## CLAIMS

What is claimed is:

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

(a) one or more nucleotide sequences encoding a polypeptide or a polypeptide complex having sucrose transporter activity;

(b) a nucleotide sequence encoding a polypeptide having fructokinase activity; ~~and~~

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

(d) a nucleotide sequence encoding a polypeptide having dehydratase activity;

wherein (a), (b) and (c) are each operably linked to the same or a different promoter,

further wherein said recombinant bacterium is capable of metabolizing sucrose to produce a product selected from the group consisting of glycerol, 1,3-propanediol and 3-hydroxypropionic acid.

2. The recombinant bacterium of claim 1 wherein the polypeptide having sucrose transporter activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:24, SEQ ID NO:26, or SEQ ID NO:28.

3. The recombinant bacterium of claim 1 wherein the polypeptide complex having sucrose transporter activity comprises:

(a) a first subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:30;

(b) a second subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:32; and

(c) a third subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:34.

4. The recombinant bacterium of claim 1 wherein the polypeptide complex having sucrose transporter activity comprises:

(a) a first subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:36;

(b) a second subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:38;

(c) a third subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:40; and

(d) a fourth subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:42.

5. The recombinant bacterium of claim 1 wherein the polypeptide having fructokinase activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:85, or SEQ ID NO:87.

6. The recombinant bacterium of claim 1 wherein the polypeptide having sucrose hydrolase activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, or SEQ ID NO:68.

7. The recombinant bacterium of claim 1 wherein the polypeptide having sucrose transporter activity consists of ~~corresponds substantially to~~ the sequence set forth in SEQ ID NO:26.

8. The recombinant bacterium of claim 1 wherein the polypeptide having fructokinase activity consists of ~~corresponds substantially to~~ the sequence set forth in SEQ ID NO:48.

9. The recombinant bacterium of claim 1 wherein the polypeptide having sucrose hydrolase activity consists of ~~corresponds substantially to~~ the sequence set forth in SEQ ID NO:58.

10. The recombinant bacterium of any of claims 1-9 wherein said bacterium is selected from the group consisting of the genera: *Escherichia*, *Klebsiella*, *Citrobacter*, and *Aerobacter*.

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

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

(a) culturing the recombinant bacterium of any of claims 1-~~9~~11 in the presence of sucrose; and

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

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

(a) culturing a ~~the~~ recombinant bacterium ~~of claim 10~~ in the presence of sucrose, said recombinant bacterium comprising in its genome or on at least one recombinant construct:

(i) one or more nucelotide sequences encoding a polypeptide or a polypeptide complex having sucrose transporter activity;

(ii) a nucleotide sequence encoding a polypeptide having

fructokinase activity; and

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

wherein (i), (ii) and (iii) are each operably liked to the same or a different promoter;

further wherein said recombinant bacterium metabolizes said sucrose to produce a product selected from the group consisting of glycerol, 1,3-propanediol and 3-hydroxypropionic acid; and

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

14. The process of claim 13 wherein the polypeptide having sucrose transporter activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:24, SEQ ID NO:26, or SEQ ID NO:28.

15. The process of claim 13 wherein the polypeptide complex having sucrose transporter activity comprises:

(a) a first subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:30;

(b) a second subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:32; and

(c) a third subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:34.

16. The process of claim 13 wherein the polypeptide complex having sucrose transporter activity comprises:

(a) a first subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:36;

(b) a second subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:38;

(c) a third subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:40; and

(d) a fourth subunit having at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:42.

17. The process of claim 13 wherein the polypeptide having fructokinase activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:85, or SEQ ID NO:87.

18. The process of claim 13 wherein the polypeptide having sucrose hydrolase activity has at least 95% sequence identity, based on a Clustal V method of alignment, when compared to an amino acid sequence as set forth in SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, or SEQ ID NO:68.

19. The process of claim 13 wherein the polypeptide having sucrose transporter activity consists of the sequence set forth in SEQ ID NO:26.

20. The process of claim 13 wherein the polypeptide having fructokinase activity consists of the sequence set forth in SEQ ID NO:48.

21. The process of claim 13 wherein the polypeptide having sucrose hydrolase activity consists of the sequence set forth in SEQ ID NO:58.

22. The process of any of claims 13-21 wherein said bacterium is selected from the group consisting of the genera: *Escherichia*, *Klebsiella*, *Citrobacter*, and *Aerobacter*.

23. The process of claim 22 wherein said bacterium is *Escherichia coli*.