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(54) Title: MICROAEROBIC CULTURES FOR CONVERTING GLYCEROL TO CHEMICALS

(57) Abstract: Glycerol or other reduced carbon sources may be used as a feedstock for the microbial production of chemical products under certain microaerobic conditions. For example, such production may occur under microaerobic or microrespiratory conditions in which electron acceptors are consumed in the reaction as quickly as they are added. In such reactions, the reaction product is at least as reduced as carbon source. Further, during such a reaction, at least some of the carbon source is used to generate cell mass. In addition, microorganisms with modified genomes are provided for carrying out the methods herein.

**MICROAEROBIC CULTURES FOR CONVERTING
GLYCEROL TO CHEMICALS**

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to US Provisional Application No. 61/109018, filed October 28, 2008 and incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under Grant Number CBET-0645188 awarded by the National Science Foundation and under Grant Number 2005-35504-16698 awarded by the United States Department of Agriculture. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] In recent years, there has been a significant increase in the production and use of biofuels, such as biodiesel and bioethanol, generally produced by transesterification using vegetable oils or animal fats and an alcohol. A byproduct of this reaction is glycerol, and there is currently a surplus of waste glycerol produced in biofuel plants.

[0004] Glycerol is a viscous liquid that is difficult to process, and it is generally disposed of by incineration or chemical processing. However, such strategies negate the positive environmental impact of using biodiesel fuels. For example, incineration of glycerol may release pollutants into the air. Rather than disposing of the glycerol, it would be better to process the glycerol into another chemically useful product.

[0005] Glycerol can be used as a feedstock in biological conversion, a process in which a microorganism enzymatically converts glycerol into specific chemical products, such as ethanol or lactic acid. Conversion of glycerol to ethanol or other products is advantageous because they have value as fuel or as feedstocks for other processes.

[0006] Anaerobic fermentation and aerobic respiration have been used for the industrial production of chemicals, and are the two methods applied to date for glycerol-based cultures. Oxygen rich respiration offers very efficient cell growth (growth rate and yield) and converts a

high percentage of the carbon source into carbon dioxide and cell mass (see table below). Anaerobic fermentation, on the other hand, results in poor cell growth, but the synthesis of several fermentation products at high yields (e.g. lactate, formate, ethanol, propionate, succinate, etc.).

Respiratory vs Fermentative Metabolism			
Variable	Anaerobic Fermentation	Anaerobic Respiration	Aerobic Respiration
Growth Rate	LOW	Intermediate	HIGH
Cell Mass	LOW	Intermediate	HIGH
Product Yields	HIGH	High/Intermediate	LOW
Capital Cost	LOW	LOW	HIGH
Energy Input	LOW	LOW	HIGH

[0007] Producing chemicals via oxygen rich processes, however, is more costly than using anaerobic methods for two reasons. First, aerobic fermenters are more expensive to build, due to both the higher cost per unit and the need for smaller fermenters with reduced economy of scale. Secondly, the aerobic fermenters are more costly to operate than their anaerobic counterparts due to low solubility of oxygen, which in turn requires high energy input to ensure appropriate supply of oxygen to the cells. This is especially relevant for the production of commodity chemicals, where fermentation costs can represent 50-90% of the total production cost.

[0008] Therefore, anaerobic methods are usually preferred where possible, and it is typical to grow cells to a large number aerobically, and then switch the cells to anaerobic culture for the production of desired molecules. Recently, another anaerobic method has been developed to biologically ferment glycerol into ethanol and other chemicals under anaerobic conditions. This method is described in co-pending WO2007115228, incorporated herein by reference in its entirety for all purposes. While an advantage of anaerobic fermentation of glycerol is the increased percentage yield of the desired end product, a disadvantage is slower bacterial growth associated with the lack of oxygen in the system. Thus, again what is needed in the art is a better system of culturing bacteria, using glycerol as a feedstock to produce high yields.

SUMMARY OF THE INVENTION

[0009] We provide herein a method of growing bacteria under microaerobic conditions that improves the yield of anaerobic cultures, yet is less costly than aerobic fermentations, using low but measurable oxygen, and sufficient to maintain redox balance, which we call “microaerobic.” Using glycerol as a feedstock, bacteria are grown under low oxygen conditions,

but with a small amount of oxygen or other electron acceptor such as nitrate or nitrite, so that ultimately the redox balance for the conversion of the substrate into the product in a stoichiometrically defined pathway is equal to or greater than zero and a fraction of the substrate is used to generate cell mass.

[00010] By “microaerobic” what is meant is 1-20 mg O₂/L/h or its equivalent. Preferably 2-15 O₂/L/h is used, and more preferably 3-10 or 5 mg O₂/L/h.

[00011] In addition to variations in the inlet gas flow rate or the composition of the inlet gas, microaerobic conditions can also be produced by decreasing the stir rate (thus decreasing the oxygenation of a large culture), or by adding more feedstock to increase the cell density (and hence higher oxygen demand), or combinations thereof.

[00012] By “deletion” (“Δ”) or “disruption” what is meant is that a gene or protein is changed such that only 10% of the activity of an appropriate control strain is retained. Preferably no detectable activity is retained. Genes can be partially or completely deleted, or interrupted with stop codons, or mutated so as to yield an inactive protein product. Proteins can also be inactivated with inhibitors or by suppression of expression or translation, and the like.

[00013] By “overexpression” what is meant is that a gene or protein is changed so as to result in at least 150% activity as compared with an appropriate control strain. Preferably as much as 2, 5 or 10 fold increases in activity are obtained. Overexpression can be achieved by mutating the protein to produce a more active form or a form that is resistant to inhibition, by removing inhibitors, or adding activators, and the like. Overexpression can also be achieved by removing repressors, adding multiple copies of the gene to the cell, or upregulating the endogenous gene, and the like.

[00014] There is provided a method for producing a chemical product in a microorganism that includes providing conditions to produce the product, wherein the degree of reduction balance for the conversion of the substrate into the product in a stoichiometrically defined pathway is equal to or greater than zero, the degree of reduction balance for the conversion of the substrate into cell mass is greater than zero, and a fraction of the substrate is used to generate cell mass. In addition, the degree of reduction balance for the conversion of the substrate into cell mass is greater than zero.

[00015] The chemical product so produced can be, but is not limited to, lactate, ethanol, and succinate.

BRIEF DESCRIPTION OF THE DRAWINGS

[00016] FIG. 1 illustrates the production of reducing equivalents generated by the metabolism of glucose, xylose, or glycerol to produce succinate, ethanol, lactate, and acetate in accordance with the present techniques;

[00017] FIG. 2 illustrates the relationship between glycerol, chemical products produced from glycerol, and cell mass; and the net production of reducing equivalents in accordance with the present techniques;

[00018] FIG. 3 illustrates the pathway for producing succinate from glycerol in accordance with the present techniques;

[00019] FIG. 4 illustrates the pathway for producing ethanol from glycerol in accordance with the present techniques;

[00020] FIG. 5 illustrates the pathway for producing lactate from glycerol in accordance with the present techniques;

[00021] FIG. 6A is a graph comparing the fermentation of glycerol in a wild-type bacterial strain under microaerobic conditions and anaerobic conditions;

[00022] FIG. 6B is a graph showing a characteristic profile of dissolved oxygen, OTR (volumetric oxygen transfer rate) and cell growth (OD_{550}) in a wild-type bacterial strain under microaerobic conditions;

[00023] FIG. 7 is a bar graph comparing the product and biomass yields of the fermentation of glycerol (solid bars), glucose (clear bars) and xylose (gray bars) in a wild-type bacterial strain under microaerobic conditions. Data is also shown for “oxygen yield”, which represents the amount of oxygen consumed in the metabolism of the specific substrate;

[00024] FIG. 8A is a graph comparing the production of ethanol, formate, and organic acids from glycerol under microaerobic conditions in a strain SY04 [pZSKLMgldA], which was engineered for the co-production of ethanol and formate (i.e. Δpta , $\Delta frdA$, $\Delta fdhF$, $gldA^+$, $dhaKLM^+$);

[00025] FIG. 8B is a graph comparing the production of ethanol, formate, and succinate from glycerol under microaerobic conditions in a mutagenic strain EH05 (pZSKLMgldA), which

was engineered for the co-production of ethanol and hydrogen (i.e. Δpta , $\Delta frdA$, $\Delta ldhA$, $gldA^+$, $dhaKLM^+$);

[00026] FIG. 9A is a bar graph comparing the product yields of the fermentation of glycerol in wild-type MG1655 and strain LA01 (pZSglpKglpD) engineered for the production of D-lactate under microaerobic conditions (i.e. $\Delta pflB$, $\Delta frdA$, $glpK^+$, $glpD^+$);

[00027] FIG. 9B is a bar graph comparing the concentration of products of the fermentation of glycerol in wild-type MG1655 and strain LA20 (pZSglpKglpD) engineered for the production of L-lactate under microaerobic conditions (i.e. $\Delta frdA$ Δpta $\Delta adhE$ $\Delta mgsA$ $\Delta ldhA$ (ldhbovis), $glpK^+$, $glpD^+$);

[00028] FIG. 9C is a bar graph comparing the concentration of products of the fermentation of glycerol in wild-type MG1655 and strain SA24 (pZSpyc) engineered for the production of succinate under microaerobic conditions (i.e. $\Delta adhE$ Δpta $\Delta poxB$ Δppc , pyc^+);

[00029] FIG. 10 illustrates the pathways engineered for the production of succinate from glycerol in exemplary mutagenic microorganisms in accordance with the present techniques;

[00030] FIG. 11 illustrates the pathways engineered for the production of ethanol from glycerol in exemplary mutagenic microorganisms in accordance with the present techniques; and

[00031] FIG. 12 illustrates the pathway engineered for the production of lactate from glycerol in exemplary mutagenic microorganisms in accordance with the present techniques.

DETAILED DESCRIPTION OF THE INVENTION

[00032] The synthesis of microbial cell mass from certain carbon sources may be harnessed under the appropriate conditions to produce a useful chemical product. The microbial synthesis of cell mass from carbon sources that are more reduced than biomass, such as glycerol, is a metabolic process that results in the net generation of reducing equivalents. Under reaction conditions in which there are substantially no electron acceptors available (e.g. under micro-respiratory or micro-aerobic conditions), conversion of some of the feedstock into a reduced product allows the reaction to maintain redox balance. The activity of this conversion to a reduced product facilitates attaining redox balance by consuming the excess reducing equivalents generated in the synthesis of cell mass from the carbon source. In many instances, a redox-balanced system allows for increased microbial growth, which in turn allows the reaction to produce increased amounts of the desired chemical product.

[00033] The present techniques may release redox constraints imposed by the incorporation of carbon sources into cellular biomass, a metabolic process that results in the generation of reducing equivalents when the carbon sources are more reduced than the biomass. For example, the low levels of oxygen available under microaerobic conditions may serve as a sink for the excess reducing equivalents, thus improving the redox balance, allowing the incorporation of a larger fraction of glycerol into cell mass, and generating additional ATP. In the present context, the terms “biomass” or “cell mass” relate to the amount of a given cell culture, *i.e.* any organism or living cell growing in a medium, that is actively growing. In general, the cell mass yield of a cell culture may be measured as gram cell mass obtained per liter of culture medium.

[00034] It is envisioned that the present techniques may be useful for the production of any suitable product wherein the degree of reduction balance for the conversion of the carbon source into the chemical product is equal to or greater than zero, *i.e.*, the conversion of glycerol into the chemical product does not consume more reducing equivalents than it produces. Such products may include alcohols, alcohol derivatives, sugar alcohols (*e.g.* ethanol, propanol, butanol, butanediol, arabitol, xylitol), organic acids (*e.g.* formate, succinate, propionate, fumarate, malate, lactate, propionate, pyruvate,), amino acids (*e.g.* alanine, asparagine, aspartic acid,), or lactones (*e.g.* gamma-butyrolactone, caprolactone/lactone).

Table 1: Analysis of redox balance for the conversion of glycerol into cell mass and selected products. In all cases, the products are synthesized through a redox-neutral or redox-generating pathway.

Pathway	Stoichiometry ^a (κ^b)	$\Delta\kappa^c$ (H ^d)
glycerol → cell mass	$C_3H_8O_3(14/3) \rightarrow 3CH_{1.9}O_{0.5}N_{0.2}(4.3)^e$	1.1 (0.55H)
glycerol → ethanol+formate ^f	$C_3H_8O_3(14/3) \rightarrow C_2H_6O(6) + CH_2O_2(2)$	0 (0H)
glycerol → succinate	$C_3H_8O_3(14/3) + CO_2(0) \rightarrow C_4H_6O_4(14/4)$	0 (0H)
glycerol → propionate	$C_3H_8O_3(14/3) \rightarrow C_3H_6O_2(14/3)$	0 (0H)
glycerol → lactate	$C_3H_8O_3(14/3) \rightarrow C_3H_6O_3(12/3)$	2 (1H)
glycerol → alanine	$C_3H_8O_3(14/3) \rightarrow C_3H_7NO_2(12/3)$	2 (1H)

^aPathway stoichiometry accounts only for carbon balance between reactants and products.

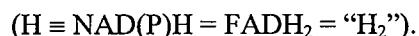
^bThe degree of reduction per carbon, K , was estimated as described elsewhere (Nielsen, J., J. Villadsen, and G. Liden. 2003. Bioreaction engineering principles, p.60-73. Kluwer Academic/Plenum Publishers, New York).

^cDegree of reduction balance ($\Delta\kappa$) is estimated as:

$$\sum_{\text{over } i \text{ reactants}} v_i c_i K_i - \sum_{\text{over } j \text{ products}} v_j c_j K_j$$

where v and c are the stoichiometric coefficients and the number of carbon atoms for each compound, respectively.

^aNet redox units, H, are expressed per mole of glycerol



^bCell mass formula is the average of reported for different microorganisms, including bacteria, yeast, and fungi (Nielsen et al., 2003). Conversion of glycerol into cell mass neglects carbon losses as 1-C metabolites. In consequence, the degree of reduction balance in this case represents the minimum amount of redox units generated.

^cSimilar results are obtained by considering the conversion of glycerol to ethanol and glycerol to H₂-CO₂.

Table 2: Analysis of redox balance for the conversion of glycerol into cell mass and selected fermentation products.

Pathway	Stoichiometry ^a (κ^b)	$\Delta\kappa^c$ (H ^d)
glycerol → cell mass	C ₃ H ₈ O ₃ (14/3) → 3CH _{1.9} O _{0.5} N _{0.2} (4.3) ^e	1.1 (0.55H)
glycerol → 1,2-PDO	C ₃ H ₈ O ₃ (14/3) → C ₃ H ₈ O ₂ (16/3)	-2 (-1H)
glycerol → 1,3-PDO	C ₃ H ₈ O ₃ (14/3) → C ₃ H ₈ O ₂ (16/3)	-2 (-1H)

^{a-f}as above.

Table 3: Analysis off redox balance for the conversion of sugars into cell mass and selected fermentation products. The synthesis of cell mass results in the net consumption of reducing equivalents (i.e., $\Delta\kappa < 0$). Products are synthesized through pathways that result in either net consumption of reducing equivalents (i.e., $\Delta\kappa < 0$) or neutral pathways (i.e., $\Delta\kappa = 0$). Redox balance in such cases can be achieved in the absence of electron acceptors.

Pathway	Stoichiometry ^a (κ^b)	$\Delta\kappa^c$ (H ^d)
glucose → cell mass	C ₆ H ₁₂ O ₆ (4) → 6CH _{1.9} O _{0.5} N _{0.2} (4.3) ^e	-1.8 (-0.9H)
glucose → ethanol+formate ^f	C ₆ H ₁₂ O ₆ (4) → 2C ₂ H ₆ O(6) + 2CH ₂ O ₂ (2)	-4 (-4H)
glucose → ethanol+CO ₂ ^f	C ₆ H ₁₂ O ₆ (4) → 2C ₂ H ₆ O(6) + 2CO ₂ (0)	0 (0H)
glucose → succinate	C ₆ H ₁₂ O ₆ (4) + 2CO ₂ (0) → 2C ₄ H ₆ O ₄ (14/4)	-4 (-2H)
glucose → propionate	C ₆ H ₁₂ O ₆ (4) → 2C ₃ H ₆ O ₂ (14/3)	-4 (-2H)
glucose → lactate	C ₆ H ₁₂ O ₆ (4) → 2C ₃ H ₆ O ₃ (12/3)	0 (1H)
glucose → alanine	C ₆ H ₁₂ O ₆ (4) → 2C ₃ H ₇ NO ₂ (12/3)	0 (1H)

^{a-e}as above.

^fTwo alternative pathways are presented for the conversion of glucose to ethanol, which differ in the co-product synthesized along with ethanol (carbon dioxide or formate) and the overall redox balance (redox consuming or redox neutral).

[00035] The present techniques address disadvantages associated with anaerobic fermentation of reduced carbon sources such as glycerol and the by-products created during the production of chemical products from glycerol. Under anaerobic conditions, the conversion of glycerol into cell mass results in the net gain of reducing equivalents (Table 1). The conversion of glycerol into succinate or lactate, for example, does not consume the excess reducing equivalents generated by the conversion of glycerol into cell mass; in the case of converting glycerol into lactate, the redox balance is further perturbed by a net gain of two reducing equivalents. This redox potential imbalance can be ameliorated through the co-production of a chemical like 1,3-

propanediol (1,3-PDO) from glycerol, which results in the net consumption of two reducing equivalents. However, while the conversion of glycerol into 1,3-PDO enables cell growth by facilitating redox-balanced conditions, it also creates an undesirable by-product that may interfere with the efficient separation of the desired target chemical from the product mixture. The techniques provided herein, through the use of limiting amounts of electron acceptors to consume excess reducing equivalents generated by the incorporation of glycerol into cell mass, reduce or eliminate the production of undesirable by-products and allow increased yield of product.

[00036] The proposed strategy is illustrated in Figures 3, 4, and 5 which schematically depict the production of succinate; or ethanol and formic acid (which is converted to ethanol and H₂); or lactate from glycerol. The advantage of using glycerol is evident when the synthesis of a product from other sugars, such as glucose, is considered, because the use of glucose, xylose or similar sugars results in a shortage of reducing equivalents that clearly limits the theoretical yield. Consequently, the maximum theoretical yield of succinate from glycerol is at least 15% higher than that from sugars such as glucose. In addition, synthesis of ethanol from sugars results in a maximum theoretical yield of approximately 51% w/w, regardless of whether glucose or xylose is used as carbon source. Accordingly, the use of glycerol as a carbon source provides **increased yield** of products such as succinate and ethanol. However, in certain embodiments, it may be useful to use other reduced carbon sources as feedstocks for the reaction.

[00037] As shown in FIG. 6, FIG. 7, FIG. 8, and FIG. 9 glycerol may be used to produce ethanol, lactic acid, and succinic acid by wild-type *E. coli*. Glycerol utilization by wild-type *E. coli* strain MG1655 under microaerobic conditions led to the synthesis of reduced compounds ethanol and succinate as the major products, although the amount of acetate was increased (FIG. 6 and FIG. 7). Moreover, much larger concentrations of succinate were produced under microaerobic conditions (FIG. 6) with improved product yields (FIG. 7) as compared to the succinate production under anaerobic conditions. In terms of productivity, 10 g/L of glycerol were completely consumed by the MG1655 wild-type strain under microaerobic conditions in about 60 hours, which corresponds to approximately 2-fold increase in productivity of the microaerobic production of succinate vs. anaerobic production of succinate.

[00038] In addition, mutant bacterial strains were evaluated for their ability to produce products whose synthesis results in no net generation or consumption of reducing equivalents. Degree of reduction analysis of the pathways involved in the conversion of glycerol to these products yields a degree of reduction balance of $\Delta\kappa = 0$. For example, production of ethanol (along with co-products formate or hydrogen) is one of the products in this category. Evaluation

of recombinant strain SY03 (pZSKLMgldA=Δ*pta*, Δ*frdA*, +*gldA*, +*dhaKLM*), a derivative of *E. coli* strain MG1655 containing mutations that reduce the synthesis of acetate (Δ*pta*), and succinate (Δ*frdA*) and overexpression of the enzymes glycerol dehydrogenase (*gldA*) and dihydroxyacetone kinase (*dhaKLM*), showed that ethanol was produced as the main fermentation product at yields close to the maximum theoretical (FIG. 8A). The ethanol yield was 0.96 mole/mole of glycerol utilized and volumetric productivities for glycerol utilization and ethanol synthesis were 4.65 mole/L/h and 4.61 mole/L/h, respectively (FIG. 8B). The high productivities realized were the result of both higher cell density and higher specific rates under microaerobic conditions, compared to those obtained with the use of anaerobic conditions. The microaerobic conditions used were characterized by a volumetric oxygen transfer rate of 5 mg O₂/L/h.

[00039] Another group of products that may be generated under microaerobic conditions according to the present techniques are those whose synthesis from glycerol or other reduced carbon sources results in the net generation of reducing equivalents ($\Delta\kappa > 0$), such as lactate. The feasibility of this approach is illustrated in FIG 9A, 9B, and 9C, which show increased production of lactic acid and succinic acid by a combination of appropriate microaerobic conditions and specific genetic manipulations. The microaerobic conditions used in these experiments were characterized by a volumetric oxygen transfer rate of 20 mg O₂/L/h.

EXAMPLE 1: MICROORGANISMS

[00040] It is envisioned that any appropriate microbial strain may be used with the present techniques, including members of the genera *Aspergillus*, *Saccharomyces*, *Zygosaccharomyces*, *Pichia*, *Kluyveromyces*, *Candida*, *Hansenula*, *Dunaliella*, *Debaryomyces*, *Mucor*, *Torylopsis*, *Bacillus*, *Paenibacillus* and *Escherichia*. A suitable microbial strain for the microbial synthesis process may be any wild type strain capable of producing the reduced chemical compound of interest. In addition, a suitable microbial strain may be obtained and/or improved by subjecting a parent strain of interest to a classical mutagenic treatment or to recombinant DNA techniques. Furthermore, such strains may then be subjected to sequential selection processes of metabolic evolution in which progeny strains are evaluated for improved performance under the desired reaction conditions. For example, such strains may be selected on the basis of high-performing biocatalysts. Markers of improved performance of a progeny strain may be increased production or yield of the desired chemical product from the glycerol feedstock. In one embodiment, metabolic evolution is conducted in the presence of decreasing amounts of oxygen, nitrate, nitrite or other electron acceptor.

[00041] Genes that will positively affect the production of the desired chemical product may be expressed in suitable hosts. For example it may be highly desirable to over-express certain enzymes in the glycerol to dihydroxyacetone pathway and/or other pathways at levels far higher than currently found in wild type cells. As shown in FIGs. 8A and B, and FIGs. 9A, 9B, and 9C the overexpression of *gldA* in a suitable microbial host in combination with the inhibition of enzymes involved in competing pathways may increase the production of succinate, ethanol, or lactic acid.

[00042] Recombinant organisms that have been genetically engineered to express one or more exogenous polynucleotide coding sequences, *i.e.*, a gene sequence that is not native, or endogenous, to the host organism can also be used in the invention. Overexpression of desired genes may be accomplished by the selective cloning of the genes encoding those enzymes into multicopy plasmids or placing those genes under a strong inducible or constitutive promoter. Methods for overexpressing desired proteins are common and well known in the art of molecular biology. It is envisioned that any of the genes provided in Table 4 may be overexpressed in a microbial strain.

Table 4: Genes Involved in the Production of Reduced Chemical Compounds

<u>Protein</u>	<u>Gene</u>	<u>GenBank Acc. No.</u>
glycerol dehydrogenase	<i>glmA</i>	ECK3937
dihydroxyacetone kinase subunit K	<i>dhaK</i>	ECK1186
dihydroxyacetone kinase subunit L	<i>dhaL</i>	ECK1187
dihydroxyacetone kinase subunit M	<i>dhaM</i>	ECK1188
glycerol kinase	<i>glpK</i>	ECK3918
glycerol-3-P dehydrogenase subunit A	<i>glpA</i>	ECK2233
glycerol-3-P dehydrogenase subunit B	<i>glpB</i>	ECK2234
glycerol-3-P dehydrogenase subunit C	<i>glpC</i>	ECK2235
glycerol-3-P dehydrogenase subunit D	<i>glpD</i>	ECK3412
phosphoenolpyruvate carboxykinase	<i>pckA</i>	ECK3390
phosphoenolpyruvate carboxylase	<i>ppc</i>	ECK3947
formate hydrogen lyase	<i>fdhF</i>	ECK4072
formate hydrogen lyase subunit	<i>hycC</i>	ECK2718
formate hydrogen lyase subunit	<i>hycD</i>	ECK2717
lactate dehydrogenase	<i>ldhA</i>	ECK1377
alcohol dehydrogenase	<i>adhE</i>	ECK1235
alcohol dehydrogenase mutant (mutant active in the presence of electron acceptors)	<i>adhE*</i>	ECK1235
glycerol dehydratase (capable of converting glycerol into hydroxyacetone or 3-hydroxypropionaldehyde)	<i>dhaB</i> (from <i>Klebsiella pneumoniae</i>)	EF634063
phosphoenolpyruvate carboxykinase	<i>pckA</i> (from <i>Actinobacillus succinogenes</i>)	Asuc_0221
dihydroxyacetone kinase subunit KL	<i>dhaKL</i> (from <i>Citrobacter freundii</i>)	DQ473522
pyruvate carboxylase	<i>pyc</i> (from <i>Lactobacillus lactis</i>)	AF068759
pyruvate carboxylase	<i>pyc</i> (from <i>Rhizobium etli</i>)	U51439
pyruvate decarboxylase	<i>pdc</i> (<i>Zymomonas mobilis</i>)	
phosphoenolpyruvate carboxykinase	<i>pckA</i> (<i>E. coli</i>)	
malic enzyme	<i>maeA</i> and <i>maeB</i> (<i>E. coli</i>)	
methylmalonyl-CoA mutase	<i>scpA</i> (<i>E. coli</i>)	
methylmalonyl-CoA decarboxylase	<i>scpB</i> (<i>E. coli</i>)	
propionyl-CoA:succinate CoA transferase	<i>scpC</i> (<i>E. coli</i>)	
GTPase that interacts with methylmalonyl-CoA mutase	<i>argK</i> (<i>E. coli</i>)	
subunit of E1p component of pyruvate dehydrogenase complex	<i>aceE</i> (<i>E. coli</i>)	
lipoate acetyltransferase / dihydrolipoamide acetyltransferase , subunit of pyruvate dehydrogenase multienzyme complex	<i>aceF</i> (<i>E. coli</i>)	
E3 monomer , subunit of pyruvate dehydrogenase multienzyme complex	<i>lpdA</i> (<i>E. coli</i>)	
Fumarate reductase	<i>frdABCD</i> (<i>E. coli</i>)	
phosphoenolpyruvate carboxylase	<i>ppc</i> (<i>E. coli</i>)	

[00043] In addition to the cells exemplified it is contemplated that the present method will be able to make use of cells having single or multiple mutations specifically designed to enhance the production of the desired end product. Cells that normally divert a carbon feed stock into non-productive pathways, or that exhibit significant catabolite repression could be mutated to avoid these phenotypic deficiencies. For example, many wild type cells are subject to catabolite repression from glucose and by-products in the media and it is contemplated that mutant strains of these wild type organisms would be particularly useful in certain embodiments of the present

techniques. In particular, it is envisioned that any of the genes in Table 5 may be mutated, either alone or in combination with other genes, in a microbial organism for use in the present techniques. As defined herein, microorganisms that lack an indicated gene are considered to be knock outs of that gene.

Table 5: Genes Involved in By-Product Pathways

Protein	Gene	GenBank Acc. No.
fumarate reductase (subunits A-D)	<i>frd</i>	ECK4147-ECK4150
lactate dehydrogenase	<i>ldhA</i>	ECK1377
D-lactate dehydrogenase, membrane-bound	<i>dld</i>	ECK2126
L-lactate dehydrogenase, membrane-bound	<i>lldD</i>	ECK3595
methylglyoxal synthase	<i>mgsA</i>	ECK0954
glyoxalase I	<i>gloA</i>	ECK1647
glyoxalase II	<i>gloB, gloC</i>	ECK0212
acetaldehyde dehydrogenase subunit	<i>aldA</i>	ECK1408
acetaldehyde dehydrogenase subunit	<i>aldB</i>	ECK3577
phosphate acetyltransferase	<i>pta</i>	ECK2291
acetate kinase	<i>ackA</i>	ECK2290
alcohol dehydrogenase	<i>adhE</i>	ECK1235
ethanol dehydrogenase	<i>adhP</i>	ECK1472
pyruvate formate-lyase	<i>pflB</i>	ECK0894
pyruvate oxidase	<i>poxB</i>	ECK0862
pyruvate dehydrogenase	<i>aceE, aceF, lpdA</i>	ECK0113-ECK0115
nitrite reductase nrf operon	<i>nrf ABCDEFG</i>	ECK4063-ECK4069
nitrite reductase nap operon	<i>nap CBHGADF</i>	ECK2194-ECK2200
nitrite/nitrate transporter subunits ABD	<i>nir</i>	ECK3353-ECK3355
nitrate/nitrite regulatory protein	<i>nar LXKGHJI</i>	ECK1215-ECK1221
Formate dehydrogenase	<i>fdnG</i>	ECK1468
Formate dehydrogenase	<i>fdoG</i>	ECK3887
Formate dehydrogenase	<i>fdhF</i>	ECK4072
triose phosphate isomerase	<i>tpiA</i>	ECK3911
fumarate reductase	<i>fumA, fumB, fumC</i>	ECK1607
fumarate reductase	<i>fumA, fumB, fumC</i>	ECK4115
fumarate reductase	<i>fumA, fumB, fumC</i>	ECK1606
F0F1-ATPase	<i>atpF, atpD</i>	ECK3729
F0F1-ATPase	<i>atpF, atpD</i>	ECK3725
phosphoenolpyruvate synthase	<i>pps</i>	ECK1700
phosphoenolpyruvate carboxykinase	<i>pckA</i>	ECK3390
phosphoenolpyruvate carboxylase	<i>ppc</i>	ECK3947
Malate dehydrogenase	<i>mdh</i>	ECK3225

[00044] For example, as noted above, FIG. 10 depicts a schematic pathway for the production of succinate or propionate from glycerol in accordance with the present techniques. In such an embodiment, it may be advantageous to provide an organism in which the one or more genes involved in the pathway to convert acetyl-CoA to ethanol are mutated or inhibited in some way such that their catalytic activity is reduced. In a specific embodiment, a suitable microorganism may include a mutation of the *adhE* gene. Additional mutations may involve the mutation of the *pta*, *ackA*, or *poxB* genes involved in acetate formation; the *ppc* gene involved in the conversion of phosphoenolpyruvate into oxaloacetate; the *glpABC* operon, *glpD*, or *glpK*, involved in the conversion of glycerol to glycerol-3-P to dihydroxyacetone phosphate; or *dhaKLM*

involved in the conversion of dihydroxyacetone to dihydroxyacetone phosphate. These mutations or combinations thereof may be combined with the overexpression of either endogenous or heterologous genes, including but not limited to: *gldA* from *E. coli* and comparable genes from other organisms; *dhaKLcf* from *Citrobacter freundii*; *pepck* from *Actinobacillus succinogenes*; or *pyc* from *Rhizobium etli*.

[00045] In another embodiment, shown in FIG. 11, ethanol production from glycerol may be increased through the inhibition of competing pathways that produce acetate and succinate by-products. These mutations may involve the mutation of the *pta*, *ackA*, or *poxB* genes involved in acetate formation; the *frdABCD* operon involved in succinate formation; the *glpABC* operon, *glpD* or *glpK*, involved in the conversion of glycerol to dihydroxyacetone phosphate. These mutations or combinations thereof may be combined with the overexpression of either endogenous or heterologous genes, including but not limited to: *gldA* from *E. coli* and comparable genes from other organisms or *dhaKLcf* from *Citrobacter freundii*.

[00046] In an additional embodiment, shown in FIG. 12, lactate production from glycerol may be increased through the inhibition of competing pathways that produce acetate, succinate, and ethanol by-products. These mutations may involve the mutation of the *pta*, *ackA*, or *poxB* genes involved in acetate formation; the *frdABCD* operon involved in succinate formation; the *adhE* gene involved in ethanol formation. Further genetic alterations may involve overexpression of the *glpABC* operon, *glpD* or *glpK*, involved in the conversion of glycerol to dihydroxyacetone phosphate.

[00047] Methods of creating mutants are common and well known in the art. For example, wild type cells may be exposed to a variety of agents such as radiation or chemical mutagens and then screened for the desired phenotype. Specific methods for creating mutants using radiation or chemical agents are well documented in the art. After mutagenesis has occurred, mutants having the desired phenotype may be selected by a variety of methods. Random screening is most common where the mutagenized cells are selected for the ability to produce the desired product. Alternatively, selective isolation of mutants can be performed by growing a mutagenized population on selective media where only resistant colonies can develop. In one embodiment, cells may be subjected to mutagenesis prior to or during selection for metabolic evolution. Targeted mutagenesis through recombinant techniques can also be employed separately, or in combination with random mutagenic techniques.

EXAMPLE 2: MEDIA AND GROWTH CONDITIONS

[00048] Typically cells are grown at 37°C in appropriate media, although some bacteria have temperature optima at 35, 37, 39, or 41°C. Preferred growth media according to the present techniques may include minimal media or minimal salt media. For example, suitable media may include 4-morpholinepropanesulfonic acid media (MOPS). In certain embodiments, the phosphate salts in the media may be replaced with sodium salts. Glycerol feedstock may be provided in any suitable amount. For example, glycerol may be provided at 10g/L.

[00049] Suitable pH ranges for the fermentation may be between pH 5.0 to pH 9.0. It is envisioned that alkaline pH may be suitable for improved yield of certain products while acidic pH may be suitable for improved yield of other products. For example, acidic pH may promote production of ethanol and hydrogen while alkaline pH may promote the production of ethanol and formic acid.

[00050] Fermentations may be conducted in any suitable microaerobic or microrespiratory fermentation system. It is envisioned that room air, oxygen, and/or nitrogen may be provided to the system in suitable amounts and at a suitable rate such that, as the growth rate of the microbes approaches log phase, there are substantially no detectable electron acceptors in the culture.

[00051] The present process may employ a batch method of fermentation. As used herein, “fermentation” may refer to microbial growth under microaerobic or microrespiratory conditions suitable for the production of reduced chemical products from glycerol. A classical batch fermentation may be a closed system where the composition of the media is set at the beginning of the fermentation and not subject to artificial alterations during the fermentation. Thus, at the beginning of the fermentation the media is inoculated with the desired organism or organisms and fermentation is permitted to occur adding nothing to the system. Typically, however, a “batch” fermentation is batch with respect to the addition of carbon source and attempts are often made at controlling factors such as pH and oxygen concentration. In batch systems the metabolite and biomass compositions of the system change constantly up to the time the fermentation is stopped. Within batch cultures cells progress through a static lag phase to a high growth log phase and finally to a stationary phase where growth rate is diminished or halted.

[00052] Sequential fermentation processes are also suitable in the present invention and comprise a typical batch system with the exception that the substrate is added in increments as the fermentation progresses. A fed-batch strategy, for example, may be advantageous. A fed-batch fermentation is an open system where a defined fermentation medium is added at the beginning of

the fermentation and is inoculated with the desired organism or organisms and the fermentation is permitted to occur. In addition to the adjustments typically made in a batch fermentation, to pH or oxygen concentration, for example, a fed-batch fermentation involves the periodic or continuous addition of the carbon source and any additional limiting nutrients, with little or no removal of culture medium from the fermentation reaction during the fermentation process.

[00053] It is contemplated that the present techniques would also be adaptable to continuous fermentation methods. Continuous fermentation is an open system where a defined fermentation media is added continuously to a bioreactor and an equal amount of conditioned media is removed simultaneously for processing. Continuous fermentation generally maintains the cultures at a constant high density where cells are primarily in log phase growth. Continuous fermentation allows for the modulation of one factor or any number of factors that affect cell growth or end product concentration. It is contemplated that the present invention may be practiced using either batch, fed-batch or continuous processes and that any known mode of fermentation would be suitable. Additionally, it is contemplated that cells may be immobilized on a substrate as whole cell catalysts and subjected to fermentation conditions for production of reduced products from glycerol.

[00054] While the invention may be susceptible to various modifications and alternative forms, specific embodiments have been shown by way of example in the drawings and have been described in detail herein. However, it should be understood that the invention is not intended to be limited to the particular forms disclosed. Rather, the invention is to cover all modifications, equivalents, and alternatives falling within the spirit and scope of the invention as defined by the following appended claims.

[00055] What is claimed is:

1. A method for producing a redox-neutral or oxidized chemical product in a microorganism from a reduced carbon source, the method comprising:
 - providing electron acceptors to the microorganism at a rate where the electron acceptors are consumed at least as quickly as they are provided;
 - and, providing the reduced carbon source as a feedstock for the microorganism such that the redox-neutral or oxidized product and at least some cell mass are generated from the reduced carbon source and wherein the reduced carbon source is more reduced than the cell mass;
 - wherein the degree of reduction balance for the conversion of the reduced carbon source into the reduced chemical product is equal to or greater than zero, and where the degree of reduction balance for the conversion of carbon source into cell mass is greater than zero.
2. The method according to claim 1, wherein the reduced carbon source comprises glycerol.
3. The method according to claim 1, wherein the redox-neutral or oxidized chemical product comprises an alcohol, an organic acid, an amino acid, or a lactone.
4. The method according to claim 1, wherein the redox-neutral or oxidized chemical product comprises succinate, propionate, ethanol, lactate, or alanine.
5. The method according to claim 1, wherein the electron acceptors comprise atmospheric air, oxygen, nitrates, nitrites, or combinations thereof.
6. The method according to claim 4, wherein the electron acceptors are provided to the microorganism at a rate within the range of 1 milligram of oxygen per gram of cell mass per hour to 15 milligrams of oxygen per gram of cell mass per hour.

7. The method according to claim 1, wherein the microorganism belongs to the genus *Escherichia, Bacillus, Paenibacillus, or Saccharomyces*.

8. The method according to claim 1 wherein the chemical product comprises succinate and the microorganism comprises one or more of:

a) a disruption in a gene involved in the conversion of acetyl-CoA to ethanol, a disruption in a gene involved in the conversion of acetyl-CoA to acetyl-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetate, a disruption in a gene involved in the conversion of pyruvate to lactate, a disruption in a gene involved in the conversion of phosphoenolpyruvate to oxaloacetate, a disruption in a gene involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetyl-CoA, a disruption in a gene involved in the conversion of phosphoenolpyruvate to pyruvate, a disruption in a gene involved in the conversion of glycerol to dihydroxyacetone, a disruption in a gene involved in the conversion of glycerol-3-phosphate to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of glycerol to glycerol-3-phosphate, a disruption in a gene involved in the conversion of dihydroxyacetone-phosphate to methylglyoxal; and

b) an exogenous gene expressing an enzyme involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, wherein the enzyme uses ATP as a cofactor and produces ADP as a co-product; an exogenous gene expressing an enzyme involved in the conversion of glycerol-3-phosphate to dihydroxyacetone-phosphate, wherein the enzyme passes the reducing equivalents to fumarate; an exogenous gene expressing an enzyme involved in the conversion of fumarate to succinate, wherein the enzyme accepts reducing equivalents from the oxidation of glycerol-3-phosphate; an exogenous gene expressing an enzyme involved in the conversion of pyruvate and CO₂ to oxaloacetate, wherein the enzyme uses ATP as a cofactor and produces ADP as a co-product; an exogenous gene expressing an enzyme involved in the conversion of phosphoenolpyruvate and CO₂ to oxaloacetate; an exogenous gene expressing an enzyme involved

in the conversion of phosphoenolpyruvate and CO₂ to oxaloacetate, wherein the enzyme uses ADP as a cofactor and produces ATP as a co-product; or an exogenous gene expressing an enzyme involved in the conversion of pyruvate and CO₂ to malate, wherein the enzyme uses NADH as a cofactor.

9. The method according to claim 1 wherein the chemical product comprises propionate and the microorganism comprises one or more of:

a) a disruption in a gene involved in the conversion of acetyl-CoA to ethanol, a disruption in a gene involved in the conversion of acetyl-CoA to acetyl-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetate, a disruption in a gene involved in the conversion of pyruvate to lactate, a disruption in a gene involved in the conversion of phosphoenolpyruvate to oxaloacetate, a disruption in a gene involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetyl-CoA, a disruption in a gene involved in the conversion of phosphoenolpyruvate to pyruvate, a disruption in a gene involved in the conversion of glycerol to dihydroxyacetone, a disruption in a gene involved in the conversion of glycerol-3-phosphate to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of glycerol to glycerol-3-phosphate, a disruption in a gene involved in the conversion of dihydroxyacetone-phosphate to methylglyoxal; and

b) an exogenous gene expressing an enzyme involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, wherein the enzyme uses ATP as a cofactor and produces ADP as a co-product; an exogenous gene expressing an enzyme involved in the conversion of glycerol-3-phosphate to dihydroxyacetone-phosphate, wherein the enzyme passes the reducing equivalents to fumarate; an exogenous gene expressing an enzyme involved in the conversion of fumarate to succinate, wherein the enzyme accepts reducing equivalents from the oxidation of glycerol-3-phosphate; an exogenous gene expressing an enzyme involved in the conversion of pyruvate and CO₂ to oxaloacetate, wherein the enzyme uses ATP as a cofactor and produces ADP as a co-

product; an exogenous gene expressing an enzyme involved in the conversion of phosphoenolpyruvate and CO₂ to oxaloacetate; an exogenous gene expressing an enzyme involved in the conversion of phosphoenolpyruvate and CO₂ to oxaloacetate, wherein the enzyme uses ADP as a cofactor and produces ATP as a co-product; or an exogenous gene expressing an enzyme involved in the conversion of pyruvate and CO₂ to malate, wherein the enzyme uses NADH as a cofactor; an exogenous gene or overexpression of an endogenous gene coding for the enzymes converting succinyl-CoA to methylmalonyl-CoA, and methylmalonyl-CoA to propionyl-CoA and CO₂, and propionyl-CoA and succinate to propionate and succinyl-CoA.

10. The method according to claim 1 wherein the chemical product comprises ethanol and the microorganism comprises at least one of:

a) a disruption in a gene involved in the conversion of acetyl-CoA to acetyl-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetate, a disruption in a gene involved in the conversion of fumarate to succinate, a disruption in a gene involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of glycerol to dihydroxyacetone, a disruption in a gene involved in the conversion of glycerol-3-phosphate to dihydroxyacetone-phosphate, a disruption in a gene involved in the conversion of glycerol to glycerol-3-phosphate, a disruption in a gene involved in the conversion of formate to CO₂ and hydrogen, a disruption in a gene involved in the conversion of pyruvate to lactate, a disruption in a gene involved in the conversion of dihydroxyacetone-phosphate to methylglyoxal; and

b) an exogenous gene involved in the conversion of glycerol to dihydroxyacetone, an exogenous gene or overexpression of an endogenous gene involved in the conversion of dihydroxyacetone to dihydroxyacetone-phosphate, an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol to glycerol-3-P, or an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol-3-P to dihydroxyacetone-phosphate, an

exogenous gene involved in the conversion of pyruvate to acetaldehyde and CO₂, an exogenous gene or overexpression of an endogenous gene involved in the conversion of pyruvate to acetyl-CoA, CO₂, and NADH, an exogenous gene or overexpression of an endogenous gene involved in the conversion of pyruvate to acetyl-CoA and formate, an exogenous gene or overexpression of an endogenous gene involved in the conversion of formate to CO₂ and NADH .

11. The method according to claim 1 wherein the chemical product comprises lactate and the microorganism comprises at least one of:

a) a disruption in a gene involved in the conversion of acetyl-CoA to ethanol, a disruption in a gene involved in the conversion of acetyl-CoA to acetyl-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetate, a disruption in a gene involved in the conversion fumarate to succinate, a disruption in a gene involved in the conversion of pyruvate to acetyl-CoA, a disruption in a gene involved in the conversion of dihydroxyacetone-phosphate to methylglyoxal, a disruption in a gene involved in the conversion of pyruvate to D-lactate; and

b) an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol to dihydroxyacetone, an exogenous gene or overexpression of an endogenous gene involved in the conversion of dihydroxacetone to dihydroxyacetone-phosphate, an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol to glycerol-3-P, an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol-3-P to dihydroxyacetone-phosphate, an exogenous gene or overexpression of an endogenous gene involved in the conversion of pyruvate to L- or D-lactate.

12. The method according to claim 1 wherein the chemical product comprises lactate and the microorganism comprises at least one of:

a) a disruption in a gene involved in the conversion of acetyl-CoA to ethanol, a disruption in a gene involved in the conversion of acetyl-CoA to acetyl-phosphate, a disruption in a gene involved in the conversion of pyruvate to acetate, a disruption in a gene involved in the conversion fumarate to succinate, a disruption in a gene involved in the conversion of pyruvate to acetyl-CoA, a disruption in a gene involved in the conversion of dihydroxyacetone-phosphate to methylglyoxal, a disruption in a gene involved in the conversion of pyruvate to D-lactate; and

b) an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol to dihydroxyacetone, an exogenous gene or overexpression of an endogenous gene involved in the conversion of dihydroxacetone to dihydroxyacetone-phosphate, an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol to glycerol-3-P, an exogenous gene or overexpression of an endogenous gene involved in the conversion of glycerol-3-P to dihydroxyacetone-phosphate; an exogenous gene or overexpression of an endogenous gene involved in the conversion of pyruvate to alanine.

13. An *Escherichia coli* strain comprising:

a disruption in one or more of a *adhE* gene, a *pta* gene, a *poxB* gene, a *ppc* gene, or a *dhaK* gene;

an exogenous *Citrobacter freundii dhaKL* gene; and

an exogenous *Actinobacillus succinogenes pckA* gene.

14. An *Escherichia coli* strain comprising:

an overexpressed *gldA* gene or an overexpressed *dhaKLM* operon;

a disruption in at least one of a *frdA*, *frdB*, *frdC*, or *frdD* gene; and

a disruption in a *pta* gene or a disruption in a *poxB* gene.

15. An *Escherichia coli* strain comprising:

an overexpressed *gldA* gene or an overexpressed *dhaKLM* operon; and

a disruption in one or more of a *adhE* gene, a *pta* gene, a *poxB* gene; a *frdA* gene, a *frdB* gene, *frdC* gene, or a *frdD* gene.

16. A method of culturing bacteria to produce a metabolite, comprising the following steps:

- a. inoculating a culture medium comprising glycerol as a feedstock with a bacteria capable of producing a metabolite,
- b. cultivating said bacteria under microaerobic conditions of ≤ 20 mg O₂/L/h, but not aerobic or anaerobic conditions, in said reactor so as to convert said glycerol into a metabolite, wherein the conversion of glycerol into the metabolite does not consume more reducing equivalents than it produces.

17. The method of claim 16, wherein said bacteria is *E. coli* comprising Δpta , $\Delta frdA$ and overexpressed *gldA* and *dhaKLM*.

18. The method of claim 16, wherein said metabolite is selected from the groups consisting of ethanol, lactate, succinate, propionate, alanine, and combinations thereof.

19. The method of claim 16, wherein said metabolite is selected from the groups consisting of ethanol, lactate, propionate, succinate, and combinations thereof.

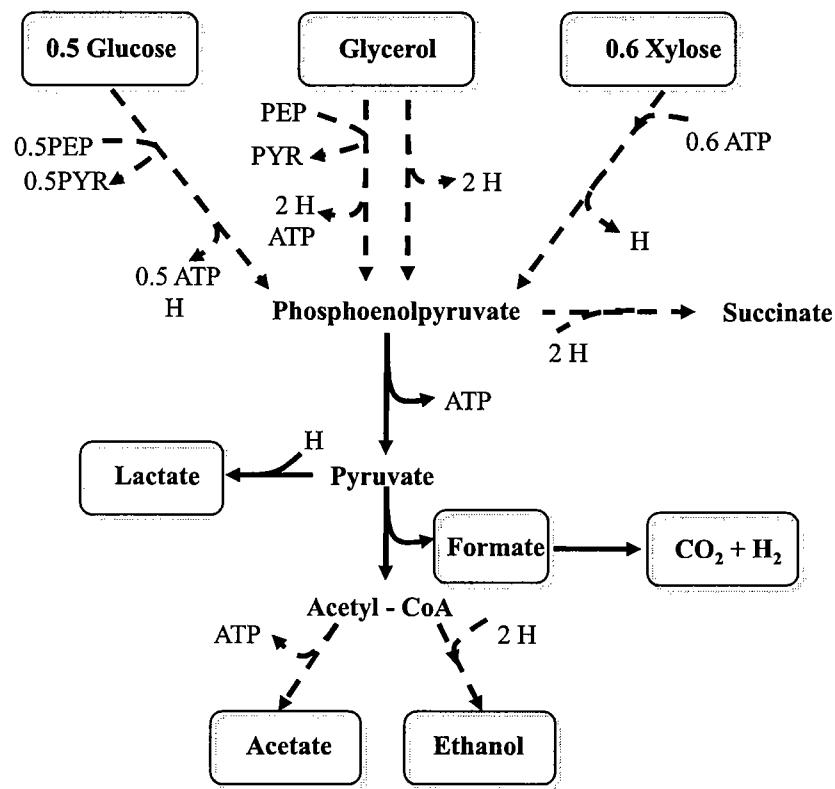
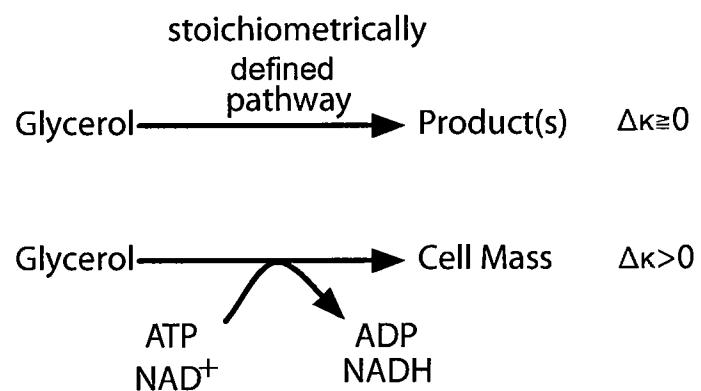


FIG. 1

**FIG. 2**

3/12

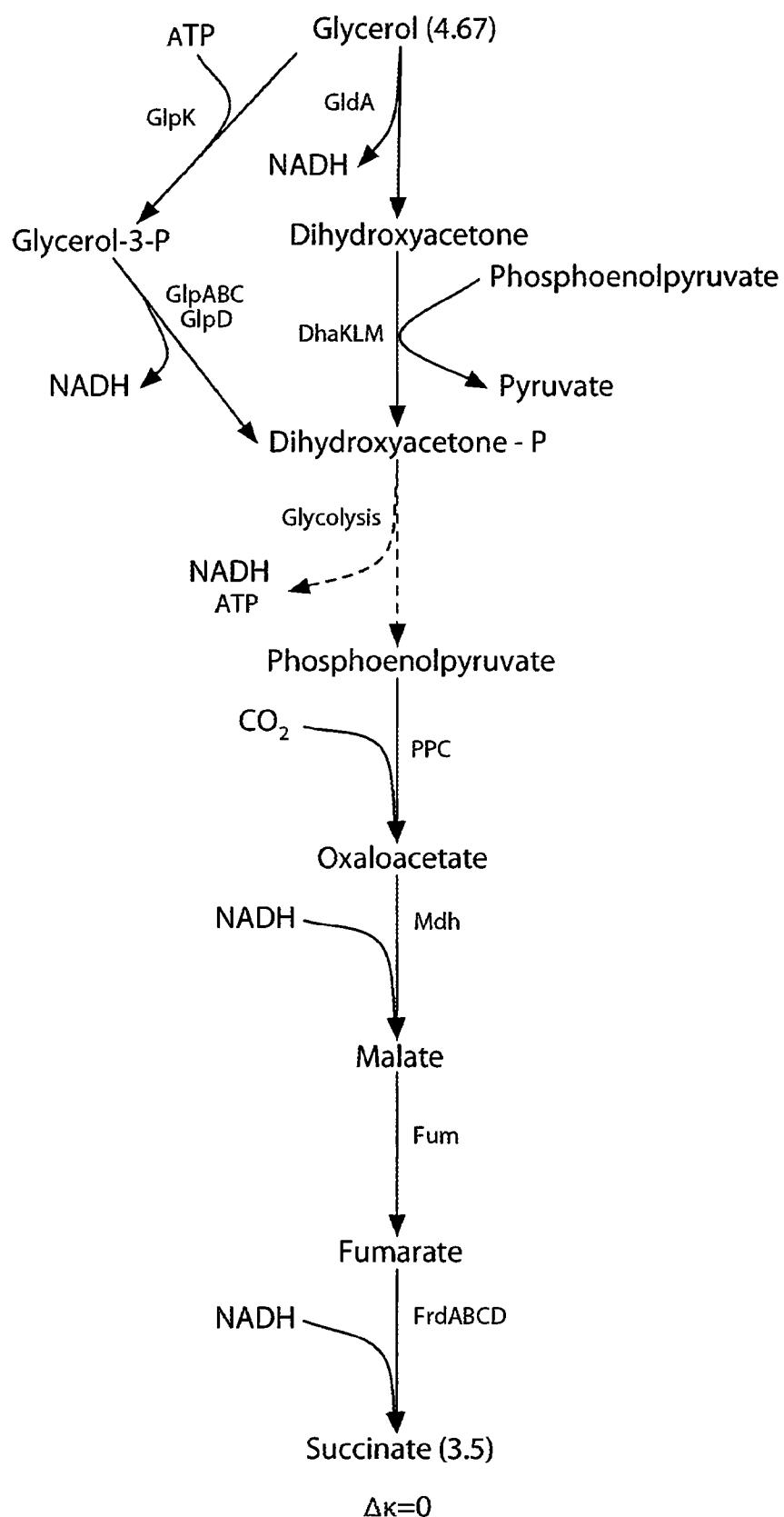


FIG. 3

4/12

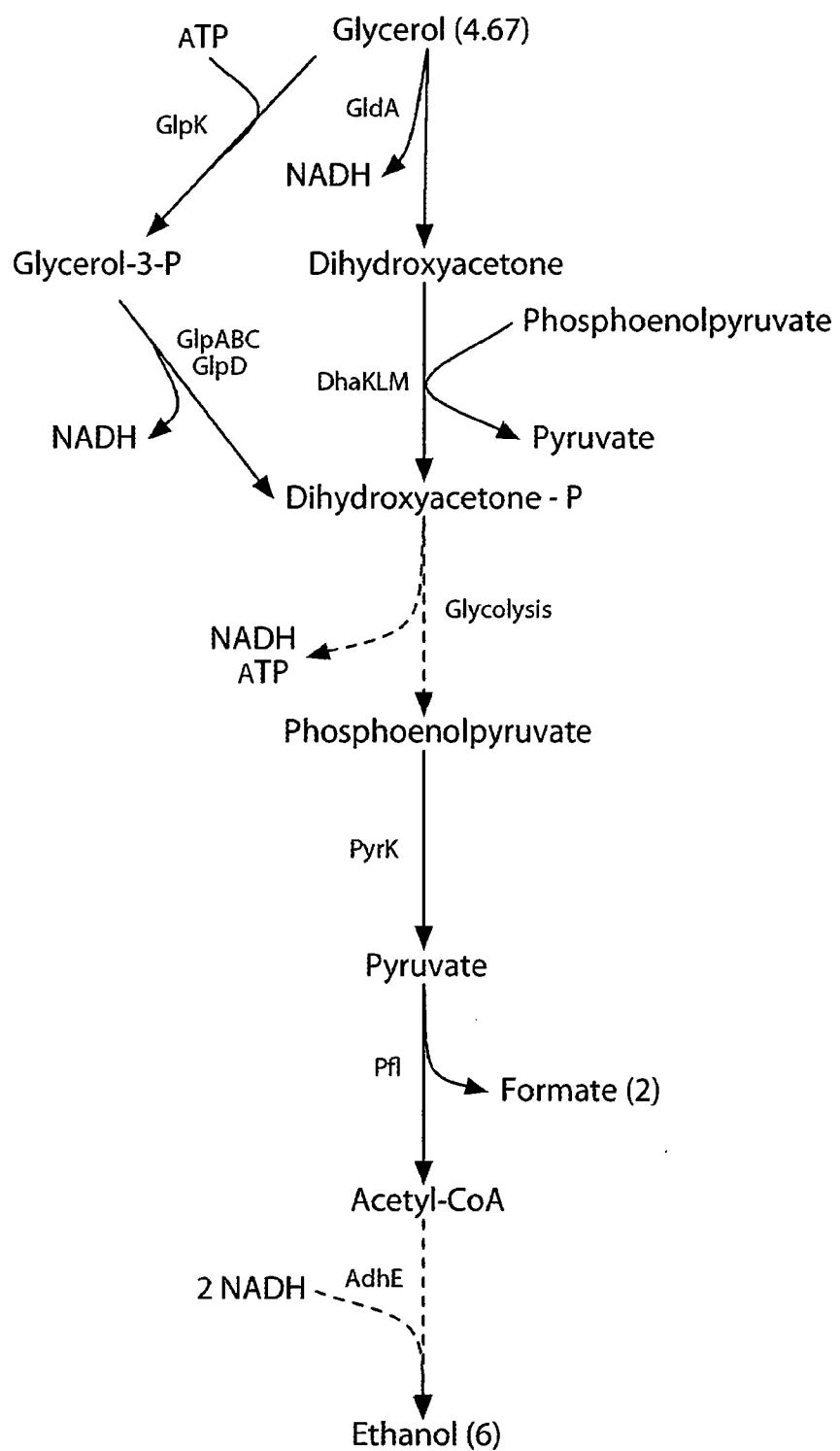
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FIG. 4

5/12

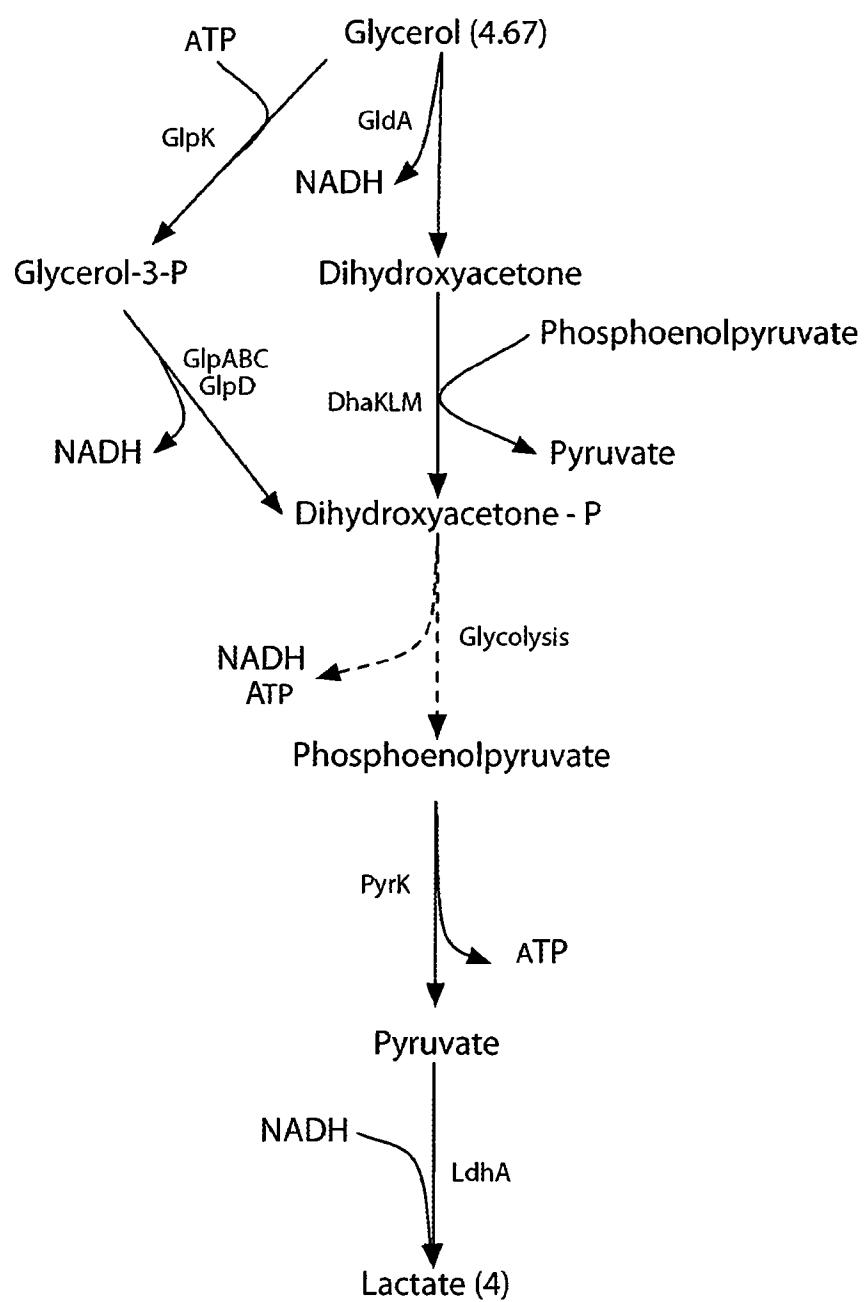
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FIG. 5

6/12

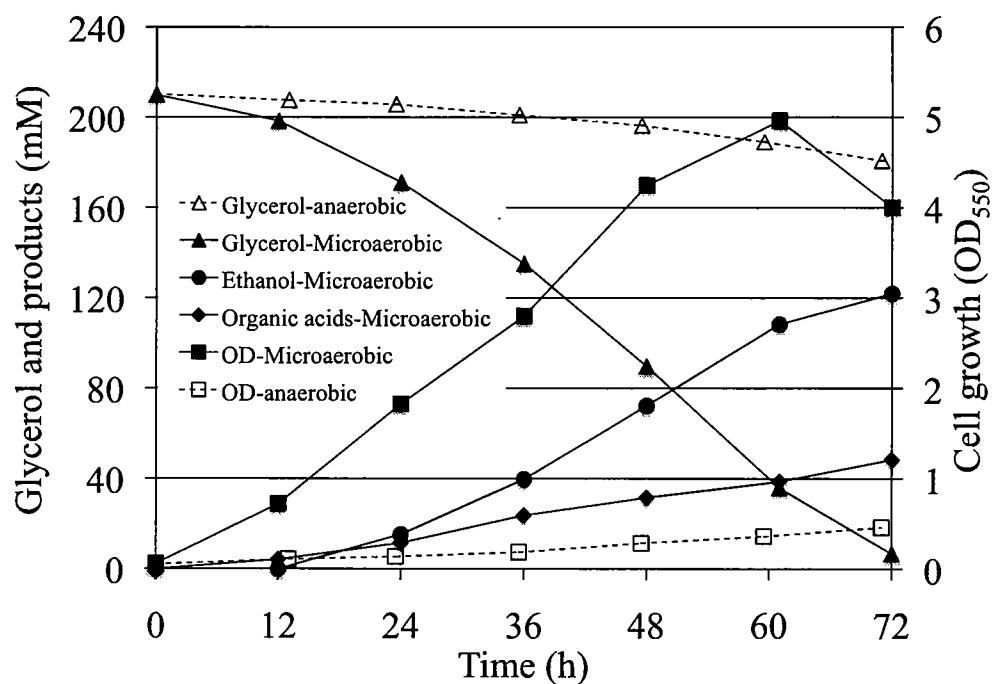


FIG. 6A

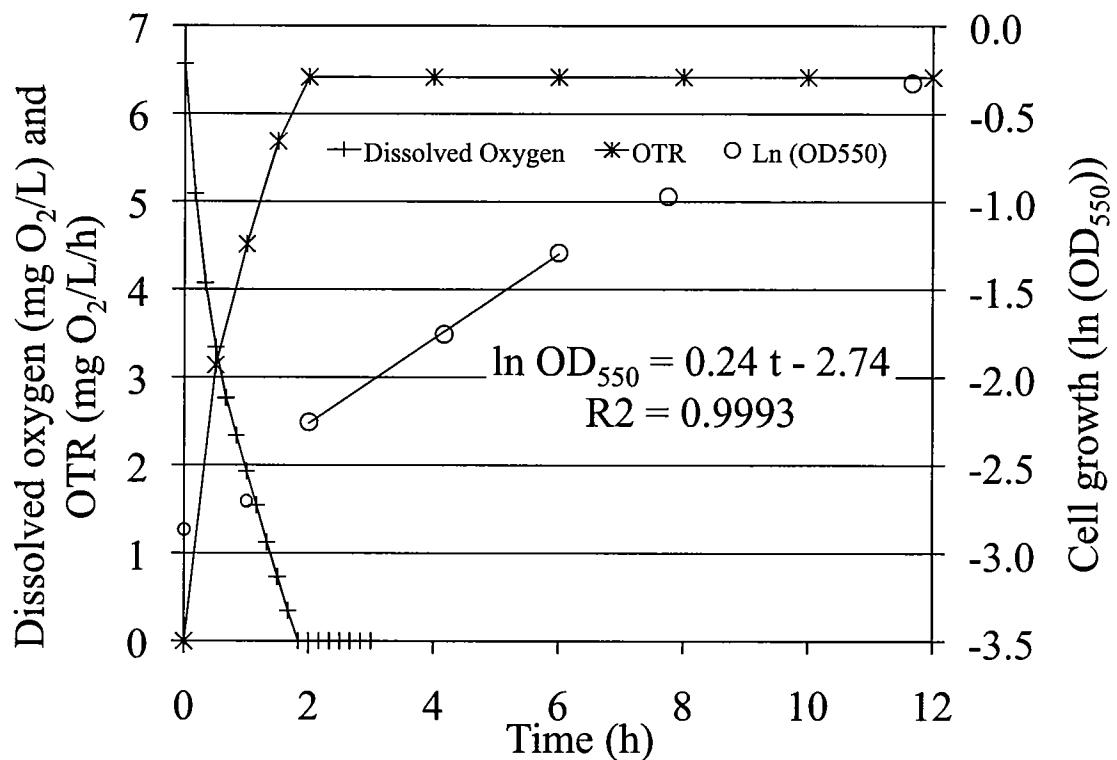


FIG. 6B

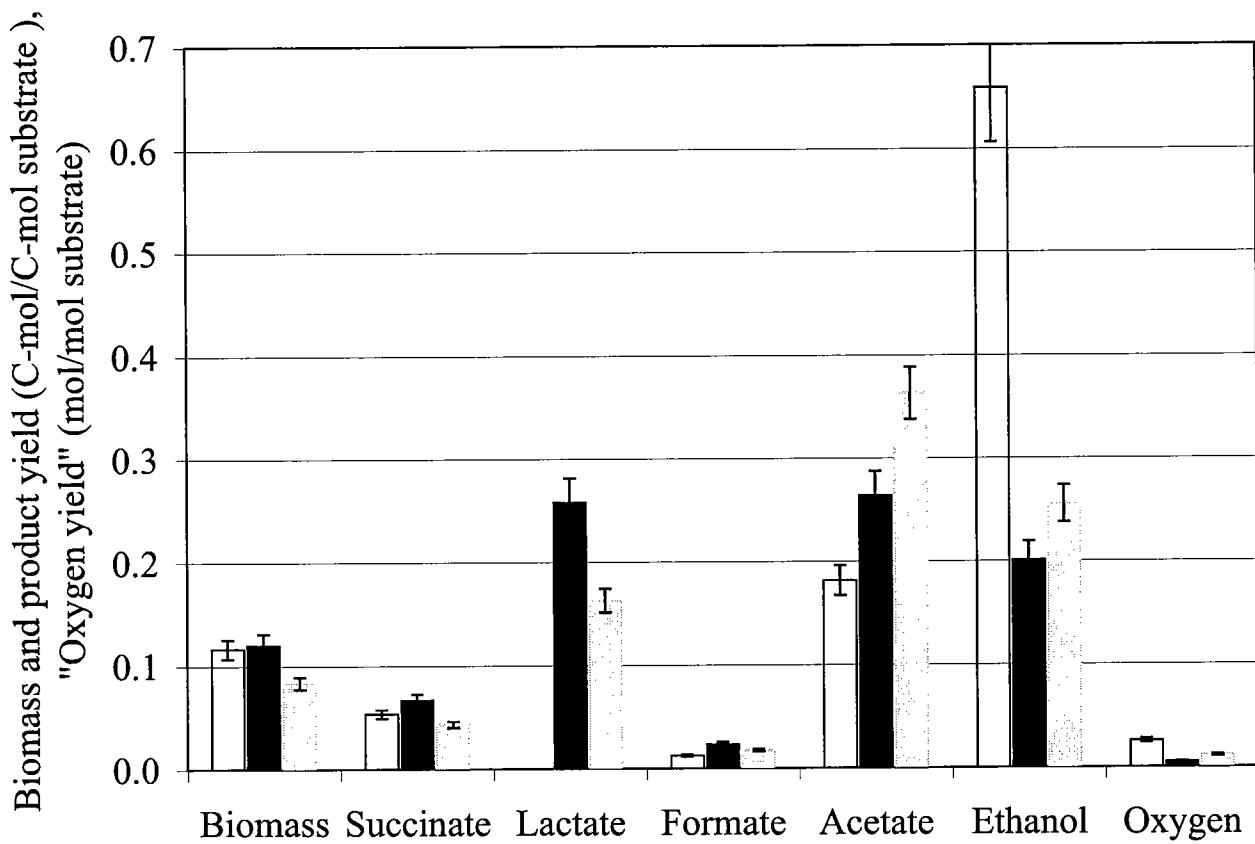


FIG. 7

8/12

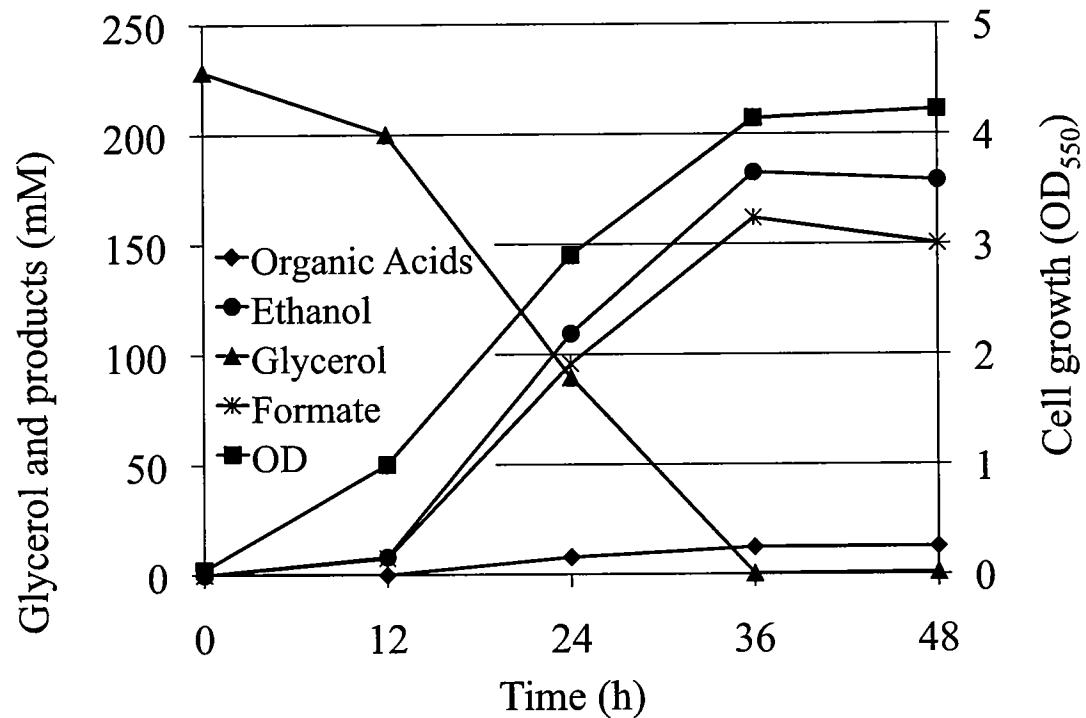


FIG. 8A

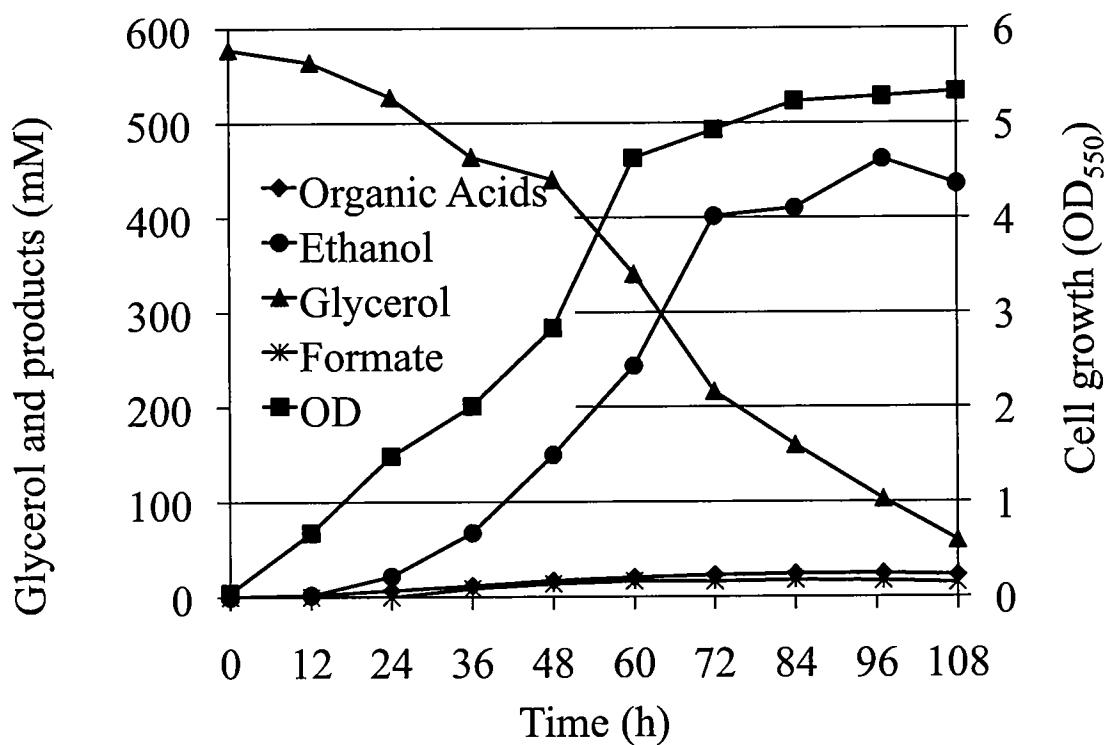


FIG. 8B

9/12

FIG. 9A

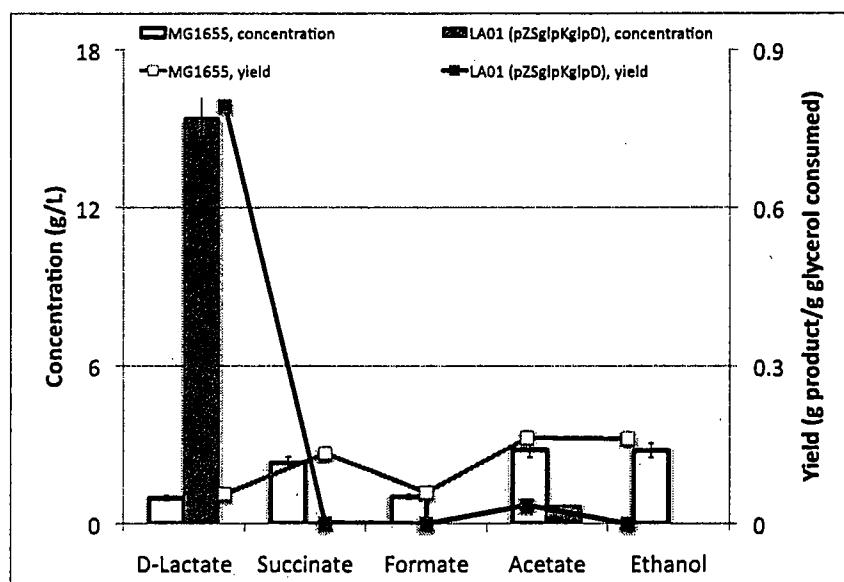


FIG. 9B

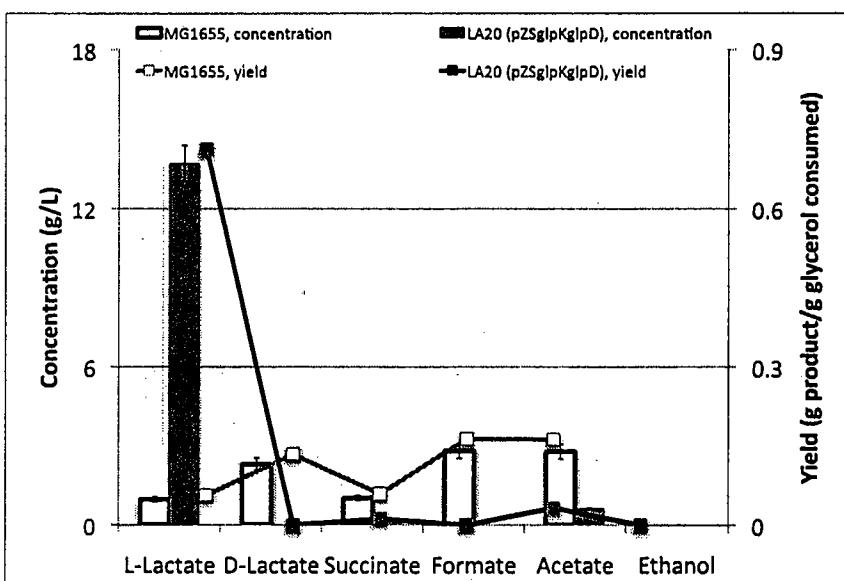
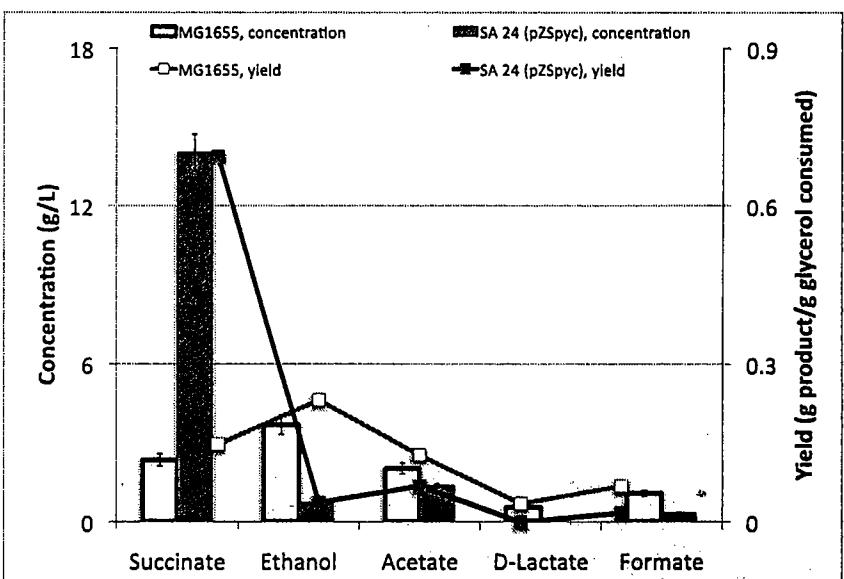


FIG. 9C



10/12

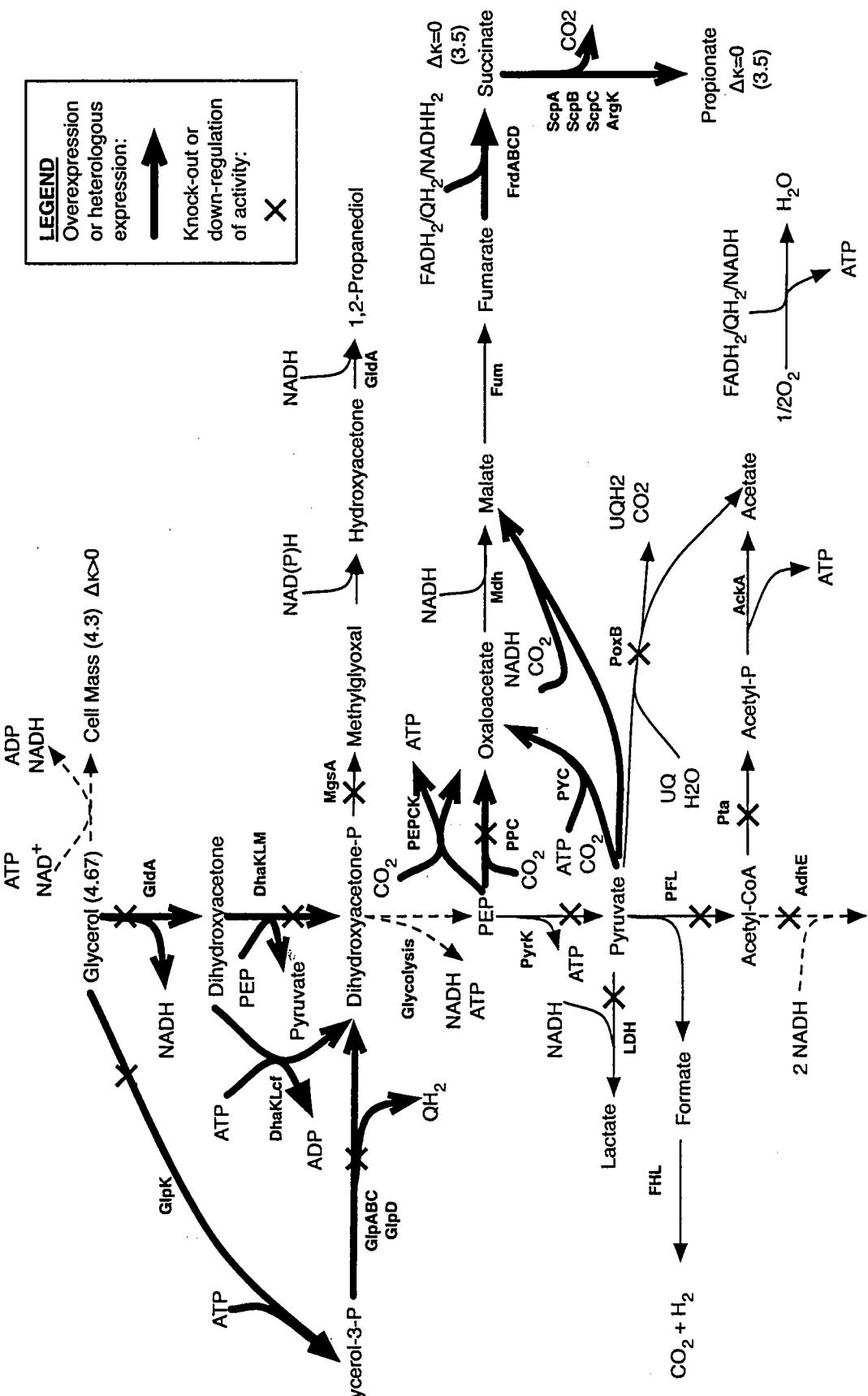


FIG. 10

11/12

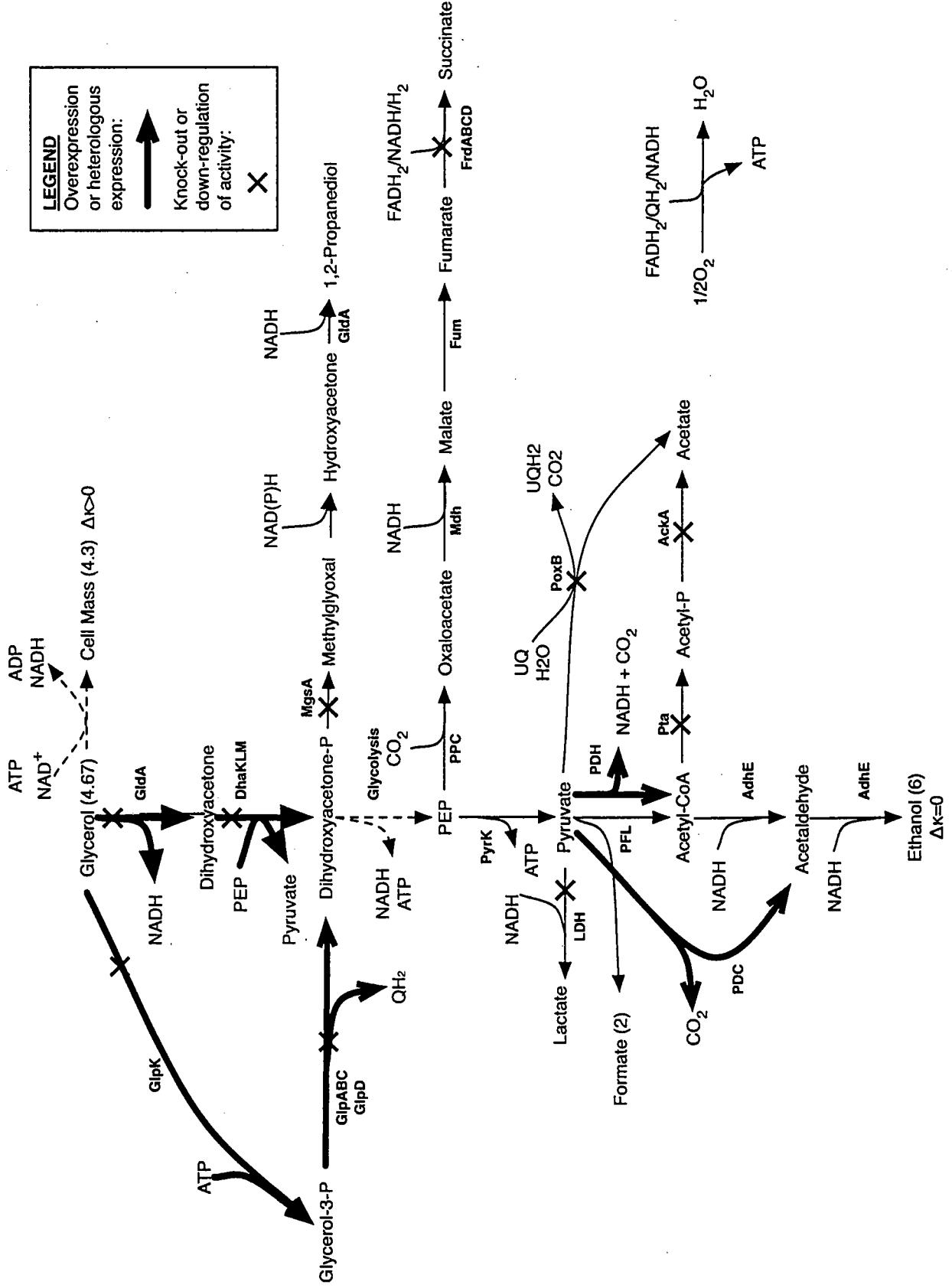


FIG. 11

12/12

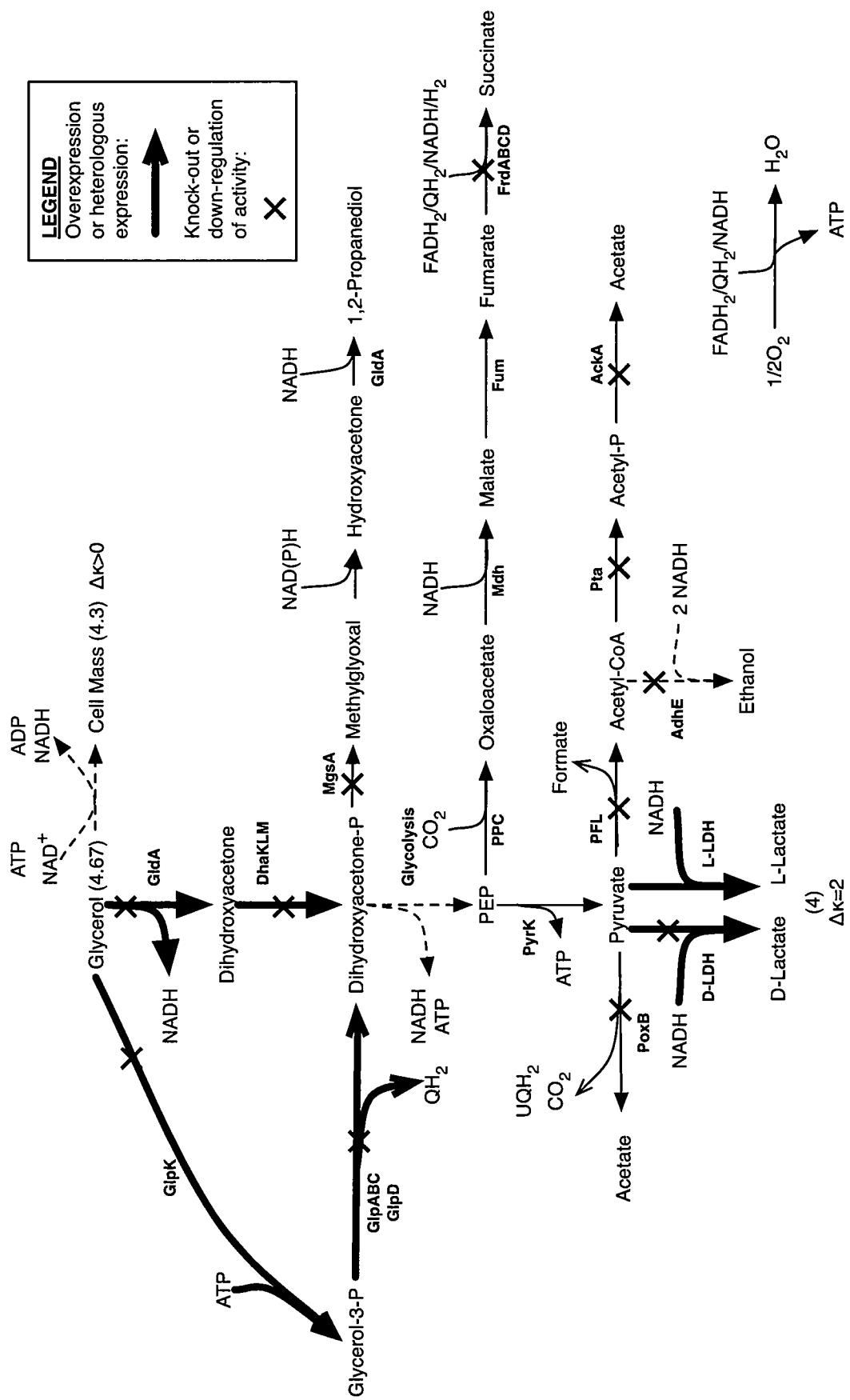


FIG. 12

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 09/62440

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12P 7/20 (2009.01)

USPC - 435/159

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

USPC: 435/159

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
USPC: 435/7.32; 435/7.37; 435/190; 435/252.31; 435/252.33; 435/252.8; 435/254.21 (text search - see terms below)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

PubWEST (USPT, PGPB, USOC, EPAB, JPAB); Google Scholar

Search Terms: alcohol, amino acid, carbon, disruption, electron, Escherichia, exogenous, feedstock, gene, glycerol, metabolize, microaerobic, microorganism, organic acid, overexpression, redox

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---	WO 2007/115228 A2 (Gonzalez) 11 October 2007 (11.10.2007), pg 1, ln 12-16, 22-23; pg 2, ln 20 - pg 3, ln 2; pg 3, ln 14-16, 23-25; pg 9, ln 12-23; pg 11, ln 7-10; pg 14, ln 18-24; pg 16, ln 21 -29; pg 17, ln 16 - pg 20, ln 2; pg 21, ln 20-22; pg 22, ln 1-3, 15-19	13-15 ----- 1-12, 16-19
Y	US 2008/0199926 A1 (Burgard et al.) 21 August 2008 (21.08.2008), para [0003]; [0006]; [0007]; [0068]; [0101]; [0132]; [0134]	1-12
Y	US 2007/0048849 A1 (Laffend et al.) 1 March 2007 (01.03.2007), abstract; para [0012]; [0017]; [0058]-[0060]; [0194]	5, 16-19

Further documents are listed in the continuation of Box C.

* Special categories of cited documents:

- “A” document defining the general state of the art which is not considered to be of particular relevance
- “E” earlier application or patent but published on or after the international filing date
- “L” document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- “O” document referring to an oral disclosure, use, exhibition or other means
- “P” document published prior to the international filing date but later than the priority date claimed

“T” later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

“X” document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

“Y” document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

“&” document member of the same patent family

Date of the actual completion of the international search

9 December 2009 (09.12.2009)

Date of mailing of the international search report

18 DEC 2009

Name and mailing address of the ISA/US

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