six OD_{600} (OD) measurements of parent strains and strains carrying the MALT434 expression plasmid grown in SC media with maltotriose as the sole carbon and doxycycline to induce plasmid expression. N=3, standard deviation in parentheses. The control was grown in SC+0.04% glucose+doxycycline to reflect the approximate amount of growth expected from contamination with other carbon sources when using 98% pure maltotriose.

FIG. **6** is a graph showing growth of the chimeric MALT constructs the change in OD 600 over 7 days of growth of *S. eubayanus* strains expressing MALT434 (yHEB1878), MALT334 (yHJC1-2), or MALT433 (yHJC3-4) from an inducible vector in 2% maltotriose medium, compared to *S. eubayanus* lacking heterologous transporter expression (yHKS210) grown in 2% maltotriose and 0.04% glucose. Points and bars show the mean +/− standard error of three technical replicates randomly distributed on a 96-well plate. p-values from two-sided t test.

DETAILED DESCRIPTION

Here, the present inventors in the non-limiting Examples used directed evolution to identify strains of *S. eubayanus* that can consume maltotriose or maltose as the sole carbon source in a growth media. The present inventors repeatedly passaged wild strains of *S. eubayanus* for hundreds of generations in 0.1% glucose (so that cells would divide and accumulate mutations) and 2% maltotriose or 2% maltose (to select for advantageous mutations). After directed evolution, the inventors identified strains that evolved the ability to consume maltotriose as the sole carbon source. They further show that in one of their evolved strains this trait is stable, genetically inherited, and maps to a single genetic locus that encodes a novel chimeric MALT3/MALT4 protein. This strain is descended from a wild isolate from Sheboygan, Wis. (yHKS210) that could not originally consume maltotriose, but could consume maltose.

The present inventors also identified six *S. eubayanus* strains (yHEB1585-90) that evolved the ability to consume both maltose and maltotriose. These strains are descended from strain yHRVM108, a wild isolate from Durham, N.C., that could not originally consume either maltose or maltotriose. By identifying these strains and demonstrating that the parent strain contains a gene encoding a maltotriose transporter capable of conferring maltotriose transport when overexpressed in *S. eubayanus,* the inventors have discovered that increasing the expression of AGT1 (alpha-glucoside transporter) or AGT1-related proteins in, for example, *S. eubayanus* cells, confers the ability to consume maltotriose or maltose as the sole carbon source.

Based on their directed evolution studies, the present inventors demonstrate that increasing the expression or

maltose/maltotriose transport activity of maltose/maltotriose transporter proteins in yeast cells, such as *S. eubayanus* cells, is sufficient to allow those yeast cells to consume maltotriose or maltose as the sole carbon source.

Polypeptides

In one aspect, the present invention relates to polypeptides. The polypeptides may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 4 (MALT4) and include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid substitution(s) to SEQ ID NO: 4 (MALT4) at position(s) S468, I503, G504, N505, V508, I512, N522, F534, L536, V538, or I540; or a functional fragment of the polypeptide thereof.

The polypeptides may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 4 (MALT4) and include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid substitution(s) to SEQ ID NO: 4 (MALT4) selected from the group consisting of S468F, S468Y, S468W, I503M, I503S, I503C, I503T, G504A, G504V, G504L, G504I, N505C, N505S, N505T, N505M, V508T, V508S, V508C, V508M, I512T, I512S, I512C, I512M N522D, N522E, F534L, F534I, F534V, F534G, F534A, L536F, L536Y, L536W, V538T, V538S, V538C, V538M, I540V, I540G, I540A, I540L, and I540I.

In some embodiments, the polypeptide may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 4 (MALT4) and may include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 amino acid substitution(s) to SEQ ID NO: 4 (MALT4) selected from the group consisting of S468F, I503M, G504A, N505C, V508T, I512T, N522D, F534L, L536F, V538T, and I540V.

Suitably, the polypeptide may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to any one of SEQ ID NO: 1 (MALT434), SEQ ID NO: 2 (MALT433 Chimeric Protein), or SEQ ID NO: 3 (MALT334 Chimeric Protein), or a functional fragment of the polypeptide thereof.

As used herein, the terms "protein" or "polypeptide" or "peptide" may be used interchangeably to refer to a polymer of amino acids. A "polypeptide" as contemplated herein typically comprises a polymer of naturally occurring amino acids (e.g., alanine, arginine, asparagine, aspartic acid, cysteine, glutamine, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, and valine). The proteins contemplated herein may be further modified in vitro or in vivo to include non-amino acid moieties. These modifications may include but are not limited to acylation (e.g., O-acylation (esters), N-acylation (amides), S-acylation (thioesters)), acetylation (e.g., the addition of an acetyl group, either at the N-terminus of the protein or at lysine residues), formylation, lipoylation (e.g., attachment of a lipoate, a C8 functional group), myristoylation (e.g., attachment of myristate, a C14 saturated acid), palmitoylation (e.g., attachment of palmitate, a C16 saturated acid), alkylation (e.g., the addition of an alkyl group, such as an methyl at a lysine or arginine residue), isoprenylation or prenylation (e.g., the addition of an isoprenoid group such as farnesol or geranylgeraniol), amidation at C-terminus, glycosylation (e.g., the addition of a glycosyl group to either asparagine, hydroxylysine, serine, or threonine, resulting in a glycoprotein). Distinct from glycation, which is regarded as a non-enzymatic attachment of sugars, enzymatic addition such as polysialylation (e.g., the addition of polysialic acid), glypiation (e.g., glycosylphosphatidylinositol (GPI) anchor formation, hydroxylation, iodination (e.g., of thyroid hormones), and phosphorylation (e.g., the addition of a phosphate group, usually to serine, tyrosine, threonine or histidine) are also contemplated.

The polypeptides provided herein are evolved polypeptides representing substitution mutants of the wild-type polypeptide. The polypeptides disclosed herein may include "mutant" polypeptides and variants thereof. As used herein the term "wild-type" is a term of the art understood by skilled persons and means the typical form of an organism, strain, gene or characteristic as it occurs in nature as distinguished from mutant or variant forms. As used herein, a "variant" refers to a polypeptide molecule having an amino acid sequence that differs from a reference protein or polypeptide molecule. A variant may have one or more insertions, deletions, or substitutions of an amino acid residue relative to a reference molecule. A variant may include a fragment of a reference molecule. For example, a polypeptide variant molecule may have one or more insertions, deletions, or substitution of at least one amino acid residue relative to the mutant polypeptides described herein.

The amino acid sequence of the "wild-type" proteins from yeast are presented as SEQ ID NO: 4 (MALT4), SEQ ID NO: 5 (MALT3), SEQ ID NO: 6 (lgAGT1), SEQ ID NO: 7 (ncAGT1), SEQ ID NO: 8 (AGT1), and SEQ ID NO: 15 (scAGT1). Some of the amino acid sequences for evolved mutant polypeptides disclosed herein are provided as SEQ ID NO: 1 (MALT434), SEQ ID NO: 2 (MALT433 Chimeric Protein), and SEQ ID NO: 3 (MALT334 Chimeric Protein). These sequences may be used as reference sequences.

The polypeptides provided herein may be full-length polypeptides (i.e., SEQ ID NOS: 1-8, 15) or may be functional fragments of the full-length polypeptide. As used herein, a "fragment" or "functional fragment" is a portion of an amino acid sequence that is identical in sequence to but shorter in length than a reference sequence. A fragment may comprise up to the entire length of the reference sequence, minus at least one amino acid residue. For example, a fragment may comprise from 5 to 155 contiguous amino acid residues of a reference polypeptide, respectively. In some embodiments, a fragment may comprise at least 5, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or 150 contiguous amino acid residues of a reference polypeptide. Fragments may be preferentially selected from certain regions of a molecule. The term "at least a fragment" encompasses the full-length polypeptide. A fragment of a polypeptide may comprise or consist essentially of a contiguous portion of an amino acid sequence of the full-length polypeptide (SEQ ID NOS: 1-8, 15). A fragment may include an N-terminal truncation, a C-terminal truncation, or both truncations relative to the full-length polypeptide. Preferably, a fragment of a polypeptide includes amino acid residues corresponding to amino acid residues 468, 503, 504, 505, 508, 512, 522, 534, 536, 538, or 540 of SEQ ID NO: 4 (MALT4).

The polypeptides disclosed herein may be useful for a variety of reasons. For example, polypeptides which contain the substitutions noted above can be used inter alfa for raising antibodies. Such polypeptides are typically less than full-length proteins. Preferably such residues are at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 19, 21, 23, 25, 30, 40, 50 or more residues in length. As an example, if the polypeptide is 6 residues in length, than it can comprise residues including the substitution site. Sufficient residues are desired to form a good immunogen or blocking antigen for use in assays. It may be desirable to conjugate or genetically fuse additional sequences to the polypeptide, for example, to

boost immunogenicity, to enhance purification, to facilitate production or expression, or to facilitate detection. Any sequences as are convenient may be used for these or other purposes. The size of these additional sequences may vary greatly, but typically will be at least 2, 4, 6, or 8 amino acid residues in length. Suitably the additional sequences will be less than 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 amino acids in length.

The polypeptides are also useful for conferring maltotriose utilization to yeast cells such as, without limitation, *S. eubayanus* cells.

A "deletion" in a polypeptide refers to a change in the amino acid sequence that results in the absence of one or more amino acid residues. A deletion may remove at least 1, 2, 3, 4, 5, 10, 20, 50, 100, 200, or more amino acids residues. A deletion may include an internal deletion and/or a terminal deletion (e.g., an N-terminal truncation, a C-terminal truncation or both of a reference polypeptide).

"Insertions" and "additions" in a polypeptide refer to changes in an amino acid sequence resulting in the addition of one or more amino acid residues. An insertion or addition may refer to 1, 2, 3, 4, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or more amino acid residues. A variant of a polypeptide may have N-terminal insertions, C-terminal insertions, internal insertions, or any combination of N-terminal insertions, C-terminal insertions, and internal insertions.

Regarding polypeptides, the phrases "percent identity," "% identity," and "% sequence identity" refer to the percentage of residue matches between at least two amino acid sequences aligned using a standardized algorithm. Methods of amino acid sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail below, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide. Percent identity for amino acid sequences may be determined as understood in the art. (See, e.g., U.S. Pat. No. 7,396,664, which is incorporated herein by reference in its entirety). A suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST), which is available from several sources, including the NCBI, Bethesda, Md., at its website. The BLAST software suite includes various sequence analysis programs including "blastp," that is used to align a known amino acid sequence with other amino acids sequences from a variety of databases.

As described herein, variants of the polypeptides disclosed herein may have 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% amino acid sequence identity relative to a reference molecule (e.g., relative to SEQ ID NOS: 1-8, 15). Suitably the MALT protein variants include the MALT4 substitution mutations identified herein.

Polypeptide sequence identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70, or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

The amino acid sequences of the polypeptide variants as contemplated herein may include conservative amino acid substitutions relative to a reference amino acid sequence. For example, a variant or derivative polypeptide may include conservative amino acid substitutions relative to a reference molecule. "Conservative amino acid substitutions" are those substitutions that are a substitution of an amino acid for a different amino acid where the substitution is predicted to interfere least with the properties of the reference polypeptide. In other words, conservative amino acid substitutions substantially conserve the structure and the function of the reference polypeptide. Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

The amino acid sequences of the polypeptide variants as contemplated herein may include modifications made apparent by a sequence alignment of the polypeptides disclosed herein and other polypeptides. A person of ordinary skill in the art may easily align the polypeptides disclosed herein with other polypeptides from, for example, other species to determine what additional variants (i.e. substitutions, insertions, deletions, etc.) could be made to the polypeptides. For example, a person of ordinary skill in the art would appreciate that modifications in a reference polypeptide (i.e., SEQ ID NOS: 1-8, 15) could be based on alternative amino acid residues that occur at the corresponding position in other homologous polypeptides from other species or strains.

The disclosed polypeptides, mutants, or variants described herein may have one or more functional or biological activities exhibited by a reference polypeptide (e.g., one or more functional or biological activities exhibited by SEQ ID NOS: 1-8). For example, the disclosed polypeptides, mutants, variants, or derivatives thereof may have increased maltotriose transport activity or localization to a particular part a cell.

Polynucleotides

In another aspect, polynucleotides encoding any of the polypeptides disclosed herein are also provided. The terms "polynucleotide," "polynucleotide sequence," "nucleic acid," and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide (which terms may be used interchangeably), or any fragment thereof. These phrases also refer to DNA or RNA of genomic, natural, or synthetic origin (which may be single-stranded or double-stranded and may represent the sense or the antisense strand).

Isolated polynucleotides homologous to the polynucleotides described herein are also provided. Those of skill in the art also understand the degeneracy of the genetic code and that a variety of polynucleotides can encode the same polypeptide. In some embodiments, the polynucleotides may be codon-optimized for expression in a particular cell such as, without limitation, a yeast cell. While particular nucleotide sequences, which are found in yeasts, are disclosed herein any nucleotide sequences may be used which encode a desired form of the substituted polypeptides described herein. Thus non-naturally occurring sequences may be used. These may be desirable, for example, to enhance expression in heterologous expression systems of polypeptides or proteins. Computer programs for generating degenerate coding sequences are available and can be used for this purpose as well as other means.

In some embodiments, the polynucleotide may include at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% to SEQ ID NO: 9 (MALT434 polynucleotide sequence).

The isolated polynucleotides or polypeptides provided herein may be prepared by methods available to those of skill in the art. Isolated indicates that the polynucleotides or proteins are not in their naturally occurring state. Such preparations may be cell-free preparations. The polynucleotide or polypeptides may be extracted from the cells by breaking the cell membrane and optionally removing non-desired components. The polypeptides may be made as secreted polypeptides and further isolated using means known to those of skill in the art. Alternatively, desired proteins or nucleic acids can be purified using sequence-specific reagents, including but not limited to oligonucleotide probes, primers, and antibodies. Techniques for isolating cell-free preparations are well known in the art, and any that are convenient can be used. The term "substantially isolated or purified" refers to polypeptides or polynucleotides that are removed from their natural environment, and are at least 60% free, preferably at least 75% free, and more preferably at least 90% free, even more preferably at least 95% free from other components with which they are naturally associated.

DNA Constructs

In still another aspect, DNA constructs are provided. The DNA constructs may include a promoter operably linked to any one of the polynucleotides described herein. The promoter may be a heterologous promoter or an endogenous promoter associated with the polypeptide described herein.

Additionally, the DNA constructs may include a heterologous promoter operably linked to a polypeptide having at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 6 (lgAGT1), SEQ ID NO: 7 (ncAGT1), SEQ ID NO: 8 (AGT1), or SEQ ID NO: 15 (scAGT1), or a functional fragment of the polypeptide thereof.

As used herein, the term "DNA construct" refers to recombinant DNA polynucleotides which may be single-stranded or double-stranded and may represent the sense or the antisense strand. Recombinant polynucleotides are polynucleotides formed by laboratory methods that include polynucleotide sequences derived from at least two different natural sources or they may be synthetic. Constructs thus may include new modifications to endogenous genes introduced by, for example, genome-editing technologies. Constructs may also include recombinant polynucleotides created using, for example, recombinant DNA methodologies.

The DNA constructs provided herein may be prepared by methods available to those of skill in the art. Notably each of the DNA constructs claimed are recombinant molecules and as such do not occur in nature. Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, and recombinant DNA techniques that are well known and commonly employed in the art. Standard techniques available to those skilled in the art may be used for cloning, DNA and RNA isolation, amplification, and purification. Such techniques are thoroughly explained in the literature.

As used herein, the terms "heterologous promoter," "promoter," "promoter region," or "promoter sequence" refer generally to transcriptional regulatory regions of a gene, which may be found at the 5' or 3' side of the polynucleotides described herein, or within the coding region of the polynucleotides, or within introns in the polynucleotides. Typically, a promoter is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. The typical 5' promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence is a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

In some embodiments, the disclosed polynucleotides are operably connected to the promoter. As used herein, a polynucleotide is "operably connected" or "operably linked" when it is placed into a functional relationship with a second polynucleotide sequence. For instance, a promoter is operably linked to a polynucleotide if the promoter is connected to the polynucleotide such that it may effect transcription of the polynucleotides. In various embodiments, the polynucleotides may be operably linked to at least 1, at least 2, at least 3, at least 4, at least 5, or at least 10 promoters.

Heterologous promoters useful in the practice of the present invention include, but are not limited to, constitutive, inducible, temporally-regulated, developmentally regulated, chemically regulated, tissue-preferred and tissue-specific promoters. The heterologous promoter may be a yeast, fungal, or bacterial promoter. In yeast cells, typical promoters include, without limitation, galactose inducible promoters (i.e., GAL1) and doxycycline-inducible promoters. Other promoters include the T3, T7, and SP6 promoter sequences, which are often used for in vitro transcription of RNA. Those of skill in the art are familiar with a wide variety of additional promoters for use in various cell types.

Vectors

In a further aspect, vectors, including any one of the DNA constructs or polynucleotides described herein, are provided. The term "vector" is intended to refer to a polynucleotide capable of transporting another polynucleotide to which it has been linked. In some embodiments, the vector may be a "plasmid," which refers to a circular double-stranded DNA loop into which additional DNA segments may be ligated. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., yeast vectors having an origin of replication). Other vectors can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome, such as some viral vectors or transposons. Yeast artificial chromosomes or YACS represent another suitable vector for use herein. Vectors may carry genetic elements, such as those that confer resistance to certain drugs or chemicals.

Yeast Cells

In another aspect, yeast cells are provided. The yeast cells may include any one of the polypeptides described herein, any one of the polynucleotides described herein, any one of the DNA constructs described herein, or any one of the vectors described herein.

The "yeast cells" disclosed herein may be, without limitation, ascomycetes and fungi that lack fruiting bodies or experience yeast phases of their life cycles. Suitable yeast species may be from the family Saccharomycetaceae. In some embodiments, the yeast species are from the genus *Saccharomyces*. Suitable *Saccharomyces* species may include, without limitation, *Saccharomyces eubayanus, Saccharomyces cerevisiae, Saccharomyces paradoxus, Saccharomyces mikatae, Saccharomyces arboricola, Saccharomyces kudriavzevii, Saccharomyces jurei,* and *Saccharomyces*

uvarum. Suitable *Saccharomyces* species may also include any taxonomic synonyms of these species or any newly discovered species to be members of the genus *Saccharomyces*.

In some embodiments, the yeast cell may be selected from unevolved yeast strains such as, without limitation, yHKS210, yHRVM108, FM1318, CRUB 1568^T=PYCC 6148^T=CBS 12357^T. These strains may be modified with the compositions and according to the methods disclosed herein.

In some embodiments, the yeast cell may be an evolved yeast strain such as, without limitation, yHEB1505, yHEB1506, yHEB1585, yHEB1586, yHEB1587, yHEB1588, yHEB1589, or yHEB1590.

The yeast cells of the present invention may be modified to increase, as compared to a control yeast cell, the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter polypeptide. Based on their directed evolution studies, the present inventors demonstrate that increasing the expression or maltose/maltotriose transport activity of maltose/maltotriose transporter proteins in yeast cells is sufficient to allow those yeast cells to consume maltotriose or maltose as the sole carbon source.

The present inventors conjecture that the findings from their directed evolution studies suggest that increasing the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter protein at the plasma membrane of a yeast cell would allow the yeast cell to consume maltotriose or maltose as the sole carbon source. In other words, yeast cells have the enzymes and other proteins necessary to use maltotriose or maltose as a carbon source internally, but some yeast cells may lack the ability to grow on maltotriose or maltose because the cells lack the ability to transport the maltotriose or maltose across the plasma membrane of the yeast cell. Accordingly, in some embodiments, the modified yeast cells may have increased expression or increased maltose/maltotriose transport activity of the maltose/maltotriose transporter polypeptide, as compared to a control yeast cell, at the plasma membrane of the yeast cell.

The increased maltose/maltotriose transport activity or expression of the maltose/maltotriose transporter polypeptide is relative to a "control yeast cell." A "control yeast cell" is a yeast cell that has not been modified as described herein. Exemplary control yeast cells may include, without limitation, the unevolved yeast strains used by the inventors in the non-limiting Examples, such as FM1318, CRUB 1568^T=PYCC 6148^T=CBS 12357^T, yHKS210, or yHRVM108.

As used herein, "maltose/maltotriose transport activity" refers to the ability of a maltose/maltotriose transporter polypeptide to transport maltose or maltotriose across a membrane. In some embodiments, the maltose/maltotriose transport activity of the maltose/maltotriose transporter polypeptide is increased by at least 30%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 150%, 200%, 300%, 500% or 1000% as compared to a control yeast cell.

As used herein, the term "expression" may refer either to the levels of an RNA encoding a protein in a cell or the levels of the protein in a cell. In some embodiments, the expression of the maltose/maltotriose transporter polypeptide is increased by at least 30%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 150%, 200%, 300%, 500% or 1000% as compared to a control yeast cell.

The yeast cells may be modified to increase as compared to a control yeast cell the maltose/maltotriose transport activity or expression of a maltose/maltotriose transporter polypeptide. As used herein, the terms "modified" or "modifying" refer to using any laboratory methods available to those of skill in the art including, without limitation, directed evolution, genetic engineering techniques (i.e. CRISPR/Cas techniques or gene overexpression technologies), traditional breeding/selection techniques, or forward genetic techniques to affect the maltose/maltotriose transport activity or expression of a maltose/maltotriose transporter polypeptide. It will be readily apparent to one of ordinary skill in the art that there are multiple potential ways to increase the maltose/maltotriose transport activity or expression of a maltose/maltotriose transporter polypeptide, by modifying the gene encoding the maltose/maltotriose transporter polypeptide, for example, introducing targeted mutations, by modifying a mRNA (or levels thereof) encoding the maltose/maltotriose transporter polypeptide, for example, gene overexpression techniques.

In some embodiments, the yeast cell may be modified to increase the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter polypeptide by introducing into the yeast cell, using for example techniques known in the art, any one of the polypeptides described herein, any one of the polynucleotides described herein, any one of the DNA constructs described herein, or any one of the vectors described herein or via combinations thereof. For example the expression of the maltose/maltotriose transporter may be increased and the activity of the maltose/maltotriose transporter may also be increased by combining the mutations in the polypeptides described herein.

The yeast may also be modified to introduce a hypermorphic mutation(s) in a polynucleotide (i.e., gene) encoding the maltose/maltotriose transporter polypeptide. A "hypermorphic mutation" is an alteration in a gene that results in an increased level of activity, or in which the wild-type gene product is expressed at an increased level. It will be readily apparent to those of skill in the art that a variety of hypermorphic mutations may be introduced (using, for example, directed evolution, CRISPR/Cas or other genome engineering techniques) into a polynucleotide encoding the maltose/maltotriose transporter polypeptide described herein to arrive at embodiments of the present invention. For example, a person of ordinary skill may introduce alterations (i.e., substitutions or deletions) into the promoter of a gene encoding a maltose/maltotriose transporter polypeptide described herein that result in additional expression of the maltose/maltotriose transporter polypeptide. Still further modifications contemplated herein include mutations that impact one or more of the domains of the maltose/maltotriose transporter polypeptide.

As used herein, a "maltose/maltotriose transporter polypeptide" may include any polypeptide that can transport maltose or maltotriose across a membrane. Suitable maltose/maltotriose transporter polypeptides may include, without limitation, AGT1 or AGT-like (alpha-glucoside transporter), MTT1/MTY1, or MPH polypeptides. In some embodiments, the maltose/maltotriose transporter protein may include a polypeptide having at least 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 6 (lgAGT1), SEQ ID NO: 7 (ncAGT1), SEQ ID NO: 8 (AGT1), or SEQ ID NO: 15 (scAGT1), or a functional fragment of the maltose/maltotriose transporter protein thereof.

In some embodiments, the yeast cell may be a *Saccharomyces eubayanus* cell modified to increase, as compared to a control *Saccharomyces eubayanus* cell, the expression or maltose/maltotriose transport activity of a maltose/

maltotriose transporter polypeptide at the plasma membrane of the *Saccharomyces eubayanus* cell.

Methods for Making a Fermentation Product

In a still further aspect, the present invention relates to methods for making a fermentation product. The methods may include culturing any one of the yeast cells described herein with a fermentable substrate to produce the fermentation product.

As used herein, "culturing" refers to mixing the yeast cells into any medium including a fermentable substrate.

The fermentable substrate may include maltose or maltotriose. In some embodiments, the fermentable substrate may include wort or malt extract.

The fermentation product may be a beer product, a wine product, an alcoholic beverage, a biochemical, or a biofuel. In some embodiments, the fermentation product is a lager beer.

The present disclosure is not limited to the specific details of construction, arrangement of components, or method steps set forth herein. The compositions and methods disclosed herein are capable of being made, practiced, used, carried out and/or formed in various ways that will be apparent to one of skill in the art in light of the disclosure that follows. The phraseology and terminology used herein is for the purpose of description only and should not be regarded as limiting to the scope of the claims. Ordinal indicators, such as first, second, and third, as used in the description and the claims to refer to various structures or method steps, are not meant to be construed to indicate any specific structures or steps, or any particular order or configuration to such structures or steps. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to facilitate the disclosure and does not imply any limitation on the scope of the disclosure unless otherwise claimed. No language in the specification, and no structures shown in the drawings, should be construed as indicating that any non-claimed element is essential to the practice of the disclosed subject matter. The use herein of the terms "including," "comprising," or "having," and variations thereof, is meant to encompass the elements listed thereafter and equivalents thereof, as well as additional elements. Embodiments recited as "including," "comprising," or "having" certain elements are also contemplated as "consisting essentially of" and "consisting of" those certain elements.

Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. For example, if a concentration range is stated as 1% to 50%, it is intended that values such as 2% to 40%, 10% to 30%, or 1% to 3%, etc., are expressly enumerated in this specification. These are only examples of what is specifically intended, and all possible combinations of numerical values between and including the lowest value and the highest value enumerated are to be considered to be expressly stated in this disclosure. Use of the word "about" to describe a particular recited amount or range of amounts is meant to indicate that values very near to the recited amount are included in that amount, such as values that could or naturally would be accounted for due to manufacturing tolerances, instrument and human error in forming measurements, and the like. All percentages referring to amounts are by weight unless indicated otherwise.

No admission is made that any reference, including any non-patent or patent document cited in this specification, constitutes prior art. In particular, it will be understood that, unless otherwise stated, reference to any document herein does not constitute an admission that any of these documents forms part of the common general knowledge in the art in the United States or in any other country. Any discussion of the references states what their authors assert, and the applicant reserves the right to challenge the accuracy and pertinence of any of the documents cited herein. All references cited herein are fully incorporated by reference, unless explicitly indicated otherwise. The present disclosure shall control in the event there are any disparities between any definitions and/or description found in the cited references.

Unless otherwise specified or indicated by context, the terms "a", "an", and "the" mean "one or more." For example, "a protein" or "an RNA" should be interpreted to mean "one or more proteins" or "one or more RNAs," respectively.

The following examples are meant only to be illustrative and are not meant as limitations on the scope of the invention or of the appended claims.

EXAMPLES

Example 1

Old and New Maltotriose Transporters in *Saccharomyces eubayanus*

Previous studies have shown that the primary hindrance to maltotriose utilization in *Saccharomyces* is the inability of cells to transport the sugar across the plasma membrane (Wang et al. 2002; Rautio and Londesborough 2003). In yeasts that are capable of maltotriose consumption, the sugar is taken up by a small number maltose transporters encoded by genes in the MALT family (Han et al. 1995; Dietvorst et al. 2005; Salema-Oom et al. 2005; Brown et al. 2010). While a number of transporters in this family have been characterized that can carry maltose and other sugars (Brown et al. 2010), maltotriose transporters are more rare, reflecting the general difficultly of transporting higher molecular weight sugars, such as dextrins and starch (Barnett 1992; Briggs D. E., Brookes P. A., Stevens R. 2004 p. 123,125). Here we characterize native MALT genes found in *S. eubayanus* for their ability to enable the transport of maltotriose and describe a novel chimeric maltotriose transporter that resulted from directed evolution of *S. eubayanus* for maltotriose consumption.

Materials and Methods

Strains

All strains discussed in this paper are listed in Table 1. Briefly, FM1318 is a monosporic derivative of the type strain of *S. eubayanus* (CRUB 1568^T=PYCC 6148^T=CBS 12357^T), which was isolated from Patagonia (Libkind et al. 2011). yHRVM108 was isolated from Durham, N.C. and is closely related to the *S. eubayanus* strains that hybridized with *S. cerevisiae* to give rise to lager-brewing yeasts (Pens & Langdon et al., 2016). yHKS210 was isolated from Sheboygan, Wis. and is an admixture between populations A and B of *S. eubayanus* (Peris et al. 2014). Of these strains, FM1318 and yHKS210 grew well on maltose, but did not grow on maltotriose. yHRVM108 grew sluggishly on maltose and did not grow on maltotriose (Table 1). yHAB47 is synonymous with Weihenstephan 34/70 (Peris & Langdon et al., 2016), a representative of the Frohberg or Group II (Magalhães et al. 2016) lineage of lager-brewing hybrids. CDFM21L.1 is a strain of *S. eubayanus* isolated from Tibet (Bing et al. 2014) and closely related to yHRVM108. Of known *S. eubayanus* strains, CDFM211-1 is the most genetically similar to the *S. eubayanus* parents of lager-brewing hybrids.

TABLE 1

Strains and plasmids used in this Example

Strain	Species	Background	Relavent genotype	MAL	MalTri	Description	Source
FM1318	*S. eubayanus*	—	—	+	–	monosporic derivative of the type strain of *S. eubayanus*	Libkind & Hittinger et al. (*PNAS*, 2011)
yHRVM108	*S. eubayanus*	—	—	(+/–)	–	Member of the holoartic subpopulation population of isolated from Durham, North Carolina	Peris & Langdon et al. (*PLOS Genetics*, 2016)
yHKS210	*S. eubayanus*	—	MALT4/ MALT4	+	–	Admixture of *S. eubayanus* populations A and B isolated from Sheboygan, Wisconsin	Peris et al. (*Molecular Ecology*, 2014)
yHEB1403	*S. eubayanus*	yHKS210	—	+	+	Sample taken from the 86th passage of yHKS210.	This study
yHEB1505	*S. eubayanus*	yHKS210	MALT434/ MALT434	+	+	single colony isolate taken from the evolution of yHKS210 in maltotriose after 86 passages.	This study
yHEB1506	*S. eubayanus*	yHKS210	—	+	+	single colony isolate taken from the evolution of yHKS210 in maltotriose after 86 passages.	This study
yHEB1593	*S. eubayanus*	yHKS210 × yHEB1505	MALT434/ MALT4	+	+	Backcross between yHEB1505 and yHKS210	This study
yHEB1853	*S. eubayanus*	yHKS210 × yHEB1505	MALT434/ malt4Δ:: NatMX	+	+	yHEB1593 with original MALT4 allele replaced with NatMX marker	This study
yHEB1854	*S. eubayanus*	yHKS210 × yHEB1505	malt434 Δ::NatMX/ MALT4	+	–	yHEB1593 with chimeric MALT434 allele replaced with NatMX marker	This study
yHEB1881	*S. eubayanus*	yHKS210	MALT4/ MALT4 [pBM5155-MALT434]	+	+	yHKS210 with pBM5155 based plasmid for MALT434 expression	This study
yHEB1878	*S. eubayanus*	yHRVM108	[pBM5155-MALT434]	+	+	yHRVM108 with pBM5155 based plasmid for MALT434 expression	This study
yHEB1870	*S. eubayanus*	yHRVM108	[pBM5155-MALT1]	(+/–)	–	yHRVM108 with pBM5155 based plasmid for MALT1 expression	This study
yHEB1872	*S. eubayanus*	yHRVM108	[pBM5155-MALT3]	(+/–)	–	yHRVM108 with pBM5155 based plasmid for MALT3 expression	This study
yHEB1877	*S. eubayanus*	yHRVM108	[pBM5155-MALT2/4]	(+/–)	–	yHRVM108 with pBM5155 based plasmid for MALT2/4 expression	This study
yHEB1885	*S. eubayanus*	yHRVM108	[pBM5155-IgAGT1]	+	+	yHRVM108 with pBM5155 based plasmid for AGT1 from lager brewing yeast expression	This study
yHEB1882	*S. eubayanus*	yHKS210	[pBM5155-IgAGT1]	+	+	yHKS210 with pBM5155 based plasmid for expression of the lager allele of AGT1	This study

TABLE 1-continued

Strains and plasmids used in this Example

Strain	Species	Background	Relavent genotype	MAL	MalTri	Description	Source
yHEB1883	*S. eubayanus*	yHRVM108	[pBM5155-ncAGT1]	+	+	yHRVM108 with pBM5155 based plasmid for expression of the North Carolinian allele of AGT1	This study
yHEB1884	*S. eubayanus*	yHRVM108	[pBM5155-IgAGT1]	+	+	yHRVM108 with pBM5155 based plasmid for expression of the lager brewing yeast allele of AGT1.	This study
yHAB47	*S. eubayanus* × *S. cerevisiae*	—	—	+*	+*	Weihenstephan 34/70; Frohberg lineage of lager brewing yeast hybrids *(Magalhaes et al. 2016)	Peris & Langdon et al. (*PLOS Genetics*, 2016)
yHEB1585	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate A of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1586	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate A of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1587	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate A of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1588	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate B of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1589	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate B of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1590	*S. eubayanus*	yHRVM108	—	+	+	single colony isolate taken from replicate B of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1778	*S. eubayanus*	yHRVM108	—	+	−	Single-colony isolate taken from replicate C of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1779	*S. eubayanus*	yHRVM108	—	+	−	Single-colony isolate taken from replicate C of the evolution of yHRVM108 in maltose after 86 passages.	This study
yHEB1780	*S. eubayanus*	yHRVM108	—	+	−	Single-colony isolate taken from replicate C of the evolution of yHRVM108 in maltose after 86 passages.	This study

TABLE 1-continued

Strains and plasmids used in this Example

Strain	Species	Background	Relavent genotype	MAL	MalTri	Description	Source
pBM5155	plasmid	—	—	na	na	plasmid for doxycycline inducible gene expression (GenBank KT725394.1)	Alexander et al. 2016 (*Fungal Genet. Biol*)
pHEB7	plasmid	—	—	na	na	pBM5155 with ncAGT1 gap repaired into the NotI site	This study
pHEB11	plasmid	—	—	na	na	pBM5155 with IgAGT1 gap repaired into the NotI site	This study
pHEB16	plasmid	—	—	na	na	pBM5155 with MALT1 gap repaired into the NotI site	This study
pHEB17	plasmid	—	—	na	na	pBM5155 with MALT3 gap repaired into the NotI site	This study
pHEB18	plasmid	—	—	na	na	pBM5155 with MALT4 gap repaired into the NotI site	This study
pHEB19	plasmid	—	—	na	na	pBM5155 with MALT434 gap repaired into the NotI site	This study

Identification of MALT Genes

Previously, we identified four genes with homology to the genes encoding the maltose transporters of *S. cerevisiae* and lager-brewing hybrids in the genome assembly of FM1318 published by Baker et al. 2015. These genes were previously designated MALT1-4. Only a partial contig was available for MALT4 in this assembly, but a BLAST (Altschul et al. 1997) search of the Okuno et al. 2016 assembly of the type strain of *S. eubayanus* (of which FM1318 is a monosporic derivative) allowed us to annotate the full-length sequence of MALT4. MALT4 has 99.7% identity to MALT2 at the nucleotide level and 100% identity at the amino acid level. The regions from 900 bp downstream ofMALT2 and MALT4 and upstream to the ends of chromosomes V and XVI (regions of approximately 12 kb in the Okuno et al. 2016 assembly), respectively, share 99.1% nucleotide identity. The 10 kb outside of this region only share 49.8% nucleotide identity. Thus, MALT2 and MALT4 are close paralogs that are likely related by a recent subtelomeric duplication and/or translocation event.

Reads for homologs of AGT1 were retrieved using the functional AGT1 sequence from lager yeast (lgAGT1) as the query sequence (Nakao et al. 2009) in a BLAST search of the SRA databases of NCBI for yHRVM108 (SRR2586159) and CDFM21L.1(SRR1507225). All reads identified in the BLAST searches were downloaded and assembled using the de novo assembler in Geneious v. 9.0.3 (http://www.geneious.com, Kearse et al., 2012). The homologs identified in yHRVM108 and CDFM21L.1 were designated ncAGT1 (for North Carolinian AGT1) and tbAGT1 (for Tibetan AGT1) respectively. The presence and sequence of ncAGT1 in yHRVM108 was further verified by PCR amplification and Sanger sequencing (Table 2). CDFM21L.1 was not available at the time of this work for further verification of the presence of tbAGT1.

TABLE 2

Oligonucleotides used in this Example

Name	Sequence	Description
oHECPB75	TATAGACACGCAAACACAAATACACACACT AAATTAATGAAGGGATTATCCTCATTAATA (SEQ ID NO: 17)	amplifies MTT1 for cloning into pBM5155 over NotI site by gap repair
oHECPB76	TCAAGAAATTCGCTTATTTAGAAGTGGCGC GAATTCACTATCATTTGTTCACAACAGATG (SEQ ID NO: 18)	amplifies MTT1 for cloning into pBM5155 over NotI site by gap repair
oHECPB77	CACGCAAACACAAATACACACACTAAATTA ATGAAAAATATACTTTCGCTGGTAGGAAGA (SEQ ID NO: 19)	amplifies IgAGT1 for cloning into pBM5155 over NotI site by gap repair
oHECPB78	CAAGAAATTCGCTTATTTAGAAGTGGCGCG AATTCACTATCATAACGCCTGTTGACTCGC (SEQ ID NO: 20)	amplifies IgAGT1 for cloning into pBM5155 over NotI site by gap repair

TABLE 2 -continued

Oligonucleotides used in this Example

Name	Sequence	Description
oHECPB104	ACACGCAAACACAAATACACACACTAAATT AATGAAGAATATCATTTCGCTGGTAAGAA G (SEQ ID NO: 21)	amplifies ncAGT1 for cloning into pBM.5155 over NotI site by gap repair
oHECPB105	GAAATTCGCTTATTTAGAAGTGGCGCGAAT TCACTATTATAATGCCTGCTGACTCATGCT (SEQ ID NO: 22)	amplifies ncAGT1 for cloning into pBM.5155 over NotI site by gap repair
oHECPB124	CCTATGCTTCTGAAGTTTGC (SEQ ID NO: 23)	primer to confirm sequence of IgAGT1 and ncAGT1 in pBM5155
oHECPB125	CCTGCCAAACCAAGACAG (SEQ ID NO: 24)	primer to confirm sequence of IgAGT1 and ncAGT1 in pBM5155
oHECPB128	GCTTGTTTATGTTGGGTCGGTC (SEQ ID NO: 25)	primer to confirm sequence of MTT1 in pBM5155
oHECPB129	GACCGACCCAACATAAACAAGC (SEQ ID NO: 26)	primer to confirm sequence of MTT1 in pBM5155
oHECPB138	ACACGCAAACACAAATACACACACTAAATT AATGAAGGGTCTATCCTCAATGATAAATAG (SEQ ID NO: 27)	amplifies MALT4 (and or MALT2) from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB139	CGCTTATTTAGAAGTGGCGCGAATTCACTA TCAATCCATTAGAGATGGGGTGCTTTGCTC (SEQ ID NO: 28)	amplifies MALT4 (and or MALT2) from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB140	CACGCAAACACAAATACACACACTAAATTA ATGAAGGGTCTATCTTCAATATTGAATAGA (SEQ ID NO: 29)	amplifies MALT1 from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB141	CGCTTATTTAGAAGTGGCGCGAATTCACTA TCAAATCGTAAGAGATGGGGTAGTTAATTC (SEQ ID NO: 30)	amplifies MALT1 from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB142	CACGCAAACACAAATACACACACTAAATTA ATGAAGGGCTTATCCTCACTGATAAACAGA (SEQ ID NO: 31)	amplifies MALT3 from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB143	CGCTTATTTAGAAGTGGCGCGAATTCACTA TCATAAATTCGTAATAGATGGTGTGCTTCG (SEQ ID NO: 32)	amplifies MALT3 from *S. eubayanus* for cloning into pBM5155 over NotI site by gap repair
oHECPB156	ATATTATGGTAGATATGACCTTTACG (SEQ ID NO: 33)	primer to confirm sequence of MALT2/4 in pBM5155
oHECPB157	GGTTGATTTCATCAGAGATTGCTTTGG (SEQ ID NO: 34)	primer to confirm sequence of MALT2/4
oHECPB158	CGTAAAGGTCATATCTACCATAATAT (SEQ ID NO: 35)	primer to confirm sequence of MALT2/4 in pBM5155
oHECPB159	CCAATGTCTGACTGTGTCTTATGCCTC (SEQ ID NO: 36)	primer to confirm sequence of MALT2/4 in pBM5155
oHECPB160	GAGGCATAAGACACAGTCAGACATTGG (SEQ ID NO: 37)	primer to confirm sequence of MALT2/4 in pBM5155
oHECPB161	CTGTCTTGGTTTGGCAGG (SEQ ID NO: 38)	primer to confirm sequence of IgAGT1 and ncAGT1 in pBM5155
oHECPB162	CTGTGAAAGTTTAGGGATGATTGCGG (SEQ ID NO: 39)	primer to confirm sequence of MALT1 in pBM5155
oHECPB163	CCGCAATCATCCCTAAACTTTCACAG (SEQ ID NO: 40)	primer to confirm sequence of MALT1 in pBM5155
oHECPB164	CCTGTATATGTTGGATCGGTCAAAC (SEQ ID NO: 41)	primer to confirm sequence of MALT1 in pBM5155
oHECPB165	GTTTGACCGATCCAACATATACAGG (SEQ ID NO: 42)	primer to confirm sequence of MALT1 in pBM5155

TABLE 2 -continued

Oligonucleotides used in this Example

Name	Sequence	Description
oHECPB166	CCTTTGGCTTTAAGATACTACC (SEQ ID NO: 43)	primer to confirm sequence of MALT3 in pBM5155
oHECPB167	GGTAGTATCTTAAAGCCAAAGG (SEQ ID NO: 44)	primer to confirm sequence of MALT3 in pBM5155
oHECPB168	GGATGCTCTGATACTCACGG (SEQ ID NO: 45)	primer to confirm sequence of MALT3 in pBM5155
oHECPB169	CCGTGAGTATCAGAGCATCC (SEQ ID NO: 46)	primer to confirm sequence of MALT3 in pBM5155
oHECPB170	GGARAGTGATACCTTATCATCTGCTGCGCT AAGAGTCAAGATCTGTTTAGCTTGCCTT (SEQ ID NO: 47)	amplifies MX-driven drug markers with overhangs to the MALT4 and MALT2 loci for allele replacement
oHECPB171	ACTCAAAAAAAATTCCAAAAGCTATTAGGT AACTGAGCTCGTTTTCGACACTGGAT (SEQ ID NO: 48)	by homologous recombination with overhangs to the MALT4 and MALT2 loci for allele replacement by homologous recombination
oHECPB172	CGATATTTCCGCCGCAGCCCGAG (SEQ ID NO: 49)	specifically amplifies the MALT2 locus when used with primers oHECPB159 or oHECPB156
oHECPB173	CTTAGTAGCAGCGACATATTCAAG (SEQ ID NO: 50)	specifically amplifies the MALT4 locus when used with primers oHECPB159 or oHECPB156
oHCT770	AACTCTTGTTTTCTTCTTTTCTCTAAA (SEQ ID NO: 51)	amplifies genes inserted over NotI site in pBM5155
oHCT771	GGGACCTAGACTTCAGGTTGTC (SEQ ID NO: 52)	amplifies genes inserted over NotI site in pBM5155

Directed Evolution

Directed evolution was initiated by growing parent strains overnight in liquid YPD medium (1% yeast extract, 2% peptone, 2% glucose). One mL of maltotriose or maltose medium was inoculated with enough overnight culture to give an OD_{600} reading of ~0.1 as measured with an IMPLEN OD600 DiluPhotometer™. Evolution in maltotriose was conducted in synthetic complete (SC) medium (0.17% yeast nitrogen base, 0.5% ammonium sulfate, 0.2% complete drop out mix) with 2% maltotriose and 0.1% glucose. The addition of 0.1% glucose ensured enough growth that mutations could occur and be selected for through the ensuing generations. Directed evolution of yHRVM108 in maltose was carried out in SC with 2% maltose. Because yHRVM108 grew so poorly in maltose alone, an additional 0.1% glucose was supplemented into its medium; after increased growth was observed around generation 110 for replicate A, from which strains yHEB1585-1587 are derived, and around generation 80 for replicate B, from which strains yHEB1588-90 were derived, subsequent generations of yHRVM108 directed evolution in maltose for these replicates was conducted with 2% maltose only. The directed evolution of each strain was carried out in triplicate. Samples were grown on a culture wheel at room temperature (22° C.) and diluted 1:10 into fresh media every 3-4 days. Samples of each evolution replicate were taken every other passage and placed into long-term storage by mixing 700 uL of culture with 300 uL of 50% glycerol in a cryotube and storing it at −80° C. The number of doublings between passages was estimated from cell counts during the second and third passages. Evolution was carried out for a total of 100 passages. Strains that could not use the primary carbon source in adaptive evolution medium underwent approximately one cell division per day on average.

Sporulation and Backcrossing

To induce sporulation, strains were grown to saturation, washed twice, and then resuspended in 200 μL liquid sporulation (spo) medium (1% potassium acetate, 0.5% zinc acetate). 30 μL of this suspension was added to 1.5 mL of spo medium and incubated on a culture wheel at room temperature. Cultures were checked for sporulation after 2-5 days. Tetrads were dissected using a Singer SporePlay. For backcrossing, tetrads of the strains to be crossed were dissected on a single YPD plate. A spore from one parent was placed in close proximity to a spore from the other parent; they were observed over several hours for mating and zygote formation. Transformations of the diploid F_1 backcross strain for gene knockouts were carried out as described below in the section describing the construction of gene expression plasmids.

Construction of Gene Expression Plasmids

Genes encoding transporters of interest were cloned via gap repair into the NotI site of plasmid pBM5155 (GenBank KT725394.1), which contains the complete machinery necessary for doxycycline induction of genes cloned into this site (Alexander et al. 2016). Transformation was carried out using standard lithium acetate transformation (Daniel Gietz and Woods 2002) with modifications to optimize transformation in *S. eubayanus*. Specifically, transformation reactions were heat shocked at 34° C. After 55 minutes, 100% ethanol was added to 10% total volume, and the reactions heat shocked for another 5 minutes before they were allowed to recover overnight and plated to selective media the next day. When necessary, plasmids were recovered and ampli-

fied in *Escherichia coli* for transformation into multiple strains. The sequences of genes encoding transporters cloned into pBM5155 were verified by Sanger sequencing. *S. eubayanus* MALT1, MALT3, and MALT4 were amplified from FM1318, lgAGT1 was amplified from yHAB47, and ncAGT1 was amplified from yHRVM108. Primers used for plasmid construction and sequence verification are listed in Table 2.

Growth Assays

Growth was measured in liquid media in 96-well plates using OD_{600} measurements on a FLUOstar Omega microplate reader. To test the abilities of single-colony isolates of yHKS210 evolved in maltotriose to grow in maltotriose, strains were grown overnight in liquid YPD and washed. Yeast was inoculated into wells to give an initial OD_{600} reading of ~0.1-0.2. To test the ability of single-colony isolates of yHRVM108 evolved in maltose to use maltose and maltotriose, a single colony was used to inoculate both SC+2% maltose and SC+2% maltotriose media. For assays testing the growth of strains carrying MALT genes expressed on an inducible plasmid, strains were grown to saturation, washed twice, resuspended in liquid SC without added carbon, and starved for 24 hours. The next day, strains were diluted in SC without added carbon to OD_{600}=1.9+/−0.05 to ensure that all cultures had approximately the same starting concentration. 15 μL of each diluted culture was added to 235 μL of the test medium. Three technical replicates, randomly distributed on a 96-well plate to control for position effects, were carried out for each strain. Strains were tested in SC with 2% added carbon source and 50 ng/mL doxycycline to induce plasmid gene expression. To control for growth from the small amount of non-maltotriose sugar in 98% pure maltotriose, the parent strains of yHRVM108 and yHKS210 were also tested in SC medium+0.04% glucose, reflecting the approximate amount of other carbon sources expected in SC medium+2% maltotriose.

Bulk-Segregant Analysis

As described above, 60 spores from 15 fully viable tetrads of strain yHEB1593 (F_1 of yHKS210×yHEB1505) were dissected and individually screened for their ability to grow in SC+2% maltotriose. F_2 segregants that could grow in maltotriose were classified as MalTri$^+$, and those that could not were classified as MalTri$^-$. Each F_2 segregant was then individually grown to saturation in liquid YPD. The saturated cultures were spun down, the supernatant removed, and enough cells resuspended in liquid SC medium to give an OD_{600} measurement of between 1.9 and 1.95. Strains were pooled based on their ability to grow in maltotriose, leading to a MalTri$^+$ pool and a MalTri$^-$ pool. To pool, 1 mL of each strain dilution was added to the appropriate pool of cells and vortexed to mix. A phenol-chloroform extraction was used to isolate gDNA from the segregant pools. The gDNA was sonicated and ligated to Illumina TruSeq-style dual adapters and index sequencing primers using the NEBNext® DNA Library Prep Master Mix Set for Illumina® kit following the manufacturer's instructions. The paired-end libraries were sequenced on an Illumina MiSeq instrument, conducting a 2×250 bp run.

Analysis of Bulk-Segregant Whole-Genome Sequencing Reads

To identify fixed differences between the meiotic segregant pools, whole-genome assemblies were made for the MalTri$^-$ group of segregants using the meta-assembler iWGS with default settings (Zhou et al. 2016). The final de novo genome assembly of the MalTri$^-$ pool was made by DISCOVAR (Weisenfeld et al. 2014) in iWGS. This assembly was used for reference-based genome assembly and variant calling using reads from the MalTri$^+$ pool following the protocol described in Peris and Langdon et al. 2016. Assemblies of the putative chimeric maltotriose transporter were retrieved from the MalTri$^+$ pool of reads using the program HybPiper (Johnson et al. 2016). Briefly, HybPiper uses a BLAST search of read sequences to find reads that map to a query sequence; it then uses the programs Exonerate (Slater and Birney 2005) and SPAdes (Bankevich et al. 2012) to assemble the reads into contigs. The sequence and genomic location of the chimeric transporter was further verified by PCR amplification and Sanger sequencing (Table 2).

Phylogenetic and Protein Mutation Prediction Analyses

Multiple sequence alignments between the proteins encoded by the MALT genes were carried out using MUSCLE (Edgar 2004), as implemented in Geneious v.9.0.3 (http://www.geneious.com, Kearse et al., 2012). Phylogenetic relationships were determined using codon alignments. Codon alignments were made using PAL2NAL (Suyama, Torrents, & Bork, 2006; http://www.bork.embl.de/pal2nal/) to convert the MUSCLE alignments of amino acid sequences to nucleotide alignments. A phylogenetic tree of nineteen MALT genes from *S. eubayanus, S. cerevisiae,* and lager-brewing yeasts was made as described in Baker et al. 2015 using MEGA v.6. All genes used in the phylogenetic analysis are as follows. MAL21, MAL31, and MAL61 from *S. cerevisiae;* MALT1 and MALT3 from *S. eubayanus;* MALT1, MALT2 and MPH from lager-brewing yeast; MPH2 and MPH3 from *S. cerevisiae;* AGT1 (MAL11 in Baker et al. 2015) from *S. cerevisiae;* scAGT1 (Weihen-MAL11-CB in Baker et al. 2015); and lgAGT1 (Weihen-MAL11-CA in Baker et al. 2015) were retrieved as previously described in Baker et al. 2015. Sequences for MALT2 and MALT4 were retrieved from the genome assembly of CBS12357 from Okuno et al. 2016. MAL11 was retrieved from the genome assembly of *S. cerevisiae* strain YJM456 (Strope et al. 2015). Sequences for tbAGT1 and ncAGT1 were retrieved as described above. MAL11 and AGT1 are both α-glucoside transporters located at the MAL1 locus in *S. cerevisiae* and as such are considered alleles of each other (Charron and Michels 1988; Han et al. 1995). Their shared genomic location notwithstanding, MAL11 and AGT1 are not phylogenetically closely related, with MAL11 clustering with other MAL×1 type transporters (FIG. **2**). In addition, while AGT1 can support maltotriose transport, MAL11, like other MAL×1 genes, cannot (Han et al. 1995; Brown et al. 2010). Despite their dissimilarity, AGT1 is recorded in the *Saccharomyces* Genome Database as MAL11 since the reference strain carries the AGT1 allele at the MAL1 locus (Vidgren et al. 2005, 2009). For this reason MAL11 is often used to refer to AGT1 (Brown et al. 2010; Baker et al. 2015; Brickwedde et al. 2017). For clarity, here we use MAL11 to only refer to the MAL×1 like allele and AGT1 to the distinct maltotriose transporting allele.

Protein structure predictions for MALT3, MALT4, lgAGT1, and scAGT1 were carried out using the I-TASSER server, and the structure prediction of MALT434 was carried out using the command line version of I-TASSER (https://zhanglab.ccmb.med.umich.edu/I-TASSER/,Roy, Kucukural, & Zhang, 2010; Yang et al., 2015; Zhang, 2008). The potential impact of the single residue difference between lgAGT1 and tbAGT1 was analyzed by two different methods. Prediction of the change in free energy (ΔΔG) was carried out using the STRUM server (Quan et al. 2016). A ΔΔG score of <+−0.5 was considered to be unlikely to affect function (Bromberg and Rost 2009). Homology-based predictions were made using SIFT (Ng and Henikoff 2001a,

2002, 2003, 2006; Kumar et al. 2009). The SIFT Related Sequences analysis was done using the amino acid sequences of MALT genes in the phylogenetic analysis above. Several SIFT analyses were also carried out using the SIFT Sequence analysis program. This analysis operates using the same principle as the SIFT Related Sequences analysis, but rather than being supplied by the user, homologous sequences were provided by a PSI-BLAST search of the indicated protein database. The SIFT Sequence analyses were carried out using default settings and the following databases NCBI nonredundant 2011 Mar, 2UniRef90 2011 Apr, 3UniProt-SwissProt 57.15 2011 Apr.

Results

Maltotriose Transporters in *S. eubayanus*

Previously, we identified four genes in the *S. eubayanus* genome assembly with homology to genes encoding known maltose transporters (MALT genes) (Baker et al. 2015). The complete sequence of one transporter, MALT4, was not present in the Baker et al. assembly but was found in another assembly for the type strain of *S. eubayanus* (Okuno et al. 2016). MALT4 encodes an identical amino acid sequence to MALT2, and these genes are likely related by a recent subtelomeric duplication and/or translocation event (see Material and Methods). Because of their identical amino acid sequences, we refer to these genes jointly as MALT2/4. To determine if they could enable maltotriose transport, MALT1, MALT3, and MALT2/4 were individually overexpressed using an inducible promoter in the *S. eubayanus* strain yHRVM108, a strain of *S. eubayanus* isolated from North Carolina that is unable to grow on maltotriose and, unlike other strains of *S. eubayanus,* has sluggish growth on maltose. None of these genes were able to confer growth on maltotriose when overexpressed (Table 3).

TABLE 3

Strain	Background	Transporter	Initial OD	Day 3	Day 6
yHRVM108*	North Carolinian strain	—	0.16 (+/−0.05)	0.39 (+/−0.02)	0.48 (+/−0.01)
yHRVM108	North Carolinian strain	—	0.12 (+/−0.03)	0.47 (+/−0.00)	0.46 (+/−0.03)
yHEB1870	yHRVM108	MALT1	0.13 (+/−0.03)	0.43 (+/−0.04)	0.58 (+/−0.04)
yHEB1877	yHRVM108	MALT2/4	0.11 (+/−0.00)	0.39 (+/−0.01)	0.57 (+/−0.02)
yHEB1872	yHRVM108	MALT3	0.13 (+/−0.01)	0.41 (+/−0.00)	0.62 (+/−0.5)
yHEB1883	yHRVM108	ncAGT1	0.11 (+/−0.01)	0.54 (+/−0.07)	1.34 (+/−0.10)
yHEB1884	yHRVM108	IgAGT1	0.10 (+/−0.00)	0.42 (+/−0.07)	0.94 (+/−0.09)

Growth on SC + 2% maltotriose (98% pure) of strains expressing MALT genes on a doxycycline-inducible plasmid. N = 3, standard deviation in parentheses.
*Control grown in SC + 0.04% glucose + doxycycline to reflect the approximate amount of growth expected from contamination with other carbon sources when using 98% pure maltotriose.

Although none of the transporters found in the type strain of *S. eubayanus* were able to support growth on maltotriose, there is compelling evidence from lager-brewing yeasts for the existence of maltotriose transporters within the greater *S. eubayanus* population (Dietvorst et al. 2005; Nakao et al. 2009; Vidgren et al. 2010; Cousseau et al. 2013; Baker et al. 2015). Of particular interest are the alleles of AGT1. Two versions of AGT1 are present in the genomes of lager-brewing yeasts. One, which we call scAGT1 (*S. cerevisiae*-AGT1), was donated by the *S. cerevisiae* parent of lager yeasts but is probably non-functional due to a nonsense mutation early in its sequence (Vidgren et al. 2005; Nakao et al. 2009; Magalhãs et al. 2016). The other AGT1, which we call lgAGT1 (lager-AGT1), was proposed to be of *S. eubayanus* origin based on its sequence divergence from scAGT1 and its location near *S. eubayanus* genomic regions (Nakao et al. 2009). Both lgAGT1 and scAGT1, like other AGT1 alleles(Han et al. 1995; Day et al. 2002b; Vidgren et al. 2005), can transport both maltose and maltotriose (Dietvorst et al. 2005; Vidgren et al. 2009; Vidgren and Londesborough 2012; Cousseau et al. 2013). Thus far, full-length sequences closely related to this lgAGT1 have not been described in any strain of *S. eubayanus,* but contigs containing the partial sequence of a gene with high similarity to lgAGT1 were recovered from an assembly of the genome of CDFM21L. 1, a Tibetan isolate of *S. eubayanus* (Hebly et al. 2015).

To recover a full-length sequence of lgAGT1 from *S. eubayanus* genome sequence, the nucleotide sequence of lgAGT1 was used as query sequence in an SRA-BLAST against Illumina reads deposited in NCBI for CDFM21L.1 (Bing et al. 2014) and the closely related strain yHRVM108 (Peris and Langdon et al. 2016). Both CDFM21L.1 and yHRVM108 belong to the Holarctic subpoptilation of *S. eubayanus* and are close relatives of the strains of *S. eubayanus* that hybridized with *S. cerevisiae* to form lager-brewing yeasts (Peris and Langdon et al 2016). From the reads that mapped to IgAGTI, two full-length genes with high sequence identity to lgAGT1 were assembled and designated tbAGT1 and ncAGT1, for Tibetan-AGT1 and North Carolinian-AGT1, respectively (FIGS. **1**A-**1**B).

There are two single nucleotide polymorphisms (SNPs) between the full-length sequence of tbAGT1 and lgAGT1, one of which results in a non-synonymous substitution (FIG. **1**B). This single-residue change probably has no impact on the function of tbAGT1 compared to lgAGT1 since it occurs near the N-terminus and outside of any predicted transmembrane domains (FIG. S**1**). In addition, analyses of the predicted effect of this substitution in lgAGT1 using STRUM and SIFT mutant protein prediction software (Ng and Henikoff 2001b; Quan et al. 2016) suggest that this single substitution is unlikely to significantly impact the structure or function of the protein (Table 4).

TABLE 4

	SIFT[b]			
	Related	Sequence[d]		
STRUM[a]	Sequences[c]	NCBI[1]	UniRef90[2]	SwissProt[3]
−0.4	1.00	1.00	0.57	1.00
# of sequences analyzed	19	59	18	8

Results of mutation prediction analyses for E18V, the sole non-synonymous substitution in the IgAGT1 protein-coding sequence, relative to tbAGT1.
[a]predicted ΔΔG (<0.5 likely no change in function, Bromberg and Rost 2009)
[b]provides amino acid probability score (<0.5 predicted to be deleterious)
[c]sequences used for for SIFT analysis are the same as used for the phylogenetic analysis (FIG. 2)
[d]sequences used for analysis provided by a PSI-BLAST of the indicated protein database
Protein Databases:
[1]NCBI nonredundant 2011 March,
[2]UniRef90 2011 April,
[3]UniProt-SwissProt 57.15 2011 April

In contrast to tbAGT1, ncAGT1 has 95% sequence identity with lgAGT1, with non-synonymous differences distrib-

uted throughout the sequence (FIGS. **1**A-**1**B). Despite the presence of ncAGT1, the yHRVM108 wild type strain grows poorly on maltose and is unable to grow in maltotriose, raising the question of whether the ability to transport maltotriose has been conserved between ncAGT1 and lgAGT1. Interestingly, and in contrast to all MALT genes found in the Patagonian type strain of *S. eubayanus,* overexpression of ncAGT1 in yHRVM108 conferred growth in maltotriose (Table 3), suggesting that insufficient ncAGT1 gene expression, rather than protein function, is likely the main reason for the inability of yHRVM108 to grow on maltotriose.

Phylogenetic Relationship Among Maltose Transporters

Lager-brewing yeasts inherited maltose/maltotriose transporters from both their *S. cerevisiae* and their *S. eubayanus* parents. To put the relationship between *S. eubayanus, S. cerevisiae,* and lager transporters into a phylogenetic perspective, a gene tree was constructed for these three groups of MALT genes (FIG. **2**). Consistent with previous analyses of MALT genes in *Saccharomyces* (Brown et al. 2010), the current set of MALT genes analyzed fell into 3 major clades. MPH genes, encoding maltose transporters native to *S. cerevisiae* but also present in some lager yeasts (Day et al. 2002a; Vidgren et al. 2005), formed their own small clade. The clade containing the largest number of genes was made up of MALT1-4 from *S. eubayanus,* MAL×1 genes from *S. cerevisiae,* and the lager-specific gene MTT1 (Dietvorst et al. 2005; Salema-Oom et al. 2005; Baker et al. 2015). This clade was further subdivided into a group containing only *S. eubayanus* transporter genes and their closely related lager homologs, as well as a second group consisting of MAL×1 genes, MTT1, and MALT3.

The final major clade was significantly divergent from the other two groups. This clade consisted of the AGT1 genes and was further split between the AGT1 genes from *S. cerevisiae* and the AGT1 genes from *S. eubayanus.* AGT1 genes isolated from lager yeasts were found in both subclades.

Evolution of Maltotriose Consumption

Since yHRVM108 already contains a functional maltotriose transporter, we decided to see if it could readily evolve maltotriose consumption. We also decided to try to evolve maltotriose utilization in FM1318 (Libkind et al. 2011) and in yHKS210 (Peris et al. 2014), strains that lack transporters capable of conferring maltotriose utilization, even when overexpressed (Table 3). A search of the available genome sequence reads for FM1318 and yHKS210 indicated that neither of these strains contain AGT1 homologs. Since none of these strains can grow on maltotriose, a small amount of glucose was also added to the media to permit a limited number of cell divisions to allow for mutation and selection to occur. Each strain was setup in triplicate and evolved by serial passaging in liquid media. Strains that could not use the primary carbon source in the directed evolution medium underwent approximately one cell division per day on average.

Over the course of 100 passages, representing approximately 3,150 cell divisions in total between all the strains and replicates, only a single replicate evolved the ability to grow in maltotriose. Surprisingly, it was not a replicate of yHRVM108, but one of yHKS210 that evolved maltotriose consumption. Two single-colony isolates (yHEB1505-6) from this replicate were isolated and confirmed to be able to grow on maltotriose without added glucose (FIG. **3**A, Table 5).

TABLE 5

Strain	Background	Evolved in	Initial OD	Day 3	Day 6
yHKS210*	Admixture strain	—	0.22 (+/−0.01)	0.68 (+/−0.07)	0.60 (+/−0.04)
yHKS210	Admixture strain	—	0.14 (+/−0.02)	0.41 (+/−0.01)	0.39 (+/−0.05)
yHEB1505	yHKS210	maltotriose	0.16 (+/−0.01)	1.46 (+/−0.01)	1.82 (+/−0.03)
yHEB1506	yHKS210	maltotriose	0.15 (+/−0.01)	1.44 (+/−0.02)	1.76 (+/−0.09)
yHRVM108*	North Carolinian strain	—	0.22 (+/−0.01)	0.47 (+/−0.01)	0.48 (+/−0.03)
yHRVM108	North Carolinian strain	—	0.12 (+/−0.03)	0.47 (+/−0.00)	0.46 (+/−0.03)
yHEB1585	yHRVM108	maltose	0.12 (+/−0.00)	0.79 (+/−0.01)	1.28 (+/−0.06)
yHEB1586	yHRVM108	maltose	0.12 (+/−0.01)	0.81 (+/−0.05)	1.31 (+/−0.07)
yHEB1587	yHRVM108	maltose	0.11 (+/−0.01)	0.77 (+/−0.01)	1.32 (+/−0.06)
yHEB1588	yHRVM108	maltose	0.13 (+/−0.00)	0.44 (+/−0.01)	0.82 (+/−0.10)
yHEB1589	yHRVM108	maltose	0.12 (+/−0.01)	0.56 (+/−0.01)	0.87 (+/−0.05)
yHEB1590	yHRVM108	maltose	0.11 (+/−0.03)	0.58 (+/−0.01)	1.00 (+/−0.03)

Growth on maltotriose of single-colony isolates from adaptive evolution experiments. Strains were evolved with either maltotriose or maltose as the primary carbon source (2%) with 0.1% added glucose. N = 3.
*Control grown in SC + 0.04% glucose to reflect the approximate amount of growth expected from contamination with other carbon sources when using 98% pure maltotriose.

To determine the genetic architecture of maltotriose utilization, we setup an F_1 backcross between yHEB1505 and the parent strain (yHKS210), producing strain yHEB1593, a putative heterozygote capable of growth on maltotriose (FIGS. **3**B and **3**E). In a test of 15 fully viable tetrads, maltotriose utilization segregated in a perfect 2:2 manner (FIG. **3**C). These results suggest that the ability of the evolved strain to use maltotriose was conferred by a dominant mutation at a single genetic locus. We performed bulk-segregant analysis (Brauer et al. 2006; Segre et al. 2006; Ehrenreich et al. 2010) using strains derived from the F_2 spores, dividing them between those that could (MalTri$^+$) and those that could not (MalTri$^-$) use maltotriose (FIG. **3**C), with a total of 30 strains in each category. Twelve 1-kb regions were identified as containing fixed differences between the MalTri$^+$ and MalTri$^-$ strains. Of these regions, eight mapped to genes encoding ribosomal proteins and most likely represent assembly artefacts due to the presence of many closely related paralogs. Three other regions contained fixed changes between the MalTri$^+$ and MalTri$^-$ groups but had no clear relationship to carbon metabolism. The final 1-kb region mapped to the MALT4 locus of FM1318. The coding sequence of MALT4 from the MalTri$^+$ group contained 54 SNPs relative to the MALT4 allele found in FM1318. Four of these SNPs were synonymous differences that were present in yHKS210 before the start of directed evolution. The remaining 50 SNPs occurred within a single 230-bp region. Of these, 11 were predicted to lead to non-synonymous changes (FIGS. **3**F and **3**H). Closer inspection revealed that the changes within the 230-bp region were the result of a recombination event between

MALT4 and MALT3, creating a chimeric gene (FIGS. 3F-H), likely through ectopic gene conversion. We call this chimeric MALT4 gene MALT434 after the arrangement of sequences from its parent genes. The sequence of MALT3 was not impacted by this mutation event.

To confirm that MALT434 was the causative locus of maltotriose utilization, we replaced MALT434 with the NatMX marker in the heterozygous Fibackcross strain (FIG. 3D), leaving only the original non-chimeric MALT4 gene. This knockout eliminated that strain's ability to utilize maltotriose (FIG. 3E), demonstrating that MALT434 is required for maltotriose utilization. Conversely, replacing the parental, non-chimeric allele of MALT4 in the heterozygous F_1 backcross strain had no impact on maltotriose utilization. Furthermore, overexpression of MALT434 in both the unevolved parent, yHKS210, and in the yHRVM108 background (FIG. 5) supported growth in maltotriose, demonstrating that its overexpression is sufficient to confer maltotriose utilization (Table 3). These results confirm that the mutant MALT434 gene encodes a functional maltotriose transporter.

It was surprising that a sequence from MALT3 permitted MALT4 to now encode a maltotriose transporter because neither MALT3 nor MALT4 supported maltotriose utilization on their own (Table 3). Malt3 and Malt4 share about 80% amino acid identity overall and 85% amino acid identity in the chimeric region specifically (FIG. 3H). Most residues in the chimeric region had high similarity between Malt3 and Malt4, as measured by Blosum62 similarity matrix (FIG. 3I) (Henikoff and Henikoff 1992), but there were a handful of low similarity amino acids as well. To gain insight into what changes may be driving the new functionality of MALT434, we used I-TASSER (Zhang 2008; Roy et al. 2010; Yang et al. 2015) to predict the protein structure of Malt3, Malt4, and Malt434. I-TASSER predicts a proteins' structure based on its homology to proteins whose structures have already been solved. I-TASSER determined that Malt3, Malt4, and Malt434 all had homology with members of the Major Facilitator Superfamily (MFS) of transporters, consistent with other studies on the structure of maltose transporters in *Saccharomyces* (Cheng and Michels 1989; Han et al. 1995; Barrett et al. 1999; Yan 2015). Based on these protein structure predictions, the structure of the chimeric region is likely conserved between Malt3 and Malt4. I-TASSER predicted that the chimeric region encompasses one full transmembrane domain and parts of two other transmembrane domains (FIG. 3J). I-TASSER also predicted that this region contains four maltose-binding sites. These same domains and predicted binding residues were identified within Malt434 as well. Interestingly, I-TASSER predicted that two of the alpha helices in the chimeric region were shorter in Malt434 than in the parent proteins. Towards the N-terminal end of the protein, another two alpha helices were also predicted to be shortened in Malt434 relative to its parents (FIG. 4). The regions covered by these alpha helices were otherwise predicted to be conserved between both Malt3 and Malt4, as well as the phylogenetically more distant maltotriose transporters lgAgt1 and scAgt1 (FIG. 3J, FIG. 4). Slightly decreasing the amount of structure in the protein by shortening these key alpha helices could have increased the overall flexibility of the protein, potentially making it easier to accommodate maltotriose, which contains an extra glucose moiety relative to maltose.

In a further attempt to define the portion of MALT434 that is critical for growth on maltotriose, we tested a further set of strains expressing MALT434 (yHEB1878), MALT334 (yHJC1-2) and MALT 433 (yHJC3-4). The results are shown in FIG. 6. Strain yHKS210 served as the wild-type control which was unable to grow on maltotrise. These strains allow a direct comparison between the MALT434 which confers maltotriose transport and allows for growth on maltotriose with the related chimeric proteins all having the same region from MALT 3 that MALT 434 has. The MALT334 strain was not capable of growing on or utilizing maltotriose any better than the wild-type strain, whereas the MALT433 strain was capable of utilizing maltotriose similar to MALT434. Thus the N-terminal portion of MALT4 seems necessary for maltotriose utilization. The C-terminus can be derived from either parent polypeptide.

Discussion

A Chimeric Path to Novel Substrate Utilization

We found that a chimeric protein constituted a novel maltotriose transporter, despite the fact that neither of the parent proteins was able to transport maltotriose. Since the MALT3 region recombined into MALT4 was not able to support maltotriose in its native background, epistatic interactions with other sequence(s) in MALT4 must be important for this gain of function. Comparison of predicted protein structures suggested that several alpha helixes may be shortened in Malt434 compared to the parent proteins. The regions covered by these helixes were otherwise predicted to be conserved, even out to the distantly related Malt transporters lgAgt1 and scAgt1 (FIG. 2, FIG. 3J, FIG. 4). The predicted shortening of some alpha helixes within the chimeric protein compared to both its parents suggests that recombining the MALT3 region into MALT4 may have decreased the overall rigidity of the encoded chimeric protein, allowing it to accommodate bulkier substrates, such as maltotriose.

A previous study characterizing residues important for transporting maltotriose in scAgt1 found two residues that were important for its ability to transport maltotriose, while not affecting its ability to transport maltose (Smit et al. 2008). One of these residues lies within the chimeric region we observed in Malt434, and the other is 10 amino acid residues downstream (FIG. 3J). As the overall structure of maltose/maltotriose transporters is conserved (Cheng and Michels 1989; Han et al. 1995; Barrett et al. 1999; Yan 2015), the area in and around the chimeric region in Malt434 may itself be important for substrate specificity.

Replacement of the MALT4 sequence in this region with sequence from MALT3 may then have facilitated maltotriose transport in two ways. First, the mutation may have increased the overall flexibility of the encoded transporter, allowing it to accommodate the larger maltotriose molecule. Second, it could also have specifically altered an important substrate interface for better interaction with maltotriose, possibly by also making this region more flexible. Testing these biophysical and structural models will require future experiments, such as solving the crystal structures for Malt3, Malt4, and Malt434 as complexes with maltose and/or maltotriose.

Challenges of Evolving Maltotriose Utilization

Based on the results of our directed evolution experiments, which led to a single novel maltotriose transporter, the evolution of a protein that can transport maltotriose seems to be relatively rare, much rarer than one would expect if it could have been achieved with a single point mutation. The drastic mutation required to convert MALT4 into a gene encoding a maltotriose transporter and the phylogenetic placement of the rare known maltotriose transporters suggest that maltotriose transporters are generally difficult to evolve. Of the known MALT genes, only MTT1 and the AGT1 clade encode maltotriose transporters (Han et

al. 1995; Dietvorst et al. 2005; Salema-Oom et al. 2005; Vidgren and Londesborough 2012). Other MALT genes described in *S. eubayanus* were not found to be able to encode maltotriose transporters (Table 3), and no MALx1-type genes are known to encode maltotriose transporters (Horak 2013). MAL11 is sometimes described as being able to transport maltotriose (Brown et al. 2010; Baker et al. 2015; Brickwedde et al. 2017), but this discrepancy is the result of confusion over the naming of AGT1 in S288C and has been noted before (see Materials and Methods and Vidgren et al. 2005, 2009).

But what of the evolution of expression of a maltotriose transporter that was already present? Initially, we anticipated that it would be simple for yHRVM108 to evolve the ability to utilize maltotriose because we knew it already contained a transporter whose expression allows for strong maltotriose utilization in the parent background (Table 3). However, over the course of 100 passages, representing around 1,050 generations in yHRVM108, no maltotriose-utilizing lineage of yHRVM108 arose. While evolving yHRVM108 under our maltotriose selection regime was not successful, we were surprised to find an alternative and indirect selection regime could evolve maltotriose utilization in this background. When we began directed evolution of *S. eubayanus* to maltotriose, we also started another directed evolution experiment to try and improve yHRVM108's sluggish growth in maltose. Here, all three replicates of yHRVM108 eventually evolved the ability to grow rapidly on maltose. On average, single-colony isolates from these replicates grew four times as fast as the unevolved parent over two days in maltose (Table 6). Interestingly, isolates from the first two replicates that gained the ability to grow on maltose also gained the ability to utilize maltotriose (Table 5), despite never being exposed to maltotriose during the course of directed evolution.

TABLE 6

Strain	Background	Evolved in	Initial OD	Day 2
yHRVM108*	North Carolinian strain	—	0.22 (+/−0.01)	0.43 (+/−0.00)
yHRVM108	North Carolinian strain	—	0.15 (+/−0.03)	0.37 (+/−0.02)
yHEB1585	yHRVM108	maltose	0.16 (+/−0.02)	1.49 (+/−0.01)
yHEB1586	yHRVM108	maltose	0.14 (+/−0.01)	1.48 (+/−0.01)
yHEB1587	yHRVM108	maltose	0.16 (+/−0.01)	1.49 (+/−0.02)
yHEB1588	yHRVM108	maltose	0.17 (+/−0.01)	1.40 (+/−0.01)
yHEB1589	yHRVM108	maltose	0.18 (+/−0.01)	1.46 (+/−0.03)
yHEB1590	yHRVM108	maltose	0.18 (+/−0.01)	1.43 (+/−0.04)

Growth on maltose of single-colony isolates. Isolated from adaptive evolution of yHRVM108 on 2% maltose + 0.1% glucose. N = 3.
*Control grown in SC + 0.04% glucose to reflect the approximate amount of growth expected from contamination with other carbon sources when using 98% pure maltotriose.

The fact that maltotriose consumption independently evolved at least twice under directed evolution for maltose utilization suggests that our maltotriose selection regime itself may have played a role in restraining evolution. In other experiments to evolve *Saccharomyces* yeasts to carbon limitation or maltotriose consumption, the parent strains already had some capacity to use the supplied carbon source (Dunham et al. 2002; Brickwedde et al. 2017). For our experiments, this was true for directed evolution for maltose utilization, but it was not the case for directed evolution for maltotriose utilization.

Upregulation of MAL genes first requires maltose (or presumably maltotriose) to enter the cell (Wang et al. 2002). In the absence of glucose, at least one of the MALT transporters is ostensibly expressed at some level to allow this to occur (Wang et al. 2002). As yHRVM108 is unable to grow in maltotriose (Table 5), it seems unlikely that appreciable ncAGT1 is expressed. Nonetheless, under the maltose evolution conditions, cells started with some limited capacity to take up maltose, presumably from another MALT that was expressed, and thereby likely induced expression of MAL genes. Any regulatory mutations that loosened negative regulation or enhanced induction of ncAGT1 and other MALT genes in the absence of glucose and the presence of maltose would have been favored by selection (Horak 2013). As a result, relatively simple changes may have been sufficient to allow for ncAGT1 expression during evolution in maltose. Such changes would have been selected for since expression of ncAGT1 could help increase maltose uptake. However, during evolution in maltotriose, the MAL genes would have remained repressed since no maltose was present in the culture medium. As a consequence, rarer (and never observed) mutations might have been necessary to achieve expression of ncAGT1 in maltotriose. In retrospect, what appeared to be a simple request, to turn on the ncAGT1 gene in the condition being selected for, may in fact have been quite difficult by simple mutations, whereas our indirect selection regime on maltose proved more effective.

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Met Glu Gln Ala Lys Lys Ser Leu Glu Arg Thr Leu Ser Gly Lys Gly
305                 310                 315                 320

Pro Glu Lys Glu Leu Leu Val Ser Met Glu Leu Asp Lys Ile Lys Val
                325                 330                 335

Thr Ile Glu Lys Glu Gln Lys Met Ser Asp Ser Glu Gly Ser Tyr Trp
            340                 345                 350

Asp Cys Val Lys Asp Cys Ile Asn Arg Arg Arg Thr Arg Ile Ala Cys
        355                 360                 365

Leu Cys Trp Ile Gly Gln Thr Thr Cys Gly Thr Gln Leu Ile Gly Tyr
    370                 375                 380

Ser Thr Tyr Phe Tyr Glu Lys Ala Gly Val Ser Thr Glu Thr Ala Phe
385                 390                 395                 400

Thr Phe Ser Ile Ile Gln Tyr Cys Leu Gly Ile Val Ala Thr Leu Leu
                405                 410                 415

Ser Trp Trp Ala Ser Lys Tyr Phe Gly Arg Phe Asp Leu Tyr Ala Phe
            420                 425                 430

Gly Leu Ala Ile Gln Thr Val Leu Leu Phe Ile Ile Gly Gly Leu Gly
        435                 440                 445

Cys Ser Asp Thr His Gly Ala Gln Met Gly Ser Gly Ala Leu Leu Met
    450                 455                 460

Val Val Ala Phe Phe Tyr Asn Leu Gly Ile Ala Pro Val Val Phe Cys
465                 470                 475                 480

Leu Val Ser Glu Ile Pro Ser Ser Arg Leu Arg Thr Lys Ser Ile Ile
                485                 490                 495

Leu Ala Arg Asn Ala Tyr Asn Met Ala Cys Ile Val Thr Ala Val Leu
            500                 505                 510

Thr Leu Tyr Gln Leu Asn Ser Glu Lys Trp Asp Trp Gly Ala Lys Ser
        515                 520                 525

Gly Phe Phe Trp Gly Gly Leu Cys Phe Ala Thr Leu Val Trp Ala Val
    530                 535                 540

Phe Asp Leu Pro Glu Thr Ala Gly Arg Thr Phe Ile Glu Ile Asn Glu
545                 550                 555                 560

Leu Phe Arg Leu Gly Val Pro Ala Arg Lys Phe Lys Ser Thr Lys Val
                565                 570                 575

Asp Pro Phe Ala Ala Ala Lys Ala Ile Ser Asp Glu Ile Asn His Lys
            580                 585                 590

Asp Pro Lys Glu Asp Met Lys Ala Ser Ala Glu Glu Arg Glu Gln Ser
        595                 600                 605

Thr Pro Ser Leu Met Asp
    610
```

<210> SEQ ID NO 4
<211> LENGTH: 613
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(613)
<223> OTHER INFORMATION: FM1318 Malt4

<400> SEQUENCE: 4

```
Met Lys Gly Leu Ser Ser Met Ile Asn Arg Lys Lys Cys Asn Gly Asn
1               5                   10                  15

Ser Ser Ser Ile Glu Thr Glu Gly Gly Phe Gly Ala Ala Glu Cys Asn
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           20                  25                  30

Ser Ile Glu Leu Glu Glu Gln Gly Lys Lys Thr Asp Phe Asp Leu Ala
        35                  40                  45

His Leu Glu Tyr Gly Gln Gly Pro Ala Ala Leu Ser Glu Asn Asp Glu
    50                  55                  60

Val Thr Pro Asn Ile Leu Asp Ala Ala Gln Asp Ala Lys Glu Ala Asp
65                  70                  75                  80

Asp Ser Glu Arg Glu Met Pro Leu Met Thr Ala Leu Lys Thr Tyr Pro
                85                  90                  95

Lys Ala Ala Ala Trp Ser Leu Leu Val Ser Thr Thr Leu Ile Gln Glu
            100                 105                 110

Gly Tyr Asp Thr Ala Ile Leu Gly Ser Phe Tyr Ala Leu Pro Val Phe
        115                 120                 125

Gln Lys Lys Tyr Gly Ser Leu Asn Ala Arg Thr Gly Glu Trp Glu Ile
    130                 135                 140

Ser Val Ser Trp Gln Ile Gly Leu Cys Leu Cys Tyr Met Ala Gly Glu
145                 150                 155                 160

Ile Val Gly Leu Gln Leu Thr Gly Pro Ser Val Asp Leu Met Gly Asn
                165                 170                 175

Arg Tyr Thr Leu Ile Met Ala Leu Met Phe Leu Thr Ala Phe Ile Phe
            180                 185                 190

Ile Leu Tyr Phe Cys Lys Ser Leu Gly Met Ile Ala Ala Gly Gln Ala
        195                 200                 205

Leu Cys Gly Met Pro Trp Gly Cys Phe Gln Cys Leu Thr Val Ser Tyr
    210                 215                 220

Ala Ser Glu Ile Cys Pro Met Ala Leu Arg Tyr Tyr Leu Thr Thr Tyr
225                 230                 235                 240

Ser Asn Leu Cys Trp Leu Phe Gly Gln Leu Phe Ala Ala Gly Ile Met
                245                 250                 255

Lys Asn Ser Gln Asn Lys Tyr Ala Asp Ser Asp Leu Gly Tyr Thr Leu
            260                 265                 270

Pro Phe Ala Leu Gln Trp Ile Trp Pro Val Pro Leu Ala Ile Ala Ile
        275                 280                 285

Phe Phe Ala Pro Glu Ser Pro Trp Trp Leu Val Lys Lys Gly Arg Leu
    290                 295                 300

Glu Gln Ala Lys Arg Ser Leu Glu Arg Thr Leu Ser Gly Lys Gly Ala
305                 310                 315                 320

Glu Lys Glu Ser Leu Val Ala Met Glu Leu Asp Lys Ile Lys Met Thr
                325                 330                 335

Ile Glu Lys Glu Lys Lys Leu Ser Asp Asp Glu Gly Ser Tyr Leu Asp
            340                 345                 350

Cys Leu Arg Gly Lys Val Asn Arg Arg Arg Thr Arg Ile Ala Cys Leu
        355                 360                 365

Cys Trp Ala Gly Gln Thr Val Cys Gly Ala Ser Leu Ile Gly Tyr Ser
    370                 375                 380

Thr Tyr Phe Tyr Glu Lys Ala Gly Val Ser Thr Glu Thr Ala Phe Thr
385                 390                 395                 400

Phe Ser Ile Ile Gln Tyr Cys Leu Gly Ile Ala Ala Thr Phe Leu Ser
                405                 410                 415

Trp Trp Ala Ser Lys Tyr Tyr Gly Arg Tyr Asp Leu Tyr Ala Cys Gly
            420                 425                 430

Leu Ala Phe Gln Thr Val Ile Leu Phe Ile Ile Gly Gly Leu Gly Cys
        435                 440                 445
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Ser Asp Thr His Gly Ala Lys Met Gly Ser Gly Ala Leu Leu Met Val
    450                 455                 460

Val Ala Phe Ser Tyr Asn Leu Gly Ile Ala Pro Val Val Phe Cys Leu
465                 470                 475                 480

Val Ser Glu Ile Pro Ser Ser Arg Leu Arg Thr Lys Ser Ile Ile Leu
                485                 490                 495

Ala Arg Asn Ala Tyr Asn Ile Gly Asn Ile Val Val Ala Val Leu Ile
            500                 505                 510

Leu Tyr Gln Leu Asn Ser Glu Lys Trp Asn Trp Gly Ala Lys Ser Gly
        515                 520                 525

Phe Phe Trp Gly Gly Phe Cys Leu Ala Val Leu Ile Trp Ala Val Phe
    530                 535                 540

Asp Leu Pro Glu Thr Ala Gly Arg Thr Phe Ile Glu Ile Asn Glu Leu
545                 550                 555                 560

Phe Arg Leu Gly Val Pro Ala Arg Lys Phe Lys Ser Thr Lys Val Asp
                565                 570                 575

Pro Phe Ala Ala Ala Lys Ala Ile Ser Asp Glu Ile Asn His Lys Asp
            580                 585                 590

Pro Lys Glu Asp Met Lys Ala Ser Ala Glu Glu Arg Glu Gln Ser Thr
        595                 600                 605

Pro Ser Leu Met Asp
    610


<210> SEQ ID NO 5
<211> LENGTH: 614
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(614)
<223> OTHER INFORMATION: FM1318 Malt3

<400> SEQUENCE: 5

Met Lys Gly Leu Ser Ser Leu Ile Asn Arg Lys Lys Asn Lys Ile Asp
1               5                   10                  15

Ser Asn Ser Asn Glu Ile Glu Asn Gly Met Asn Ser Thr Asp Leu Asn
            20                  25                  30

Ser Ile Glu Met Gln Glu Gln Gly Lys Lys Ser Asp Phe Asp Leu Ser
        35                  40                  45

His Ile Glu Tyr Gly Gln Asp Ser Arg Val Pro Lys Asp Asp Asp Glu
    50                  55                  60

Glu Val Pro Asp Leu Leu Asp Glu Ala Met Gln Asp Ala Lys Glu Ala
65                  70                  75                  80

Asp Glu Ser Glu Arg Gly Met Pro Leu Leu Gln Ala Leu Lys Thr Tyr
                85                  90                  95

Pro Lys Ala Ala Ala Trp Ser Leu Leu Val Ser Thr Thr Leu Ile Gln
            100                 105                 110

Glu Gly Tyr Asp Thr Ala Ile Leu Gly Ser Phe Tyr Ala Leu Pro Val
        115                 120                 125

Phe Gln Lys Glu Tyr Gly Ser Leu Asn Ser Lys Thr Gly Glu Tyr Glu
    130                 135                 140

Ile Ser Val Ser Trp Gln Ile Gly Leu Ser Leu Cys Ile Val Ala Gly
145                 150                 155                 160

Glu Ile Val Gly Leu Gln Met Thr Gly Pro Phe Val Asp Tyr Met Gly
                165                 170                 175
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Asn Arg Tyr Thr Leu Ile Val Ala Leu Phe Phe Leu Ala Ala Phe Thr
            180                 185                 190

Phe Ile Leu Tyr Phe Cys Lys Ser Leu Gly Met Ile Ala Val Gly Gln
        195                 200                 205

Val Leu Cys Gly Met Pro Trp Gly Cys Phe Gln Cys Leu Thr Val Ser
    210                 215                 220

Tyr Ala Ser Glu Ile Cys Pro Leu Ala Leu Arg Tyr Tyr Leu Thr Thr
225                 230                 235                 240

Tyr Ser Asn Leu Cys Trp Thr Phe Gly Gln Leu Phe Ala Ala Gly Ile
                245                 250                 255

Met Lys Asn Ser Gln Asn Lys Tyr Pro Asp Ser Asp Leu Gly Tyr Lys
            260                 265                 270

Leu Pro Phe Ala Leu Gln Trp Ile Trp Pro Leu Pro Leu Ala Ile Gly
        275                 280                 285

Ile Phe Phe Ala Pro Glu Ser Pro Trp Trp Leu Ile Lys Lys Gly Arg
    290                 295                 300

Met Glu Gln Ala Lys Lys Ser Leu Glu Arg Thr Leu Ser Gly Lys Gly
305                 310                 315                 320

Pro Glu Lys Glu Leu Leu Val Ser Met Glu Leu Asp Lys Ile Lys Val
                325                 330                 335

Thr Ile Glu Lys Glu Gln Lys Met Ser Asp Ser Glu Gly Ser Tyr Trp
            340                 345                 350

Asp Cys Val Lys Asp Cys Ile Asn Arg Arg Arg Thr Arg Ile Ala Cys
        355                 360                 365

Leu Cys Trp Ile Gly Gln Thr Thr Cys Gly Thr Gln Leu Ile Gly Tyr
    370                 375                 380

Ser Thr Tyr Phe Tyr Glu Lys Ala Gly Val Ser Thr Glu Thr Ala Phe
385                 390                 395                 400

Thr Phe Ser Ile Ile Gln Tyr Cys Leu Gly Ile Val Ala Thr Leu Leu
                405                 410                 415

Ser Trp Trp Ala Ser Lys Tyr Phe Gly Arg Phe Asp Leu Tyr Ala Phe
            420                 425                 430

Gly Leu Ala Ile Gln Thr Val Leu Leu Phe Ile Ile Gly Gly Leu Gly
        435                 440                 445

Cys Ser Asp Thr His Gly Ala Gln Met Gly Ser Gly Ala Leu Leu Met
    450                 455                 460

Val Val Ala Phe Phe Tyr Asn Leu Gly Ile Ala Pro Val Val Phe Cys
465                 470                 475                 480

Leu Val Ser Glu Ile Pro Ser Ser Arg Leu Arg Thr Lys Ser Ile Ile
                485                 490                 495

Leu Ala Arg Asn Ala Tyr Asn Met Ala Cys Ile Val Thr Ala Val Leu
            500                 505                 510

Thr Leu Tyr Gln Leu Asn Ser Glu Lys Trp Asp Trp Gly Ala Lys Ser
        515                 520                 525

Gly Phe Phe Trp Gly Gly Leu Cys Phe Ala Thr Leu Val Trp Ala Val
    530                 535                 540

Ile Asp Leu Pro Glu Thr Ala Gly Arg Thr Phe Met Glu Met Asn Glu
545                 550                 555                 560

Leu Phe Arg Leu Gly Ile Pro Ala Arg Lys Phe Lys Thr Thr Lys Val
                565                 570                 575

Asp Pro Phe Ala Ala Val Lys Ala Ala Lys Glu Ile Ala His Asn Asp
            580                 585                 590

Pro Lys Glu Asp Met Glu Thr Ser Met Val Glu Glu Gly Arg Ser Thr
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595 600 605

Pro Ser Ile Thr Asn Leu
610

<210> SEQ ID NO 6
<211> LENGTH: 610
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: yHAB47 lager hybrid lgAGT1

<400> SEQUENCE: 6

Met Lys Asn Ile Leu Ser Leu Val Gly Arg Lys Glu Asn Thr Pro Glu
1 5 10 15

Asp Val Thr Ala Asn Leu Ala Asp Thr Ser Ser Thr Thr Val Met Gln
20 25 30

Ala Lys Asp Leu Val Ile Glu Asp Phe Glu Glu Arg Lys Lys Asn Asp
35 40 45

Ala Phe Glu Leu Asn His Leu Glu Leu Thr Thr Asn Ala Thr Gln Leu
50 55 60

Ser Asp Ser Asp Glu Asp Lys Glu Asn Val Ile Arg Val Ala Glu Ala
65 70 75 80

Thr Asp Asp Ala Asn Glu Ala Asn Asn Glu Glu Lys Ser Met Thr Leu
85 90 95

Arg Gln Ala Leu Arg Lys Tyr Pro Lys Ala Ala Leu Trp Ser Ile Leu
100 105 110

Val Ser Thr Thr Leu Val Met Glu Gly Tyr Asp Thr Ala Leu Leu Ser
115 120 125

Ala Leu Tyr Ala Leu Pro Val Phe Gln Arg Lys Phe Gly Thr Met Asn
130 135 140

Ala Glu Gly Ser Tyr Glu Ile Thr Ser Gln Trp Gln Ile Gly Leu Asn
145 150 155 160

Met Cys Val Leu Cys Gly Glu Met Ile Gly Leu Gln Ile Thr Thr Tyr
165 170 175

Met Val Glu Phe Met Gly Asn Arg Tyr Thr Met Ile Thr Ala Leu Ser
180 185 190

Leu Leu Thr Ala Tyr Ile Phe Ile Leu Tyr Tyr Cys Lys Ser Leu Ala
195 200 205

Met Ile Ala Val Gly Gln Ile Leu Ser Ala Met Pro Trp Gly Cys Phe
210 215 220

Gln Ser Leu Ala Val Thr Tyr Ala Ser Glu Val Cys Pro Leu Ala Leu
225 230 235 240

Arg Tyr Tyr Met Thr Ser Tyr Ser Asn Ile Cys Trp Leu Phe Gly Gln
245 250 255

Ile Phe Ala Ser Gly Ile Met Lys Asn Ser Gln Glu Asn Leu Gly Asn
260 265 270

Ser Asp Leu Gly Tyr Lys Leu Pro Phe Ala Leu Gln Trp Ile Trp Pro
275 280 285

Ala Pro Leu Ile Ile Gly Ile Phe Phe Ala Pro Glu Ser Pro Trp Trp
290 295 300

Leu Val Arg Lys Asn Lys Ile Val Glu Ala Lys Lys Ser Leu Asn Arg
305 310 315 320

Ile Leu Ser Gly Thr Val Thr Glu Lys Glu Ile Gln Val Asp Ile Thr
325 330 335

Leu Lys Gln Ile Glu Met Thr Ile Glu Lys Glu Arg Leu Arg Ala Ser

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            340                 345                 350

Lys Ser Gly Ser Phe Phe Ser Cys Phe Lys Gly Val Asp Gly Arg Arg
        355                 360                 365

Thr Arg Leu Ala Cys Leu Thr Trp Val Ala Gln Asn Ser Ser Gly Ala
    370                 375                 380

Val Leu Leu Gly Tyr Ser Thr Tyr Phe Phe Glu Arg Ala Gly Met Ala
385                 390                 395                 400

Thr Asp Lys Ala Phe Thr Phe Ser Leu Ile Gln Tyr Cys Leu Gly Leu
                405                 410                 415

Ala Gly Thr Leu Gly Ser Trp Val Ile Ser Gly Arg Val Gly Arg Trp
            420                 425                 430

Thr Ile Leu Thr Tyr Gly Leu Ser Phe Gln Met Val Cys Leu Phe Ile
        435                 440                 445

Ile Gly Gly Met Gly Phe Ala Ser Gly Ser Ser Ala Ser Asn Ala Ala
    450                 455                 460

Gly Gly Leu Leu Leu Ala Leu Ser Phe Phe Tyr Asn Ala Gly Ile Gly
465                 470                 475                 480

Ala Val Val Tyr Cys Ile Val Ala Glu Ile Pro Ser Ala Glu Leu Arg
                485                 490                 495

Thr Lys Thr Ile Val Leu Ala Arg Ile Cys Tyr Asn Leu Met Ala Val
            500                 505                 510

Phe Asn Ala Ile Leu Thr Pro Tyr Met Leu Asn Val Ser Asp Trp Asn
        515                 520                 525

Trp Gly Ala Lys Thr Gly Leu Tyr Trp Gly Gly Phe Thr Ala Leu Thr
    530                 535                 540

Leu Ala Trp Val Ile Ile Asp Leu Pro Glu Thr Thr Gly Arg Thr Phe
545                 550                 555                 560

Ser Glu Ile Asn Glu Leu Phe Ser Gln Gly Val Pro Ala Arg Lys Phe
                565                 570                 575

Ala Ser Thr Val Val Asp Pro Phe Gly Lys Arg Gly Leu Gln Asn Arg
            580                 585                 590

Pro Gln Val Asp Asn Ile Ile Asp Arg Phe Ser Ser Ala Ser Gln Gln
        595                 600                 605

Ala Leu
    610


<210> SEQ ID NO 7
<211> LENGTH: 610
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(610)
<223> OTHER INFORMATION: yHRVM108 ncAGT1

<400> SEQUENCE: 7

Met Lys Asn Ile Ile Ser Leu Val Arg Arg Lys Gly Asn Thr Pro Glu
1               5                   10                  15

Asp Glu Thr Glu Asn Leu Glu Asp Thr Ser Ser Thr Thr Val Met Gln
            20                  25                  30

Ala Lys Asp Leu Asp Ile Glu Asp Phe Glu Glu Arg Lys Lys Asn Asp
        35                  40                  45

Ala Phe Glu Leu Asn His Met Glu Leu Thr Thr Asn Ala Thr Gln Leu
    50                  55                  60

Gly Asp Ser Asp Gly Asp Asn Asp Asn Ala Ile Arg Val Ala Glu Ala
65                  70                  75                  80
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Thr Asp Asp Ala Asn Glu Ala Asn Asn Glu Glu Lys Ser Met Thr Leu
                85                  90                  95

Arg Gln Ala Leu Arg Lys Tyr Pro Lys Ala Ala Leu Trp Ser Ile Leu
            100                 105                 110

Val Ser Thr Thr Leu Val Met Glu Gly Tyr Asp Thr Ala Leu Leu Ser
        115                 120                 125

Ala Leu Tyr Ala Leu Pro Val Phe Gln Arg Lys Phe Gly Thr Met Asn
    130                 135                 140

Ala Glu Gly Ser Tyr Glu Ile Thr Ser Gln Trp Gln Ile Gly Leu Asn
145                 150                 155                 160

Met Cys Val Leu Cys Gly Glu Met Ile Gly Leu Gln Met Thr Thr Tyr
                165                 170                 175

Met Val Glu Phe Met Gly Asn Arg Tyr Thr Met Ile Met Ala Leu Phe
            180                 185                 190

Leu Leu Thr Ala Tyr Ile Phe Ile Leu Tyr Tyr Cys Lys Ser Leu Ala
        195                 200                 205

Met Ile Ala Val Gly Gln Ile Leu Ser Ala Met Pro Trp Gly Cys Phe
    210                 215                 220

Gln Ser Leu Ala Val Thr Tyr Ala Ser Glu Val Cys Pro Leu Ala Leu
225                 230                 235                 240

Arg Tyr Tyr Met Thr Ser Tyr Ser Asn Ile Cys Trp Leu Phe Gly Gln
                245                 250                 255

Ile Phe Ala Ser Gly Ile Met Lys Asn Ser Gln Glu Asn Leu Gly Asp
            260                 265                 270

Ser Asp Leu Gly Tyr Lys Leu Pro Phe Ala Leu Gln Trp Ile Trp Pro
        275                 280                 285

Ala Pro Leu Ile Ile Gly Ile Phe Phe Ala Pro Glu Ser Pro Trp Trp
    290                 295                 300

Leu Val Arg Lys Asn Lys Ile Val Glu Ala Lys Lys Ser Leu Asn Arg
305                 310                 315                 320

Ile Leu Ser Gly Thr Ala Thr Glu Lys Glu Ile Gln Val Asp Ile Thr
                325                 330                 335

Leu Lys Gln Ile Glu Met Thr Ile Glu Lys Glu Arg Leu Arg Ala Ser
            340                 345                 350

Glu Ser Gly Ser Phe Phe Ser Cys Phe Lys Gly Val Asp Gly Arg Arg
        355                 360                 365

Thr Arg Leu Ala Cys Leu Thr Trp Val Ala Gln Asn Ser Ser Gly Ala
    370                 375                 380

Val Leu Leu Gly Tyr Ser Thr Tyr Phe Phe Glu Arg Ala Gly Met Asp
385                 390                 395                 400

Thr Asp Lys Ala Phe Thr Phe Ser Leu Ile Gln Tyr Cys Leu Gly Leu
                405                 410                 415

Ala Gly Thr Leu Cys Ser Trp Val Ile Ser Gly Arg Val Gly Arg Trp
            420                 425                 430

Thr Ile Leu Thr Tyr Gly Leu Ser Phe Gln Met Val Cys Leu Phe Ile
        435                 440                 445

Ile Gly Gly Met Gly Phe Ala Ser Gly Ser Ser Ala Ser Asn Ala Ala
    450                 455                 460

Gly Gly Leu Leu Leu Ala Leu Ser Phe Phe Tyr Asn Ala Gly Ile Gly
465                 470                 475                 480

Ala Val Val Tyr Cys Ile Val Ala Glu Ile Pro Ser Ala Glu Leu Arg
                485                 490                 495
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```
Thr Lys Thr Ile Val Leu Ala Arg Ile Cys Tyr Asn Leu Met Ala Val
            500                 505                 510

Phe Asn Ala Ile Leu Thr Pro Tyr Met Leu Asn Val Ser Asp Trp Asn
        515                 520                 525

Trp Gly Ala Lys Thr Gly Leu Tyr Trp Gly Gly Phe Thr Ala Leu Thr
    530                 535                 540

Leu Ala Trp Val Ile Ile Asp Leu Pro Glu Thr Thr Gly Arg Thr Phe
545                 550                 555                 560

Ser Glu Ile Asn Glu Leu Phe Asn Gln Gly Val Pro Ala Arg Lys Phe
                565                 570                 575

Ala Ser Thr Val Val Asp Pro Phe Gly Lys Ser Gly Leu Lys Asn Leu
            580                 585                 590

Pro Gln Val Asp Asp Ile Ile Asp Arg Ser Ser Ser Met Ser Gln Gln
        595                 600                 605

Ala Leu
    610


<210> SEQ ID NO 8
<211> LENGTH: 616
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(616)
<223> OTHER INFORMATION: AGT1 from strain S288c

<400> SEQUENCE: 8

Met Lys Asn Ile Ile Ser Leu Val Ser Lys Lys Lys Ala Ala Ser Lys
1               5                   10                  15

Asn Glu Asp Lys Asn Ile Ser Glu Ser Ser Arg Asp Ile Val Asn Gln
            20                  25                  30

Gln Glu Val Phe Asn Thr Glu Asp Phe Glu Glu Gly Lys Lys Asp Ser
        35                  40                  45

Ala Phe Glu Leu Asp His Leu Glu Phe Thr Thr Asn Ser Ala Gln Leu
    50                  55                  60

Gly Asp Ser Asp Glu Asp Asn Glu Asn Val Ile Asn Glu Met Asn Ala
65                  70                  75                  80

Thr Asp Asp Ala Asn Glu Ala Asn Ser Glu Glu Lys Ser Met Thr Leu
                85                  90                  95

Lys Gln Ala Leu Leu Lys Tyr Pro Lys Ala Ala Leu Trp Ser Ile Leu
            100                 105                 110

Val Ser Thr Thr Leu Val Met Glu Gly Tyr Asp Thr Ala Leu Leu Ser
        115                 120                 125

Ala Leu Tyr Ala Leu Pro Val Phe Gln Arg Lys Phe Gly Thr Leu Asn
    130                 135                 140

Gly Glu Gly Ser Tyr Glu Ile Thr Ser Gln Trp Gln Ile Gly Leu Asn
145                 150                 155                 160

Met Cys Val Leu Cys Gly Glu Met Ile Gly Leu Gln Ile Thr Thr Tyr
                165                 170                 175

Met Val Glu Phe Met Gly Asn Arg Tyr Thr Met Ile Thr Ala Leu Gly
            180                 185                 190

Leu Leu Thr Ala Tyr Ile Phe Ile Leu Tyr Tyr Cys Lys Ser Leu Ala
        195                 200                 205

Met Ile Ala Val Gly Gln Ile Leu Ser Ala Ile Pro Trp Gly Cys Phe
    210                 215                 220

Gln Ser Leu Ala Val Thr Tyr Ala Ser Glu Val Cys Pro Leu Ala Leu
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225                 230                 235                 240

Arg Tyr Tyr Met Thr Ser Tyr Ser Asn Ile Cys Trp Leu Phe Gly Gln
                245                 250                 255

Ile Phe Ala Ser Gly Ile Met Lys Asn Ser Gln Glu Asn Leu Gly Asn
            260                 265                 270

Ser Asp Leu Gly Tyr Lys Leu Pro Phe Ala Leu Gln Trp Ile Trp Pro
        275                 280                 285

Ala Pro Leu Met Ile Gly Ile Phe Phe Ala Pro Glu Ser Pro Trp Trp
    290                 295                 300

Leu Val Arg Lys Asp Arg Val Ala Glu Ala Arg Lys Ser Leu Ser Arg
305                 310                 315                 320

Ile Leu Ser Gly Lys Gly Ala Glu Lys Asp Ile Gln Val Asp Leu Thr
                325                 330                 335

Leu Lys Gln Ile Glu Leu Thr Ile Glu Lys Glu Arg Leu Leu Ala Ser
            340                 345                 350

Lys Ser Gly Ser Phe Phe Asn Cys Phe Lys Gly Val Asn Gly Arg Arg
        355                 360                 365

Thr Arg Leu Ala Cys Leu Thr Trp Val Ala Gln Asn Ser Ser Gly Ala
    370                 375                 380

Val Leu Leu Gly Tyr Ser Thr Tyr Phe Phe Glu Arg Ala Gly Met Ala
385                 390                 395                 400

Thr Asp Lys Ala Phe Thr Phe Ser Leu Ile Gln Tyr Cys Leu Gly Leu
                405                 410                 415

Ala Gly Thr Leu Cys Ser Trp Val Ile Ser Gly Arg Val Gly Arg Trp
            420                 425                 430

Thr Ile Leu Thr Tyr Gly Leu Ala Phe Gln Met Val Cys Leu Phe Ile
        435                 440                 445

Ile Gly Gly Met Gly Phe Gly Ser Gly Ser Ser Ala Ser Asn Gly Ala
    450                 455                 460

Gly Gly Leu Leu Leu Ala Leu Ser Phe Phe Tyr Asn Ala Gly Ile Gly
465                 470                 475                 480

Ala Val Val Tyr Cys Ile Val Ala Glu Ile Pro Ser Ala Glu Leu Arg
                485                 490                 495

Thr Lys Thr Ile Val Leu Ala Arg Ile Cys Tyr Asn Leu Met Ala Val
            500                 505                 510

Ile Asn Ala Ile Leu Thr Pro Tyr Met Leu Asn Val Ser Asp Trp Asn
        515                 520                 525

Trp Gly Ala Lys Thr Gly Leu Tyr Trp Gly Gly Phe Thr Ala Val Thr
    530                 535                 540

Leu Ala Trp Val Ile Ile Asp Leu Pro Glu Thr Thr Gly Arg Thr Phe
545                 550                 555                 560

Ser Glu Ile Asn Glu Leu Phe Asn Gln Gly Val Pro Ala Arg Lys Phe
                565                 570                 575

Ala Ser Thr Val Val Asp Pro Phe Gly Lys Gly Lys Thr Gln His Asp
            580                 585                 590

Ser Leu Ala Asp Glu Ser Ile Ser Gln Ser Ser Ser Ile Lys Gln Arg
        595                 600                 605

Glu Leu Asn Ala Ala Asp Lys Cys
    610                 615


<210> SEQ ID NO 9
<211> LENGTH: 1842
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces eubayanus
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1842)
<223> OTHER INFORMATION: yHEB1505 MALT434

<400> SEQUENCE: 9

atgaagggtc tatcctcaat gataaataga aagaagtgca acggtaactc gagttcaata 60

gagaccgaag gtggcttcgg cgccgctgaa tgcaactcga tagagttgga ggagcaaggc 120

aaaaaaactg attttgatct tgcccatctt gagtatggtc agggcccagc agcattaagc 180

gagaatgatg aagtaacgcc aaatattctc gacgctgcgc aggatgctaa ggaggccgac 240

gatagtgaaa gagagatgcc gctcatgaca gctttgaaaa cgtatcccaa agcagcggct 300

tggtcgttgt tggtttccac aacgctgatc caggaaggtt atgacaccgc catcctcggc 360

tctttctatg ccctacccgt ctttcagaag aagtacggct ctctaaatgc ccgtacagga 420

gaatgggaga tttcggtatc ttggcagatt gggctgtgtt tatgctacat ggcaggagag 480

atcgtgggtt tacagttgac aggtccctcg gtggatttga tgggtaaccg ctacacattg 540

attatggcgt tgatgttctt aactgccttc atttttattc tgtatttctg taaaagttta 600

gggatgatcg ctgcgggaca ggcattgtgc ggtatgccat ggggttgttt ccaatgtctg 660

actgtgtctt atgcctctga aatctgtcct atggcgctga ggtactacct gacgacatat 720

tcgaatctgt gctggttgtt tggtcagctt tttgctgcag gcatcatgaa aaattcccaa 780

aacaaatacg cagactcgga cttaggatat acgctacctt ttgctttaca gtggatctgg 840

cctgttcctc tagcaatagc gatattcttt gcacctgaat ccccatggtg gttagtcaag 900

aaaggaagac tagagcaggc aaagaggtcg ctcgaaagaa cactaagcgg taagggagcc 960

gagaaagaat cactggtggc catggaactg gataaaatca aaatgactat agagaaggag 1020

aagaagctgt cagacgatga aggctcctat ttggattgtc tgaggggcaa ggttaatcgg 1080

aggagaacga gaatagcctg tctgtgctgg gccggtcaaa ctgtttgtgg tgcgtcacta 1140

ataggttact caacttactt ctacgagaaa gccggtgtta gcacggaaac agcattcact 1200

tttagtatca ttcaatactg tctcggtatt gctgcaacat ttttatcctg gtgggcctca 1260

aaatattatg gtagatatga cctttacgct tgtggactgg ccttccagac cgttatactg 1320

ttcattatag gcggtttggg atgctccgac actcacggtg ccaaaatggg aagtggcgct 1380

cttctaatgg tggtcgcctt cttttacaac ctggggattg ctcccgttgt cttttgctta 1440

gtttctgaaa taccatcctc gaggctaaga actaaatcaa ttattctggc tcgtaacgcc 1500

tataatatgg catgtatcgt aactgctgtc ctgacattgt accaattgaa ttcagaaaaa 1560

tgggattggg gtgcaaagtc aggcttcttc tgggggggac tatgttttgc gacgttagta 1620

tgggctgtct ttgatctgcc cgaaaccgca ggtagaacct ttattgaaat aaatgaacta 1680

tttagacttg gagttccagc aagaaaattc aagtcaacaa aagtggaccc atttgccgcc 1740

gccaaagcaa tctctgatga aatcaaccat aaagatccca aggaagatat gaaagcttcc 1800

gccgaggaga gagagcaaag caccccatct ctaatggatt ga 1842

<210> SEQ ID NO 10
<211> LENGTH: 1842
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1842)
<223> OTHER INFORMATION: FM1318 Malt4

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<400> SEQUENCE: 10

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aaaaaaactg attttgatct tgcccatctt gagtatggtc agggcccagc agcattaagc 180

gagaatgatg aagtaacgcc aaatattctc gacgctgcgc aggatgctaa ggaggcagac 240

gatagtgaaa gagagatgcc gctcatgaca gctttgaaaa cgtatcccaa agcagcggct 300

tggtcgttgt tggtttccac aacgctgatc caggaaggtt atgacaccgc catcctcggc 360

tctttctatg ccctacccgt ctttcagaag aagtacggct ctctaaatgc ccgtacagga 420

gaatgggaga tttcggtatc ttggcagatt gggctgtgtt tatgctacat ggcaggagag 480

atcgtgggtt tacagttgac aggtccctcg gtggatttga tgggtaaccg ctacacattg 540

attatggcgt tgatgttctt aactgctttc atttttattc tgtatttctg taaaagttta 600

gggatgatcg ctgcgggaca ggcattgtgc ggtatgccat ggggttgttt ccaatgtctg 660

actgtgtctt atgcctctga aatctgtcct atggcgctga ggtactacct gacgacatat 720

tcgaatctgt gctggttgtt tggtcagctt tttgctgcag gcatcatgaa aaattcccaa 780

aacaaatacg cagactcgga cttaggatat acgctacctt ttgctttaca gtggatctgg 840

cctgttcctc tagcaatagc gatattcttt gcacctgaat ccccatggtg gttagtcaag 900

aaaggaagac tagagcaggc aaagaggtcg ctcgaaagaa cactaagcgg taagggagcc 960

gagaaagaat cactggtggc catggaactg gataaaatca aaatgactat agagaaggag 1020

aagaagctgt cagacgatga aggctcctat ttggattgtc tgaggggcaa ggttaatcgg 1080

aggagaacga gaatagcctg tctgtgctgg gccggtcaaa ctgtttgtgg tgcgtcacta 1140

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tttagtatca ttcaatactg tctcggtatt gctgcaacat ttttatcctg gtgggcctca 1260

aaatattatg gtagatatga cctttacgct tgtggactgg ccttccagac cgttatactg 1320

ttcattatag gcggtttggg atgctccgac actcacggtg ccaaaatggg aagtggcgct 1380

cttctaatgg tcgttgcgtt ctcatacaac ctggggattg cccctgtcgt tttttgctta 1440

gtctctgaaa taccatcgtc gaggctgaga actaaatcga tcattttagc tcgtaatgcg 1500

tacaacatag gaaatatcgt agttgctgtt ttgattttgt accaactgaa ctctgagaaa 1560

tggaactggg gtgccaagtc aggctttttc tggggaggat tctgcctggc tgttttaatt 1620

tgggctgtct ttgatctgcc cgaaaccgca ggtagaacct ttattgaaat aaatgaacta 1680

tttagacttg gagttccagc aagaaaattc aagtcaacaa aagtggaccc atttgccgcc 1740

gccaaagcaa tctctgatga aatcaaccat aaagatccca aggaagatat gaaagcttcc 1800

gccgaggaga gagagcaaag caccccatct ctaatggatt ga 1842

<210> SEQ ID NO 11
<211> LENGTH: 1845
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1845)
<223> OTHER INFORMATION: FM1318 Malt3

<400> SEQUENCE: 11

atgaagggct tatcctcact gataaacaga aaaaaaaaca agattgactc taattcaaat 60

gagatcgaga acggcatgaa cagtaccgat ctcaactcga tcgagatgca ggaacaaggc 120

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aagaaatctg actttgatct ttcccatatt gagtacggtc aagattcacg agtaccaaaa 180

gatgatgatg aggaagtccc agatcttctc gatgaggcta tgcaggatgc gaaggaggca 240

gacgaaagtg aaaggggat gccacttctg caagctttga aaacgtatcc caaagctgct 300

gcttggtcgc tattagtctc cacaacgctg attcaagaag gttatgatac tgccatcctc 360

ggatctttct atgctttgcc cgttttccag aaggaatatg gttctctgaa tagcaagaca 420

ggagaatatg aaatttcagt ttcttggcag attggtttat ctttatgtat tgtggcaggt 480

gagattgttg gtttacaaat gactggtcct tttgtagatt acatgggtaa tcgttacaca 540

ttgattgtgg cgttgttctt tttagccgct ttcacttta ttctgtattt ttgcaaaagt 600

ttgggtatga ttgccgtggg acaagtactg tgtggtatgc catggggttg tttccaatgt 660

ttgacagtct catatgcttc cgaaatctgt cctttggctt taagatacta cctgacaact 720

tattcaaact tgtgctggac ttttggccaa ctttttgctg ctggtattat gaaaaattcc 780

caaaacaagt acccagactc ggatttggga tataagctac catttgcttt acagtggatt 840

tggcctcttc ccctggcaat agggatattc tttgcacctg aatctccatg gtggttgatc 900

aagaaaggga gaatggaaca ggcgaagaaa tcacttgaaa gaacattgag tggcaaggga 960

cctgagaaag aactgctggt gagtatggaa ctagataaaa tcaaagtgac tattgaaaaa 1020

gaacaaaaaa tgtcagattc agaagggtca tactgggatt gtgtgaagga ctgtatcaac 1080

cggagaagaa caagaatagc ttgtttatgt tggattggtc aaaccacttg tggtacacaa 1140

ctgataggat attcaaccta tttttacgaa aaggctggtg ttagcactga aacagcattc 1200

acttttagta ttattcaata ctgtcttggt attgttgcaa cacttctatc ctggtgggct 1260

tcaaagtatt ttgggagatt tgacctttac gcgttcggac tggccattca gactgtttta 1320

ctgtttatta taggaggtct gggatgctct gatactcacg gtgcccaaat gggaagtggc 1380

gctcttctaa tggtggtcgc cttcttttac aacctgggga ttgctcccgt tgtcttttgc 1440

ttagtttctg aaataccatc ctcgaggcta agaactaaat caattattct ggctcgtaac 1500

gcctataata tggcatgtat cgtaactgct gtcctgacat tgtaccaatt gaattcagaa 1560

aaatgggatt ggggtgcaaa gtcaggcttc ttctgggggg gactatgttt tgcgacgtta 1620

gtatgggctg tcattgattt acccgaaact gccggtagaa cctttatgga aatgaacgaa 1680

ctatttagac tcggtattcc agcaagaaag ttcaagacga ctaaagtgga cccatttgcg 1740

gctgtcaaag cggctaaaga aattgctcat aatgatccca aggaagatat ggaaacttcc 1800

atggtggaag aagggcgaag cacaccatct attacgaatt tatga 1845

<210> SEQ ID NO 12
<211> LENGTH: 1833
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: yHAB47 lager hybrid lgAGT1

<400> SEQUENCE: 12

atgaaaaata tactttcgct ggtaggaaga aaggaaaata ccccagaaga tgtgacggcg 60

aatcttgcgg acacctcaag cactacagtt atgcaagcaa aggacttggt tattgaggac 120

tttgaagaac gaaagaaaaa cgatgcattt gagttgaatc acttggagct cactactaat 180

gcaacacagt taagcgattc tgatgaagac aaagaaaatg taatcagagt ggcagaagct 240

actgatgatg cgaacgaagc taataacgaa gagaagagca tgactttaag acaagctttg 300

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cgaaaatatc caaaggcagc gctatggtct attttggtat ctactacgct tgttatggaa 360

ggttatgata ctgcactttt aagtgcactt tatgcattgc cagtttttca gaggaagttt 420

gggactatga atgcggaagg ctcctacgaa atcacttcgc agtggcaaat tggcttgaac 480

atgtgtgttc tttgtggtga aatgattggt ctacagataa ccacttacat ggtcgagttc 540

atgggtaatc gttatacaat gattacggcg ctttctcttt tgactgctta tatctttatc 600

ctttactatt gcaagagttt ggccatgatt gctgtaggac aaattctttc ggctatgcca 660

tggggttgct tccagagtct ggctgttacc tatgcttctg aagtttgccc cctggcattg 720

agatattaca tgaccagtta ctccaacatt tgttggttgt ttggtcaaat ttttgcttct 780

ggaatcatga aaaattccca ggagaatttg ggaaactccg acttaggtta caagttacca 840

ttcgccttac aatggatctg gcctgcaccc ttaattattg gtatcttttt cgctcctgag 900

tcgccttggt ggttggtaag aaagaataag atcgtggaag ccaaaaagtc tttgaacaga 960

attctgagtg gcactgttac cgagaaggag atacaagtgg atattacttt gaagcaaatt 1020

gaaatgacca ttgagaagga aagacttcgg gcatccaaat cggggtcatt tttcagctgt 1080

ttcaagggag ttgatggaag aagaacgagg cttgcgtgtt tgacttgggt tgctcagaac 1140

agtagtggtg cagtattact tggttattcg acgtacttct ttgaaagagc aggcatggcc 1200

actgacaagg ccttcacttt ctcgctaatt caatactgtc ttggtttggc aggcacgctt 1260

ggttcctggg taatatctgg ccgtgttggt agatggacta tactgaccta tggtctttca 1320

ttccaaatgg tttgtctatt tatcattggc ggaatgggtt ttgcatccgg aagcagtgct 1380

agtaacgctg ctggtggcct actgcttgct ttatctttct tctataacgc gggtatcgga 1440

gctgtcgttt actgtattgt tgcagaaatc ccatccgcag aattaaggac caagaccatt 1500

gtgctggccc gtatttgcta caatctaatg gccgtcttca atgctattct aacgccctat 1560

atgcttaacg tgagcgactg gaactggggt gccaaaactg gtctatattg gggtggcttt 1620

accgcactca ctctggcttg ggtcattatt gatttgcccg agacaactgg cagaaccttt 1680

agcgaaatca atgaactttt cagtcaaggt gtccctgcta gaaaatttgc atctacagta 1740

gttgatccct ttggaaagag agggctacaa aatcgtccgc aagttgataa cattattgac 1800

cggttctcaa gcgcgagtca acaggcgtta tga 1833

<210> SEQ ID NO 13
<211> LENGTH: 1833
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces eubayanus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1833)
<223> OTHER INFORMATION: yHRVM108 ncAGT1

<400> SEQUENCE: 13

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tttgaagaac ggaagaaaaa cgatgcattt gagttaaatc acatggagct cactactaat 180

gcaacacagt taggcgattc tgatggagac aacgataatg caatcagagt ggcagaagct 240

actgatgatg cgaacgaagc taacaacgaa gagaaaagca tgactttaag acaagctttg 300

cgaaaatatc caaaggcagc gctatggtct attttggtat ctactacgct tgttatggaa 360

ggttatgata ccgcacttct aagtgcgctt tatgcattgc cagtttttca gaggaagttc 420

gggactatga atgcggaagg ctcctacgaa atcacttcgc agtggcaaat tggcttgaac 480

atgtgtgttc tttgtggtga aatgattggt ttacagatga ccacttacat ggtcgagttc 540

atgggcaatc gttatacaat gattatggcg ctttttcttt tgactgctta tatttttatc 600

ctttactatt gcaagagttt agccatgatt gctgtaggac aaattctttc ggctatgcca 660

tggggttgct tccagagtct ggctgttacc tatgcttctg aagtttgccc cctggctttg 720

agatattaca tgaccagtta ctccaacatt tgttggttat ttggtcaaat ttttgcttct 780

ggaatcatga aaaattctca ggagaatttg ggagactccg acttgggtta caagttacca 840

ttcgccttac aatggatctg gcctgcaccc ttaattattg gtatcttctt cgctcctgag 900

tcgccatggt ggttagtaag aaagaataag atcgtggagg ccaaaaagtc tttgaacaga 960

attctgagtg gcactgctac cgagaaggag atacaagtgg atattacttt gaagcaaatt 1020

gaaatgacca ttgagaagga aagacttcgt gcatccgaat cggggtcatt tttcagctgt 1080

ttcaagggag ttgatggaag aagaacgaga cttgcgtgtt tgacttgggt tgctcagaac 1140

agtagtggtg cagttttact tggttattcg acctatttct ttgaaagagc aggcatggac 1200

actgacaagg ctttcacttt ctcgcttatt cagtactgtc ttggtttggc aggcactctt 1260

tgttcttggg taatttctgg ccgtgttggt agatggacta tactgaccta tggtctttca 1320

ttccaaatgg tttgtctatt tatcattggc ggaatgggtt ttgcatccgg aagcagtgct 1380

agtaacgctg ctggtggcct actgcttgcg ttatcttttt tctataacgc gggtatcgga 1440

gctgtcgttt actgtattgt tgcagagatc ccatccgcgg aattaaggac caagactatt 1500

gtgctggctc gtatttgcta caatctaatg gccgtcttca atgctattct aacgccctat 1560

atgcttaacg tgagcgactg gaactggggt gccaaaactg gtctatattg gggtggcttc 1620

accgcactca ctctcgcttg ggtcattatt gatttgcccg agacaactgg cagaaccttt 1680

agcgaaatca atgaactttt caatcaaggt gtccctgcta gaaaatttgc atctacagta 1740

gttgatcctt ttggaaagag cgggttaaag aatcttccgc aagttgatga cattattgac 1800

cggtcctcaa gcatgagtca gcaggcatta taa 1833

<210> SEQ ID NO 14
<211> LENGTH: 1851
<212> TYPE: DNA
<213> ORGANISM: Saccharomyces cerevisiae
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1851)
<223> OTHER INFORMATION: AGT1 from strain S288c

<400> SEQUENCE: 14

atgaaaaata tcatttcatt ggtaagcaag aagaaggctg cctcaaaaaa tgaggataaa 60

aacatttctg agtcttcaag agatattgta aaccaacagg aggttttcaa tactgaagat 120

tttgaagaag ggaaaaagga tagtgccttt gagctagacc acttagagtt caccaccaat 180

tcagcccagt taggagattc tgacgaagat aacgagaatg tgattaatga gatgaacgct 240

actgatgatg caaatgaagc taacagcgag gaaaaaagca tgactttgaa gcaggcgttg 300

ctaaaatatc caaaagcagc cctgtggtcc atattagtgt ctactaccct ggttatggaa 360

ggttatgata ccgcactact gagcgcactg tatgccctgc cagtttttca gagaaaattc 420

ggtactttga acggggaggg ttcttacgaa attacttccc aatggcagat tggtttaaac 480

atgtgtgtcc tttgtggtga gatgattggt ttgcaaatca cgacttatat ggttgaattt 540

atggggaatc gttatacgat gattacagca cttggtttgt taactgctta tatctttatc 600

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ctctactact gtaaaagttt agctatgatt gctgtgggac aaattctctc agctatacca    660

tggggttgtt tccaaagttt ggctgttact tatgcttcgg aagtttgccc tttagcatta    720

agatattaca tgaccagtta ctccaacatt tgttggttat ttggtcaaat cttcgcctct    780

ggtattatga aaaactcaca agagaattta gggaactccg acttgggcta taaattgcca    840

tttgctttac aatggatttg gcctgctcct ttaatgatcg gtatcttttt cgctcctgag    900

tcgccctggt ggttggtgag aaaggatagg gtcgctgagg caagaaaatc tttaagcaga    960

attttgagtg gtaaaggcgc cgagaaggac attcaagttg atcttacttt aaagcagatt   1020

gaattgacta ttgaaaaaga aagactttta gcatctaaat caggatcatt ctttaattgt   1080

ttcaagggag ttaatggaag aagaacgaga cttgcatgtt taacttgggt agctcaaaat   1140

agtagcggtg ccgttttact tggttactcg acatattttt ttgaaagagc aggtatggcc   1200

accgacaagg cgtttacttt ttctctaatt cagtactgtc ttgggttagc gggtacactt   1260

tgctcctggg taatatctgg ccgtgttggt agatggacaa tactgaccta tggtcttgca   1320

tttcaaatgg tctgcttatt tattattggt ggaatgggtt ttggttctgg aagcagcgct   1380

agtaatggtg ccggtggttt attgctggct ttatcattct tttacaatgc tggtatcggt   1440

gcagttgttt actgtatcgt tgctgaaatt ccatcagcgg agttgagaac taagactata   1500

gtgctggccc gtatttgcta caatctcatg gccgttatta acgctatatt aacgccctat   1560

atgctaaacg tgagcgattg gaactggggt gccaaaactg gtctatactg gggtggtttc   1620

acagcagtca ctttagcttg ggtcatcatc gatctgcctg agacaactgg tagaaccttc   1680

agtgaaatta atgaactttt caaccaaggg gttcctgcca gaaaatttgc atctactgtg   1740

gttgatccat tcggaaaggg aaaaactcaa catgattcgc tagctgatga gagtatcagt   1800

cagtcctcaa gcataaaaca gcgagaatta aatgcagctg ataaatgtta a             1851
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<210> SEQ ID NO 15
<211> LENGTH: 616
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: yHAB47 lager hybrid scAGT1

<400> SEQUENCE: 15

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Met Lys Asn Ile Ile Ser Leu Val Ser Lys Lys Lys Ala Ala Ser Lys
1               5                   10                  15

Asn Glu Asp Lys Asn Ile Ser Glu Ser Ser Arg Asp Ile Val Asn Gln
            20                  25                  30

Gln Glu Val Phe Asn Thr Glu Asn Phe Glu Glu Gly Lys Lys Asp Ser
        35                  40                  45

Ala Phe Glu Leu Asp His Leu Glu Phe Thr Thr Asn Ser Ala Gln Leu
    50                  55                  60

Gly Asp Ser Asp Glu Asp Asn Glu Asn Met Ile Asn Glu Met Asn Ala
65                  70                  75                  80

Thr Asp Glu Ala Asn Glu Ala Asn Ser Glu Glu Lys Ser Met Thr Leu
                85                  90                  95

Lys Gln Ala Leu Leu Lys Tyr Pro Lys Ala Ala Leu Trp Ser Ile Leu
            100                 105                 110

Val Ser Thr Thr Leu Val Met Glu Gly Tyr Asp Thr Ala Leu Leu Asn
        115                 120                 125

Ala Leu Tyr Ala Leu Pro Val Phe Gln Arg Lys Phe Gly Thr Leu Asn
    130                 135                 140
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Gly Glu Gly Ser Tyr Glu Ile Thr Ser Gln Trp Gln Ile Gly Leu Asn
145                 150                 155                 160

Met Cys Val Gln Cys Gly Glu Met Ile Gly Leu Gln Ile Thr Thr Tyr
                165                 170                 175

Met Val Glu Phe Met Gly Asn Arg Tyr Thr Met Ile Thr Ala Leu Gly
            180                 185                 190

Leu Leu Thr Ala Tyr Ile Phe Ile Leu Tyr Tyr Cys Lys Ser Leu Ala
        195                 200                 205

Met Ile Ala Val Gly Gln Val Leu Ser Ala Met Pro Trp Gly Cys Phe
    210                 215                 220

Gln Gly Leu Thr Val Thr Tyr Ala Ser Glu Val Cys Pro Leu Ala Leu
225                 230                 235                 240

Arg Tyr Tyr Met Thr Ser Tyr Ser Asn Ile Cys Trp Leu Phe Gly Gln
                245                 250                 255

Ile Phe Ala Ser Gly Ile Met Lys Asn Ser Gln Glu Asn Leu Gly Asn
            260                 265                 270

Ser Asp Leu Asp Tyr Lys Leu Pro Phe Ala Leu Gln Trp Ile Trp Pro
        275                 280                 285

Ala Pro Leu Met Ile Gly Ile Phe Phe Ala Pro Glu Ser Pro Trp Trp
    290                 295                 300

Leu Val Arg Lys Asp Arg Val Ala Glu Ala Arg Lys Ser Leu Ser Arg
305                 310                 315                 320

Ile Leu Ser Gly Lys Gly Ala Glu Lys Asp Ile Gln Val Asp Leu Thr
                325                 330                 335

Leu Lys Gln Ile Glu Leu Thr Ile Glu Lys Glu Arg Leu Leu Ala Ser
            340                 345                 350

Lys Ser Gly Ser Phe Phe Asp Cys Phe Lys Gly Val Asn Gly Arg Arg
        355                 360                 365

Thr Arg Leu Ala Cys Leu Ala Trp Val Ala Gln Asn Thr Ser Gly Ala
    370                 375                 380

Cys Leu Leu Gly Tyr Ser Thr Tyr Phe Phe Glu Arg Ala Gly Met Ala
385                 390                 395                 400

Thr Asp Lys Ala Phe Thr Phe Ser Val Ile Gln Tyr Cys Leu Gly Leu
                405                 410                 415

Ala Gly Thr Leu Cys Ser Trp Val Ile Ser Gly Arg Val Gly Arg Trp
            420                 425                 430

Thr Ile Leu Thr Tyr Gly Leu Ala Phe Gln Met Val Cys Leu Phe Val
        435                 440                 445

Ile Gly Gly Met Gly Phe Gly Ser Gly Ser Gly Ala Ser Asn Gly Ala
    450                 455                 460

Gly Gly Leu Leu Leu Ala Leu Ser Phe Phe Tyr Asn Ala Gly Ile Gly
465                 470                 475                 480

Ala Val Val Tyr Cys Ile Val Ala Glu Ile Pro Ser Ala Glu Leu Arg
                485                 490                 495

Thr Lys Thr Ile Val Leu Ala Arg Ile Cys Tyr Asn Leu Met Ala Val
            500                 505                 510

Ile Asn Ala Ile Leu Thr Pro Tyr Met Leu Asn Val Ser Asp Trp Asn
        515                 520                 525

Trp Gly Ala Lys Thr Gly Leu Tyr Trp Gly Gly Phe Thr Ala Val Thr
    530                 535                 540

Leu Ala Trp Val Ile Ile Asp Leu Pro Glu Thr Thr Gly Arg Thr Phe
545                 550                 555                 560

Ser Glu Ile Asn Glu Leu Phe Asn Gln Gly Val Pro Ala Arg Lys Phe
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               565                 570                 575

Ala Ser Thr Val Val Asp Pro Phe Gly Lys Gly Lys Thr Gln His Asp
            580                 585                 590

Ser Leu Ala Asp Glu Ser Ile Ser Gln Ser Ser Ser Ile Lys Gln Arg
        595                 600                 605

Glu Leu Asn Ala Ala Asp Lys Cys
    610                 615


<210> SEQ ID NO 16
<211> LENGTH: 1851
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: yHAB47 lager hybrid scAGT1

<400> SEQUENCE: 16

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aacatttctg agtcttcaag agatattgta aaccaacagg aggttttcaa tactgaaaat    120

tttgaagaag ggaaaaagga tagtgccttt gagctagacc acttagagtt caccaccaat    180

tcagcccagt taggagattc tgacgaagat aacgagaata tgattaatga gatgaacgct    240

actgatgaag caaatgaagc taacagcgag gaaaaaagca tgactttaaa gcaggcgttg    300

ctaaaatatc caaaagcagc cctgtggtcc atattagtgt ctactaccct ggttatggaa    360

ggttatgata ccgcactact gaacgcactg tatgccctgc cagtgtttca gagaaaattc    420

ggtactttga acggggaggg ttcttacgaa attacttccc aatggcagat tggtttaaac    480

atgtgtgtcc aatgtggtga gatgattggt ttgcaaatca cgacttatat ggttgaattt    540

atggggaatc gttatacgat gattacagca cttggtttgt taactgctta tatctttatc    600

ctctactact gtaaaagttt agctatgatt gctgtgggac aagttctctc agctatgcca    660

tggggttgtt tccagggttt gactgttact tatgcttcgg aagtttgccc tttagcatta    720

agatattaca tgaccagtta ctccaacatt tgttggttat ttggtcaaat cttcgcctct    780

ggtattatga aaaactcaca agagaattta gggaactctg acttggacta taaattgcca    840

tttgctttac aatggatttg gcctgctcct ttaatgatcg gtatcttttt cgctcctgag    900

tcgccctggt ggttggtgag aaaggatagg gtcgctgagg caagaaaatc tttaagcaga    960

attttgagtg gtaaaggcgc cgagaaggac attcaagttg atcttacttt aaagcagatt   1020

gaattgacta ttgaaaaaga aagactttta gcatctaaat caggatcatt ctttgattgt   1080

ttcaagggag ttaatggaag aagaacgaga cttgcatgtt tagcttgggt agctcaaaat   1140

actagcggtg cctgtttact tggttactcg acatattttt ttgaaagagc aggtatggcc   1200

accgacaagg cgtttacttt ttctgtaatt cagtactgtc ttgggttagc gggtacactt   1260

tgctcctggg taatatctgg ccgtgttggt agatggacaa tactgaccta tggtcttgca   1320

tttcaaatgg tctgcttatt tgttattggt ggaatgggtt ttggttctgg aagcggcgct   1380

agtaatggtg ccggtggttt attgctggct ttatcattct tttacaatgc tggtatcggt   1440

gcagttgttt actgtatcgt agctgaaatt ccatcagcgg agttgagaac taagactata   1500

gtgctggccc gtatttgcta caatctcatg gccgttatca acgctatatt aacgccctat   1560

atgctaaacg tgagcgattg gaactggggt gccaaaactg gtctatactg gggtggtttc   1620

acagcagtca ctttagcttg ggtcatcatc gatctgcctg agacaactgg tagaaccttc   1680

agtgaaatta atgaactttt caaccaaggg gttcctgcca gaaaatttgc atctactgtg   1740
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gttgatccat tcggaaaggg aaaaactcaa catgattcgc tagctgatga gagtatcagt 1800

cagtcctcaa gcataaaaca gcgagaatta aatgcagctg ataaatgtta a 1851

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<212> TYPE: DNA
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<220> FEATURE:
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<210> SEQ ID NO 19
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<212> TYPE: DNA
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<400> SEQUENCE: 19

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<210> SEQ ID NO 22
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<212> TYPE: DNA
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<210> SEQ ID NO 33
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<210> SEQ ID NO 34
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<210> SEQ ID NO 38
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<400> SEQUENCE: 43

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<210> SEQ ID NO 44
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<210> SEQ ID NO 45
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ccgtgagtat cagagcatcc 20

<210> SEQ ID NO 47
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<223> OTHER INFORMATION: oHECPB173 primer

<400> SEQUENCE: 50

cttagtagca gcgacatatt caag 24

<210> SEQ ID NO 51
<211> LENGTH: 27
<212> TYPE: DNA
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<223> OTHER INFORMATION: oHCT770 primer

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aactcttgtt ttcttctttt ctctaaa 27

<210> SEQ ID NO 52
<211> LENGTH: 22
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<220> FEATURE:
<223> OTHER INFORMATION: oHCT771 primer

<400> SEQUENCE: 52

gggacctaga cttcaggttg tc 22

We claim:

1. A polynucleotide encoding a polypeptide comprising at least 95% sequence identity to SEQ ID NO: 4 and comprising at least six amino acid substitutions to SEQ ID NO: 4 at positions selected from the group consisting of S468, I503, G504, N505, V508, I512, N522, F534, L536, V538, and I540; or a functional fragment of the polypeptide thereof, wherein the polypeptide or functional fragment thereof has maltotriose transporter activity.

2. The polynucleotide of claim **1**, wherein the polynucleotide comprises SEQ ID NO: 9.

3. A DNA construct comprising a promoter operably linked to the polynucleotide of claim **1**.

4. A vector comprising the DNA construct of claim **3**.

5. A *Saccharomyces* yeast cell comprising the polynucleotide of claim **1**.

6. A *Saccharomyces* yeast cell modified to increase as compared to a control yeast cell the expression or maltose/maltotriose transport activity of a maltose/maltotriose transporter polypeptide, wherein the yeast cell comprises a polynucleotide encoding a polypeptide having at least 95% sequence identity to SEQ ID NO: 4 and comprising at least six amino acid substitutions to SEQ ID NO: 4, wherein the amino acid substitutions are at positions selected from the group consisting of S468, I503, G504, N505, V508, I512, N522, F534, L536, V538, and I540, or a functional fragment thereof having maltotriose transporter activity.

7. The yeast cell of claim **6**, wherein the increased expression or increased maltose/maltotriose transport activity of the maltose/maltotriose transporter polypeptide is at the plasma membrane of the yeast cell.

8. The yeast cell of claim **6**, wherein the expression or maltose/maltotriose transport activity of the maltose/maltotriose transporter polypeptide is increased by at least 30% as compared to the control yeast cell.

9. The yeast cell of claim **6**, wherein the yeast cell is selected from the species consisting of *Saccharomyces eubayanus, Saccharomyces cerevisiae, Saccharomyces paradoxus, Saccharomyces mikatae, Saccharomyces arboricola, Saccharomyces kudriavzevii, Saccharomyces jurei, and Saccharomyces uvarum.*

10. A method for making a fermentation product comprising culturing the yeast cells of claim **5** with a fermentable substrate to produce the fermentation product.

11. The method of claim **10**, wherein the fermentable substrate comprises wort or malt extract.

12. The method of claim **10**, wherein the fermentation product is selected from the group consisting of a beer product, a wine product, an alcoholic beverage, a biochemical, and a biofuel.

* * * * *