CLAIMS

What is claimed is:

1. A variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity to an amino acid sequence as set forth in SEQ ID NO:26 based on a Clustal W method of alignment and having an amino acid change from arginine to alanine or arginine to leucine at position 300, and comprising:

(a) at least one additional amino acid change selected from the group consisting of:

(i) glutamine to histidine at position 353

(ii) leucine to proline at position 61;

(iii) phenylalanine to leucine at position 159;

(iv) glycine to cysteine at position 162;

(v) proline to histidine at position 169;

(vi) leucine to tryptophan at position 61;

(vii) leucine to histidine at position 61;

(viii) leucine to phenylalanine at position 61; and

(ix) leucine to tyrosine at position 61; or

(b) a length of 402 to 407 amino acids from the N-terminus; or

(c) a length of 402 to 407 amino acids from the N-terminus, and having at least one of the amino acid changes of (a).

2. A variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity based on a Clustal W method of alignment to an amino acid sequence selected from the group consisting of SEQ ID NOs: 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, and 98, and comprising an amino acid at an equivalent position when compared with a reference amino acid sequence of SEQ ID NO:26 selected from the group consisting of:

(a) alanine at a position equivalent to position 300; and

(b) leucine at a position equivalent to position 300.

3. The variant sucrose transporter polypeptide of claim 2, wherein the variant sucrose transporter polypeptide further comprises:

(a) at least one of the following amino acids at an equivalent position when compared with the reference amino acid sequence of SEQ ID NO:26:

(i) histidine at a position equivalent to position 353;

(ii) proline at a position equivalent to position 61;

(iii) leucine at a position equivalent to position 159;

(iv) cysteine at a position equivalent to position 162;

(v) histidine at a position equivalent to position 169;

(vi) tryptophan at a position equivalent to position 61;

(vii) histidine at a position equivalent to position 61;

(viii) phenylalanine at a position equivalent to position 61;

(ix) tyrosine at a position equivalent to position 61; and/or

(b) truncation at a position equivalent to position 407, 406, 405, 404, 403, or 402 when compared with the reference amino acid sequence of SEQ ID NO:26.

4. A recombinant bacterium comprising in its genome or on at least one recombinant construct:

(a) a nucleotide sequence encoding a variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity based on a Clustal W method of alignment to an amino acid sequence selected from the group consisting of SEQ ID NOs:26, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, and 98,and an amino acid at an equivalent position when compared with a reference amino acid sequence of SEQ ID NO:26 selected from the group consisting of:

(i) alanine at a position equivalent to position 300; and

(ii) leucine at a position equivalent to position 300; and

(b) a nucleotide sequence encoding a polypeptide having sucrose hydrolase activity;

wherein (a) and (b) are each operably linked to the same or a different promoter, further wherein said recombinant bacterium is capable of metabolizing sucrose.

5. The recombinant bacterium of claim 4, wherein the variant sucrose transporter polypeptide further comprises:

(a) at least one of the following amino acids at an equivalent position when compared with the reference amino acid sequence of SEQ ID NO:26:

(i) histidine at a position equivalent to position 353;

(ii) proline at a position equivalent to position 61;

(iii) leucine at a position equivalent to position 159;

(iv) cysteine at a position equivalent to position 162;

(v) histidine at a position equivalent to position 169;

(vi) tryptophan at a position equivalent to position 61;

(vii) histidine at a position equivalent to position 61;

(viii) phenylalanine at a position equivalent to position 61;

(ix) tyrosine at a position equivalent to position 61; and/or

(b) truncation at a position equivalent to position 407, 406, 405, 404, 403, or 402 when compared with the reference amino acid sequence of SEQ ID NO:26.

6. The recombinant bacterium of claim 4, wherein the polypeptide having sucrose hydrolase activity is classified as EC 3.2.1.26 or EC 2.4.1.7.

7. The recombinant bacterium of claim 4 further comprising in its genome or on at least one recombinant construct, a nucleotide sequence encoding a polypeptide having fructokinase activity.

8. The recombinant bacterium of claim 7, wherein the polypeptide having fructokinase activity is classified as EC 2.7.1.4, EC

2.7.1.3, or EC 2.7.1.1.

9. The recombinant bacterium of claim 4, wherein said bacterium is selected from the group consisting of the genera: *Escherichia*, *Klebsiella*, *Citrobacter*, and *Aerobacter*.

10. The recombinant bacterium of claim 9, wherein said bacterium is *Escherichia coli*.

11. The recombinant bacterium of claim 4, wherein the recombinant bacterium produces 1,3-propanediol, glycerol, and/or 3-hydroxypropionic acid.

12. A process for making glycerol, 1,3-propanediol and/or 3-hydroxypropionic acid from sucrose comprising:

a) culturing the recombinant bacterium of claim 11 in the presence of sucrose; and

b) optionally, recovering the glycerol, 1,3-propanediol and/or 3-hydroxypropionic acid produced

What is claimed is:

1. A variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity to an amino acid sequence as set forth in SEQ ID NO:26 based on a Clustal W method of alignment and having an amino acid change from arginine to alanine or arginine to leucine at position 300, and comprising:

(a) at least one additional amino acid change selected from the group consisting of:

(i) glutamine to histidine at position 353

(ii) leucine to proline at position 61;

(iii) phenylalanine to leucine at position 159;

(iv) glycine to cysteine at position 162;

(v) proline to histidine at position 169;

(vi) leucine to tryptophan at position 61;

(vii) leucine to histidine at position 61;

(viii) leucine to phenylalanine at position 61; and

(ix) leucine to tyrosine at position 61; or

(b) a length of 402 to 407 amino acids from the N-terminus; or

(c) a length of 402 to 407 amino acids from the N-terminus, and having at least one of the amino acid changes of (a).

2. A variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity based on a Clustal W method of alignment to an amino acid sequence selected from the group consisting of SEQ ID NOs: 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, and 98, and comprising an amino acid at an equivalent position when compared with a reference amino acid sequence of SEQ ID NO:26 selected from the group consisting of:

(a) alanine at a position equivalent to position 300; and

(b) leucine at a position equivalent to position 300.

3. The variant sucrose transporter polypeptide of claim 2, wherein the variant sucrose transporter polypeptide further comprises:

(a) at least one of the following amino acids at an equivalent position when compared with the reference amino acid sequence of SEQ ID NO:26:

(i) histidine at a position equivalent to position 353;

(ii) proline at a position equivalent to position 61;

(iii) leucine at a position equivalent to position 159;

(iv) cysteine at a position equivalent to position 162;

(v) histidine at a position equivalent to position 169;

(vi) tryptophan at a position equivalent to position 61;

(vii) histidine at a position equivalent to position 61;

(viii) phenylalanine at a position equivalent to position 61;

(ix) tyrosine at a position equivalent to position 61; and/or

(b) truncation at a position equivalent to position 407, 406, 405, 404, 403, or 402 when compared with the reference amino acid sequence of SEQ ID NO:26.

4. A recombinant bacterium comprising in its genome or on at least one recombinant construct:

(a) a nucleotide sequence encoding a variant sucrose transporter polypeptide having an amino acid sequence that has at least 95% identity based on a Clustal W method of alignment to an amino acid sequence selected from the group consisting of SEQ ID NOs:26, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, and 98, and an amino acid at an equivalent position when compared with a reference amino acid sequence of SEQ ID NO:26 selected from the group consisting of:

(i) alanine at a position equivalent to position 300; and

(ii) leucine at a position equivalent to position 300; and

(b) a nucleotide sequence encoding a polypeptide having sucrose hydrolase activity;

wherein (a) and (b) are each operably linked to the same or a different promoter, wherein each of (a) and (b): (i) is on a recombinant construct; (ii) encodes a polypeptide

comprising a non-native polypeptide; (iii) comprises a foreign gene; or (iv) is any combination of (i), (ii) or (iii), and further wherein said recombinant bacterium is capable of metabolizing sucrose.

5. The recombinant bacterium of claim 4, wherein the variant sucrose transporter polypeptide further comprises:

(a) at least one of the following amino acids at an equivalent position when compared with the reference amino acid sequence of SEQ ID NO:26:

(i) histidine at a position equivalent to position 353;

(ii) proline at a position equivalent to position 61;

(iii) leucine at a position equivalent to position 159;

(iv) cysteine at a position equivalent to position 162;

(v) histidine at a position equivalent to position 169;

(vi) tryptophan at a position equivalent to position 61;

(vii) histidine at a position equivalent to position 61;

(viii) phenylalanine at a position equivalent to position 61;

(ix) tyrosine at a position equivalent to position 61; and/or

(b) truncation at a position equivalent to position 407, 406, 405, 404, 403, or 402 when compared with the reference amino acid sequence of SEQ ID NO:26.

6. The recombinant bacterium of claim 4 or claim 5, wherein the polypeptide having sucrose hydrolase activity is classified as EC 3.2.1.26 or EC 2.4.1.7.

7. The recombinant bacterium of claim 4 or claim 5 further comprising in its genome or on at least one recombinant construct, a nucleotide sequence encoding a polypeptide having fructokinase activity.

8. The recombinant bacterium of claim 7, wherein the polypeptide having fructokinase activity is classified as EC 2.7.1.4, EC 2.7.1.3, or EC 2.7.1.1.

9. The recombinant bacterium of claim 4 or claim 5, wherein said bacterium is selected from the group consisting of the genera: *Escherichia*, *Klebsiella*, *Citrobacter*, and *Aerobacter*.

10. The recombinant bacterium of claim 9, wherein said bacterium is *Escherichia coli*.

11. The recombinant bacterium of claim 4 or claim 5, wherein the recombinant bacterium produces 1,3-propanediol, glycerol, and/or 3-hydroxypropionic acid.

12. A process for making glycerol, 1,3-propanediol and/or 3-hydroxypropionic acid from sucrose comprising:

a) culturing the recombinant bacterium of claim 11 in the presence of sucrose; and

b) optionally, recovering the glycerol, 1,3-propanediol and/or 3-hydroxypropionic acid produced.