approaches for generating combustible products rely on the use of a large quantity of carbohydrate-rich feedstock such as sugar cane, rice, corn, or the like. Use of such resources to produce combustible fuel has the undesirable consequence of increasing the market pressures on feed stocks, driving up the price of the world's food supply.

[0005] Fatty acids are composed of long alkyl chains and represent nature's petroleum, being a primary metabolite used by cells for both chemical and energy storage functions. These energy-rich molecules are today isolated from plant and animal oils for a diverse set of products ranging from fuels to oleochemicals. A more scalable, controllable and economical route to this important class of chemicals would be beneficial to the development of renewable energy sources.

SUMMARY

[0006] In one ~~aspect~~ embodiment, the ~~invention~~ present disclosure provides a method of producing a lipid where the method includes providing a culture of a recombinant microorganism that includes a non-native gene encoding a dehydrogenase, and allowing the microorganism to proliferate under conditions in which the non-native gene is expressed, where the culture produces at least one lipid. In an aspect, there is provided a method of culturing a lipid-producing photosynthetic microorganism comprising: providing a culture of a recombinant photosynthetic microorganism that comprises a non-native gene encoding a dehydrogenase and at least one non-native gene encoding a thioesterase in a suitable culture medium under conditions in which the non-native gene encoding the dehydrogenase and the non-native gene encoding the thioesterase are expressed, wherein the culture produces a greater amount of the lipid than does a culture comprising a control microorganism identical in all respects except that it does not include the gene encoding a non-native dehydrogenase, further wherein the recombinant photosynthetic microorganism that comprises the non-native gene encoding a dehydrogenase has a higher growth and/or proliferation rate than the control microorganism that lacks the gene encoding the non-native dehydrogenase. Preferably, the culture produces a greater amount of the lipid than the amount of lipid produced by a control culture of a control microorganism identical in all respects to the recombinant microorganism that expresses a non-native dehydrogenase gene, except that the control microorganism does not express the gene encoding a non-native dehydrogenase. The recombinant microorganism that expresses a non-native gene encoding a dehydrogenase and produces a lipid can have a higher proliferation rate than a control microorganism that does not express a non-native dehydrogenase gene. The lipid produced by the recombinant microorganism can be any lipid, and can preferably be a fatty acid product, *e.g.*, a fatty acid, fatty acid derivative, or a triglyceride. Additionally, the recombinant microorganism may include an additional non-native gene that encodes a polypeptide that participates in the biosynthesis of a lipid. The recombinant microorganism that expresses the non-native dehydrogenase gene can be cultured in a suitable culture medium, for example, a culture medium that supports growth and/or proliferation of the recombinant microorganism. The method can further include isolating at least one lipid from the culture.

[0007] Also provided herein, in certain ~~aspects~~embodiments, is a method of improving the propagation and/or proliferation rate of a microorganism that produces a lipid, in which the method includes expressing a recombinant nucleic acid molecule that encodes a dehydrogenase in a microorganism that produces a lipid, and culturing the microorganism under conditions that support the propagation of the microorganism, wherein the propagation and/or proliferation rate of the microorganism is greater than that of a control microorganism that is cultured under the same conditions and is identical in all respects to the recombinant microorganism, except that the control microorganism does not express a recombinant nucleic acid molecule that encodes a dehydrogenase. Additionally the microorganism can include at least one additional non-native gene, in which the additional non-native gene(s) encode one or more polypeptides that participate in the synthesis of a lipid.

[0008] The dehydrogenase encoded by the non-native gene or recombinant nucleic acid molecule can be a dehydrogenase that can use NADP in oxidation reactions. Additonally or alternatively, the non-native gene can encode a dehydrogenase that is heterologous (derived from a different species) or homologous (derived from the same species) with respect to the host microorganism, and in certain ~~aspects~~ embodiments the non-native gene can be an endogenous gene engineered for overexpression in the host microorganism. In various examples, the dehydrogenase can be an aldehyde dehydrogenase (including, for example, a methylmalonate semialdehyde dehydrogenase or a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9)), a D-2-hydroxyacid dehydrogenase, a glucose-6-phosphate dehydrogenase, a 6-phosphogluconate dehydrogenase, a sorbitol dehydrogenase, an isocitrate dehydrogenase, or a malic enzyme. For example, the recombinant microorganism can include a non-native gene encoding an aldehyde dehydrogenase, which in some examples can include an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:4, SEQ ID NO:4,or SEQ ID NO:7, or an active fragment thereof. Alternatively or in addition, the recombinant microorganism can include a non-native gene encoding a methylmalonate semialdehyde dehydrogenase, and in some examples can be a methylmalonate semialdehyde dehydrogenase that includes an amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the

Geitlerinema, Gloeobacter, Gloeocapsa, Gloeothece, Halospirulina, Iyengariella, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Microcystis, Myxosarcina, Nodularia, Nostoc, Nostochopsis, Oscillatoria, Phormidium, Planktothrix, Pleurocapsa, Prochlorococcus, Prochloron, Prochlorothrix, Pseudanabaena, Rivularia, Schizothrix, Scytonema, Spirulina, Stanieria, Starria, Stigonema, Symploca, Synechococcus, Synechocystis, Thermosynechococcus, Tolypothrix, Trichodesmium, Tychonema or *Xenococcus*.

[0010] A photosynthetic host microorganism of the ~~invention~~ present disclosure can be cultured photoautotrophically for the production of a lipid, for example using inorganic carbon as substantially the sole source of carbon in the culture medium. The microorganism can be provided with inorganic carbon in the culture medium, for example, CO_2 and/or carbonate can be supplied to the culture during the culture period.

[0011] A recombinant microorganism comprising a non-native gene encoding a dehydrogenase, which may be a photosynthetic microorganism, can further include a second non-native gene encoding a polypeptide that participates in the production of a lipid, such as a fatty acid product or a triglyceride. As nonlimiting examples, a polypeptide that participates in the production of a lipid can be an acetyl-CoA carboxylase, a malonyl CoA: ACP transacylase, a beta-ketoacyl-ACP synthase, an acyl-ACP thioesterase, an acyl-CoA thioesterase, a hydroxylbenzoyl thioesterase, a polypeptide having lipolytic activity, an acyl-CoA synthetase, an acyl-CoA reductase, an acyl-ACP reductase, a carboxylic acid reductase, a wax synthase, a decarboxylase, a decarbonylase, a glycerolphosphate acyltransferase (GPAT), a lysophosphatidic acid acyltransferase (LPAAT), a phosphatidic acid phosphatase (PA), or a diacylglycerol O-acyltransferase (DGAT). The recombinant microorganism can produce, for example, a fatty acid, a fatty acid derivative such as a fatty aldehyde, a fatty alcohol, a fatty acid ester, a wax ester, an alkane, or an alkene, or can produce a triglyceride, any of which may be, in particular examples, a lipid that is not naturally produced by the microorganism when not transformed with a gene that participates in production of the lipid. For example, the recombinant microorganism can include a second non-native gene encoding a thioesterase, and can produce a fatty acid product, *e.g.*, a free fatty acid or a fatty acid derivative. The fatty acid product can include at least one acyl chain of C8-C14, for example, of C12-C24, such as from C12-C18.

[0012] The recombinant microorganism that includes a first non-native gene encoding a dehydrogenase and a second non-native gene encoding a polypeptide that participates in the

can be an aldehyde dehydrogenase, a D-2-hydroxyacid dehydrogenase, a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase, a glucose-6-phosphate dehydrogenase, a 6-phosphogluconate dehydrogenase, an isocitrate dehydrogenase, or a malic enzyme. For example the dehydrogenase can be an aldehyde dehydrogenase, and in some examples can have at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, or SEQ ID NO:7, or an active fragment thereof. Alternatively or in addition, the microorganism can include a methylmalonate semialdehyde dehydrogenase, and in some examples can be a methylmalonate semialdehyde dehydrogenase having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:18 or SEQ ID NO:19, or an active fragment thereof. Alternatively or in addition, the microorganism can include a non-native gene encoding a D-2-hydroxyacid dehydrogenase, and in some examples can be a D-2-hydroxyacid dehydrogenase that has at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15 or SEQ ID NO:16, or an active fragment thereof. Alternatively or in addition, the microorganism can include a non-native gene encoding a 6-phosphogluconate dehydrogenase. The 6-phosphogluconate in some examples has at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to the amino acid sequence of SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13, or an active fragment thereof.

[0015] The methods can further include isolating at least on lipid from the culture. Lipids can be isolated from cells, media, or whole culture. Also provided herein is a lipid produced by any of the methods or recombinant microorganisms provided herein. The lipid can be any or any combination of a fatty acid, fatty aldehyde, fatty alcohol, fatty acid ester, wax ester, alkane, alkene, phospholipid, galactolipid, or triglyceride. The lipid can comprise at least one acyl chain containing between 8 and 24 carbon atoms, such as between 12 and 24 carbon atoms, for example, between 12 and 18 carbon atoms.

[0016] In an aspect, there is provided a recombinant photosynthetic microorganism comprising a first non-native gene encoding a dehydrogenase, wherein the photosynthetic microorganism further comprises at least a second non-native gene encoding a thioesterase, wherein the photosynthetic microorganism produces a lipid, further wherein the photosynthetic microorganism has a higher growth and/or proliferation rate than an otherwise identical microorganism that lacks the non-native gene encoding a dehydrogenase. In some ~~aspects~~embodiments, the ~~invention~~ present disclosure relates to a recombinant photosynthetic microorganism comprising a first recombinant nucleic acid molecule comprising a first nucleotide sequence at

least 50% identical to SEQ ID NO:3, SEQ ID NO:9, SEQ ID NO:1, SEQ ID NO:12, SEQ ID NO:14, or SEQ ID NO:17, where the nucleic acid molecule encodes a dehydrogenase. The recombinant photosynthetic microorganism can be engineered for the production of a fatty acid product, and can include at least a second recombinant nucleic acid molecule or nucleotide sequence that encodes a polypeptide that participates in the synthesis of a lipid. For example, the photosynthetic microorganism can include a recombinant nucleotide sequence encoding a polypeptide that participates in the synthesis of a free fatty acid, fatty acid derivative, or triglyceride that is not naturally produced by the photosynthetic microorganism, which can be, for example, a cyanobacterium. For example, the photosynthetic microorganism can include a recombinant nucleotide sequence encoding an acyl-ACP thioesterase and can produce a free fatty acid or a fatty acid derivative. In illustrative examples, the acyl-ACP thioesterase can be a higher plant acyl-ACP thioesterase or a variant thereof, such as, for example, the acyl-ACP thioesterase of SEQ ID NO:21.

[0017] The ~~invention~~ present disclosure provides, in additional examples, a recombinant microorganism comprising an non-native first nucleic acid molecule comprising a nucleotide sequence encoding an aldehyde dehydrogenase or a D-2-hydroxyacid dehydrogenase, wherein the photosynthetic microorganism produces more of a fatty acid, fatty acid derivative, or lipid than is made by an otherwise identical microorganism that lacks the exogenous first nucleic acid molecule. In some embodiments, the organism further expresses at least one second non-native nucleic acid molecule encoding an enzyme selected from the group consisting of non-native acyl-ACP thioesterase, acyl-CoA thioesterase, hydroxybenzoyl thioesterase, acyl-ACP reductase, acyl-ACP reductase, wax synthase, decarbonylase, decarboxylase, acetyl-CoA carboxylase, malonyl CoA: ACP transacylase, beta-ketoacyl-ACP synthase, glycerolphosphate acyltransferase (GPAT), lysophosphatidic acid acyltransferase (LPAAT), phosphatidic acid phosphatase (PAP), or diacylglycerol O-acyltransferase (DGAT). Additionally, the microorganism may produce a fatty acid, fatty acid derivative, or glycerolipid that is not made by the microorganism in the absence of the second non-native nucleic acid molecule. The recombinant microorganism may be a photosynthetic microorganism, and may produce more of a fatty acid, fatty acid derivative, or glycerolipid than is made by an otherwise identical microorganism that lacks the first nucleic acid under photoautotrophic conditions. In some ~~aspects~~embodiments, the ~~invention~~ present disclosure relates to a method of producing a fatty acid product comprising culturing a recombinant photosynthetic

microorganism of the ~~invention~~ present disclosure that includes a first non-native gene encoding an aldehyde dehydrogenase or a D-2-hydroxyacid dehydrogenase and includes a second non-native gene encoding a polypeptide that participates in fatty acid, fatty acid derivative, or lipid biosynthesis for a sufficient amount of time to produce a fatty acid product. The fatty acid product can be a product not naturally produced by the photosynthetic microorganism.

[0018] Also provided is a recombinant photosynthetic microorganism comprising an homologous phosphogluconate dehydrogenase gene that is under the control of a heterologus promoter, *i.e.*, a promoter that does not normally regulate the phosphogluconate dehydrogenase gene. For example, the phosphogluconate dehydrogenase gene can be operably linked to a heterologous, and preferably regulatable, promoter, and can be integrated into a non-native locus within the genome of the recombinant microorganism. Alternatively, a heterologous promoter can be inserted into the host genome to become operably linked to an endogenous phosphogluconate dehydrogenase gene, such that the endogenous phosphhogluconate dehydrogenase can be overexpressed in the host microorganism. In some embodiments, the cell further expresses a second nucleic acid comprising a second nucleotide sequence encoding polypeptide that participates in the production of a lipid (*e.g.*, a fatty acid product) in which the expression of phosphogluconate dehydrogenase gene increases the propagation and/or proliferation rate of the microorganism relative to an otherwise identical microorganism that does not include a recombinant phosphogluconate dehydrogenase gene.

[0019] In some embodiments, the photosynthetic microorganism is a cyanobacterium. In some embodiments, the cyanobacterium is selected from a group consisting of *Agmenellum, Anabaena, Anabaenopsis, Anacystis, Aphanizomenon, Arthrospira, Asterocapsa, Borzia, Calothrix, Chamaesiphon, Chlorogloeopsis, Chroococcidiopsis, Chroococcus, Crinalium, Cyanobacterium, Cyanobium, Cyanocystis, Cyanospira, Cyanothece, Cylindrospermopsis, Cylindrospermum, Dactylococcopsis, Dermocarpella, Fischerella, Fremyella, Geitleria, Geitlerinema, Gloeobacter, Gloeocapsa, Gloeothece, Halospirulina, Iyengariella, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Microcystis, Myxosarcina, Nodularia, Nostoc, Nostochopsis, Oscillatoria, Phormidium, Planktothrix, Pleurocapsa, Prochlorococcus, Prochloron, Prochlorothrix, Pseudanabaena, Rivularia, Schizothrix, Scytonema, Spirulina, Stanieria, Starria, Stigonema, Symploca, Synechococcus, Synechocystis, Thermosynechococcus, Tolypothrix, Trichodesmium, Tychonema,* and *Xenococcus*.

[0020] The ~~invention~~ present disclosure also provides a method of producing free fatty acids, fatty acid derivatives, or lipids by the photosynthetic microorganism. The method can comprise culturing a photosynthetic microorganism described herein under conditions in which the first non-native nucleic acid molecule and the second nucleic acid molecule is expressed to produce at least one fatty acid or fatty acid derivative. Optionally, the photosynthetic microorganism is cultured phototrophically.

[0021] The expression of a non-native gene encoding a dehydrogenase and the expression of gene encoding a polypeptide for lipid biosynthesis in a recombinant microorganism can result in increased production of a fatty acid product, by a culture of the dehydrogenase-overexpressing microorganism relative to the production of a fatty acid product by a culture of a control microorganism cultured identically, and in which the control microorganism is substantially identical to the non-native dehydrogenase gene-expressing microorganism except that the control microorganism lacks the non-native dehydrogenase gene. In some embodiments, the amount of a free fatty acid, fatty acid derivative, or glycerolipid produced by a culture of a microorganism expressing the non-native dehydrogenase gene and a non-native lipid biosynthesis gene is at least 1%, at least 5%, at least 8%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 150%, or at least 200% more than the free fatty acid, fatty acid derivative, or glycerolipid produced by a culture of the control microorganism lacking the non-native dehydrogenase gene. The microorganism can be a photosynthetic microorganism.

[0022] Additionally or alternatively, the expression of a non-native gene encoding a dehydrogenase and the expression of gene encoding a polypeptide for lipid biosynthesis in a recombinant microorganism can increase the intracellular ratio of NADPH to $NADP^+$ relative to the ratio of NADPH to $NADP^+$ in an otherwise identical microorganism that lacks the non-native dehydrogenase gene. For example, the NADPH to $NADP^+$ ratio in cells expressing the non-native dehydrogenase gene and non-native lipid biosynthesis gene can be at least 1%, at least 5%, at least 8%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 150%, or at least 200% higher than the NADPH to $NADP^+$ ratio of an otherwise identical control microorganism lacking the non-native dehydrogenase gene during a culture period in which lipid is being produced. The microorganism can be a photosynthetic microorganism.

[0023] Further additionally or alternatively, the expression of a non-native gene encoding a dehydrogenase and the expression of gene encoding a polypeptide for lipid biosynthesis in a recombinant microorganism can increase the propagation rate and/or the proliferation rate of the engineered microorganism relative to the propagation and/or proliferation rate of an otherwise identical microorganism that lacks the non-native dehydrogenase gene. For example, the propagation rate or the proliferation rate can be at least 1%, at least 5%, at least 8%, at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 150%, or at least 200% higher than the propagation rate and/or the proliferation rate of a control microorganism that expresses the non-native lipid biosynthesis gene but does not include the non-native gene encoding a dehydrogenase. For example, a culture of the engineered microorganism that includes a non-native gene encoding a dehydrogenase and a non-native gene encoding a polypeptide for lipid biosynthesis can achieve a higher cell density after three, four, five, six, or more days in culture that can be achieved by a culture of an otherwise identical microorganism that does not include the non-native gene encoding the dehydrogenase, where the culture is producing a lipid. The microorganism can be a photosynthetic microorganism.

[0024] The amount of the free fatty acids, fatty acid derivatives, or lipids produced by the photosynthetic microorganism according to the ~~invention~~ present disclosure can be at least 290 mg, at least 330 mg, at least 370 mg, at least 400 mg, at least 500 mg, at least 600 mg per liter of culture. Additionally, the method of producing a fatty acid product can further comprise isolating at least one fatty product from the photosynthetic microorganism or from the growth media.

[0025] In a further ~~aspect~~embodiment, the ~~invention~~ present disclosure provides an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide sequence that includes an amino acid sequence at least 65% identical, at least 75% identical, at least 85% identical or at least 95% identical to SEQ ID NO:2 or SEQ ID NO:29 or an active fragment thereof. The encoded polypeptide can have dehydrogenase activity, for example, D-2-hydroxyacid dehydrogenase activity. The nucleic acid molecule can further comprise a promoter, which can be heterologous with respect to the dehydrogenase encoding sequence, and can be regulatable, for example, inducible. The nucleic acid molecule can be provided in a vector.

[0025a] In a further aspect, there is provided an expression cassette comprising a heterologous promoter operably linked to a nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence having at least 65% identity to SEQ ID NO:29 and a nucleic acid sequence encoding a thioesterase.

WHAT IS CLAIMED IS:

1. A method of culturing a lipid-producing photosynthetic microorganism comprising:

providing a culture of a recombinant photosynthetic microorganism that comprises a non-native gene encoding a dehydrogenase and at least one non-native gene encoding a ~~polypeptide for the production of a lipid~~ thioesterase in a suitable culture medium under conditions in which the non-native gene encoding the dehydrogenase and the ~~at least one~~ non-native gene ~~for~~ encoding the ~~production of a lipid~~ thioesterase are expressed,

wherein the culture produces a greater amount of the lipid than does a culture comprising a control microorganism identical in all respects except that it does not include the gene encoding a non-native dehydrogenase,

further wherein the recombinant photosynthetic microorganism that comprises the non-native gene encoding a dehydrogenase has a higher growth and/or proliferation rate than the control microorganism that lacks the gene encoding the non-native dehydrogenase.

2. The method of Claim 1, wherein the dehydrogenase is an NADP-dependent dehydrogenase.

3. The method of either Claim 1 or Claim 2, wherein the dehydrogenase is an aldehyde dehydrogenase, a methylmalonate semialdehyde dehydrogenase, a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase, a D-2-hydroxyacid dehydrogenase, a glucose-6-phosphate dehydrogenase, a 6-phosphogluconate dehydrogenase, an isocitrate dehydrogenase, or a malic enzyme.

4. The method of Claim 3, wherein the dehydrogenase is an aldehyde dehydrogenase.

5. The method of Claim 4, wherein the aldehyde dehydrogenase comprises an amino acid sequence having at least 7050% sequence identity~~, preferably at least 85% sequence identity~~ to SEQ ID NO:4 ~~or to an active fragment thereof~~.

6. The method of Claim 5, wherein the aldehyde dehydrogenase comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:4.

~~6.~~7. The method of Claim 3, wherein the dehydrogenase is a methylmalonate semialdehyde dehydrogenase.

~~7.~~8. The method of Claim ~~6~~7, wherein the methylmalonate semialdehyde dehydrogenase comprises an amino acid sequence having at least ~~50~~70% sequence identity~~, preferably at least 85% sequence identity~~ to an amino acid sequence selected from the group consisting of SEQ ID NO:18~~,~~ and SEQ ID NO:19~~, and active fragments thereof~~.

9. The method of Claim 8, wherein the methylmalonate semialdehyde dehydrogenase comprises an amino acid sequence having at least 85% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:18 and SEQ ID NO:19.

~~8.~~10. The method of Claim 3, wherein the dehydrogenase is a D-2-hydroxyacid dehydrogenase.

~~9.~~11. The method of Claim ~~8~~10, wherein the D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least ~~50~~70% sequence identity~~, preferably at least 85% sequence identity~~ to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15~~,~~ and SEQ ID NO:16~~, and active fragments thereof~~.

12. The method of Claim 11, wherein the D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least 85% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15 and SEQ ID NO:16.

~~10.~~13. The method of Claim 3, wherein the dehydrogenase is a 6-phosphogluconate dehydrogenase.

~~11.~~14. The method of Claim ~~10~~13, wherein the ~~a~~ 6-phosphogluconate dehydrogenase comprises an amino acid sequence having at least ~~50~~70% sequence identity~~, preferably at least 85% sequence identity~~ to an amino acid sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11~~,~~ and SEQ ID NO:13~~, and active fragments thereof~~.

15. The method of Claim 14, wherein the 6-phosphogluconate dehydrogenase has at least 85% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:13.

~~12.~~16. The method of Claim ~~10~~13, wherein the 6-phosphogluconate dehydrogenase is endogenous to the recombinant photosynthetic microorganism.

~~13.~~17. The method of ~~any one of~~ Claim~~s~~ 1~~–12~~, wherein the recombinant photosynthetic microorganism is a microalga~~, preferably a microalga of a species selected from the group consisting of the genera: *Achnanthes, Amphiprora, Amphora, Ankistrodesmus, Asteromonas, Bockelovia, Borodinella, Botryococcus, Bracteococcus, Chaetoceros, Carteria, Chlamydomonas, Chlorococcum, Chlorogonium, Chlorella, Chroomonas, Chrysosphaera, Cricosphaera, Crypthecodinium, Cryptomonas, Cyclotella, Dunaliella, Ellipsoidon, Emiliania, Eremosphaera, Ernodesmius, Euglena, Franceia, Fragilaria, Gloeothamnion, Haematococcus, Halocafeteria, Hymenomonas, Isochrysis, Lepocinclis, Micractinium, Monoraphidium, Nannochloris, Nannochloropsis, Navicula, Neochloris, Nephrochloris, Nephroselmis, Nitzschia, Ochromonas, Oedogonium, Oocystis*~~,

~~*Ostreococcus*, *Pavlova*, *Parachlorella*, *Pascheria*, *Phaeodactylum*, *Phagus*, *Picochlorum*, *Platymonas*, *Pleurochrysis*, *Pleurococcus*, *Prototheca*, *Pseudochlorella*, *Pseudoneochloris*, *Pyramimonas*, *Pyrobotrys*, *Scenedesmus*, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, and *Volvox*.~~

18. The method of Claim 17, wherein the recombinant photosynthetic microorganism is a species of an *Achnanthes*, *Amphiprora*, *Amphora*, *Ankistrodesmus*, *Asteromonas*, *Boekelovia*, *Borodinella*, *Botryococcus*, *Bracteococcus*, *Chaetoceros*, *Carteria*, *Chlamydomonas*, *Chlorococcum*, *Chlorogonium*, *Chlorella*, *Chroomonas*, *Chrysosphaera*, *Cricosphaera*, *Crypthecodinium*, *Cryptomonas*, *Cyclotella*, *Dunaliella*, *Ellipsoidon*, *Emiliania*, *Eremosphaera*, *Ernodesmius*, *Euglena*, *Franceia*, *Fragilaria*, *Gloeothamnion*, *Haematococcus*, *Halocafeteria*, *Hymenomonas*, *Isochrysis*, *Lepocinclis*, *Micractinium*, *Monoraphidium*, *Nannochloris*, *Nannochloropsis*, *Navicula*, *Neochloris*, *Nephrochloris*, *Nephroselmis*, *Nitzschia*, *Ochromonas*, *Oedogonium*, *Oocystis*, *Ostreococcus*, *Pavlova*, *Parachlorella*, *Pascheria*, *Phaeodactylum*, *Phagus*, *Picochlorum*, *Platymonas*, *Pleurochrysis*, *Pleurococcus*, *Prototheca*, *Pseudochlorella*, *Pseudoneochloris*, *Pyramimonas*, *Pyrobotrys*, *Scenedesmus*, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, or *Volvox*.

~~14.~~19. The method of ~~any one of~~ Claims ~~1–12~~, wherein the recombinant photosynthetic microorganism is a cyanobacterium.~~, preferably a cyanobacterium of a species selected from the group consisting of the genera: *Agmenellum*, *Anabaena*, *Anabaenopsis*, *Anacystis*, *Aphanizomenon*, *Arthrospira*, *Asterocapsa*, *Borzia*, *Calothrix*, *Chamaesiphon*, *Chlorogloeopsis*, *Chroococcidiopsis*, *Chroococcus*, *Crinalium*, *Cyanobacterium*, *Cyanobium*, *Cyanocystis*, *Cyanospira*, *Cyanothece*, *Cylindrospermopsis*, *Cylindrospermum*, *Dactylococcopsis*, *Dermocarpella*, *Fischerella*, *Fremyella*, *Geitleria*, *Geitlerinema*, *Gloeobacter*, *Gloeocapsa*, *Gloeothece*, *Halospirulina*, *Iyengariella*, *Leptolyngbya*, *Limnothrix*, *Lyngbya*, *Microcoleus*, *Microcystis*, *Myxosarcina*, *Nodularia*, *Nostoc*, *Nostochopsis*, *Oscillatoria*, *Phormidium*, *Planktothrix*, *Pleurocapsa*, *Prochlorococcus*, *Prochloron*, *Prochlorothrix*, *Pseudanabaena*, *Rivularia*, *Schizothrix*, *Scytonema*, *Spirulina*, *Stanieria*, *Starria*, *Stigonema*, *Symploca*, *Synechococcus*, *Synechocystis*, *Thermosynechococcus*, *Tolypothrix*, *Trichodesmium*, *Tychonema* and *Xenococcus*.~~

20. The method of Claim 19, wherein the recombinant photosynthetic microorganism is a species of *Agmenellum*, *Anabaena*, *Anabaenopsis*, *Anacystis*, *Aphanizomenon*, *Arthrospira*,

Asterocapsa, Borzia, Calothrix, Chamaesiphon, Chlorogloeopsis, Chroococcidiopsis, Chroococcus, Crinalium, Cyanobacterium, Cyanobium, Cyanocystis, Cyanospira, Cyanothece, Cylindrospermopsis, Cylindrospermum, Dactylococcopsis, Dermocarpella, Fischerella, Fremyella, Geitleria, Geitlerinema, Gloeobacter, Gloeocapsa, Gloeothece, Halospirulina, Iyengariella, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Microcystis, Myxosarcina, Nodularia, Nostoc, Nostochopsis, Oscillatoria, Phormidium, Planktothrix, Pleurocapsa, Prochlorococcus, Prochloron, Prochlorothrix, Pseudanabaena, Rivularia, Schizothrix, Scytonema, Spirulina, Stanieria, Starria, Stigonema, Symploca, Synechococcus, Synechocystis, Thermosynechococcus, Tolypothrix, Trichodesmium, Tychonema or *Xenococcus.*

~~15.~~21. The method of ~~either~~ Claim 1~~3 or Claim 14~~, wherein the recombinant photosynthetic microorganism is cultured photoautotrophically.

~~16.~~22. A recombinant photosynthetic microorganism comprising a first non-native gene encoding a dehydrogenase, wherein the photosynthetic microorganism further comprises at least a second non-native gene encoding ~~an enzyme that participates in the production of a lipid, wherein the enzyme is selected from the group consisting of an acyl-ACP thioesterase, an acyl-CoA thioesterase, a hydroxybenzoyl thioesterase, a polypeptide having lipolytic activity, an acyl-CoA synthetase, an acyl-CoA reductase, an acyl-ACP reductase, a carboxylic acid reductase, a wax synthase, a decarboxylase, a decarbonylase, a GPAT, an LPAAT, a PAP, and a DGAT~~a thioesterase;

wherein the photosynthetic microorganism produces a lipid;

further wherein the photosynthetic microorganism has a higher growth and/or proliferation rate than an otherwise identical microorganism that lacks the non-native gene encoding a dehydrogenase.

~~17.~~23. The recombinant photosynthetic microorganism of Claim ~~16~~22, wherein the lipid is a fatty acid, a fatty acid derivative, or a triglyceride.

~~18.~~24. The recombinant photosynthetic microorganism of either Claim ~~16 or Claim 17~~ 22, wherein the dehydrogenase is an NADP-dependent dehydrogenase.

~~19.~~25. The recombinant photosynthetic microorganism of Claim ~~18~~24, wherein the dehydrogenase is an aldehyde dehydrogenase, a methylmalonate semialdehyde dehydrogenase, a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase, a D-2-hydroxyacid dehydrogenase, a glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase, an isocitrate dehydrogenase, or a malic enzyme.

~~20.~~26. The recombinant photosynthetic microorganism of Claim ~~19~~25, wherein the dehydrogenase is an aldehyde dehydrogenase.

~~21.~~27. The recombinant photosynthetic microorganism of Claim ~~20~~26, wherein the aldehyde dehydrogenase comprises an amino acid sequence having at least ~~50~~70% identity~~, preferably at least 85% sequence identity~~ to SEQ ID NO:4 ~~or active fragments thereof~~.

28. The recombinant photosynthetic microorganism of Claim 27, wherein the aldehyde dehydrogenase comprises an amino acid sequence having at least 85% identity to SEQ ID NO:4.

~~22.~~29. The recombinant photosynthetic microorganism of Claim ~~19~~25, wherein the dehydrogenase is a methylmalonate semialdehyde dehydrogenase.

~~23.~~30. The recombinant photosynthetic microorganism of Claim ~~22~~29, wherein the ~~aldehyde~~ methylmalonate semialdehyde dehydrogenase comprises an amino acid sequence having at least ~~50~~70%~~, preferably at least 85%~~ identity to an amino acid sequence selected from the group consisting of SEQ ID NO:18~~,~~ and SEQ ID NO:19~~, and active fragments thereof~~.

31. The recombinant photosynthetic microorganism of Claim 30, wherein the methylmalonate semialdehyde dehydrogenase comprises an amino acid sequence having at least 85% identity to an amino acid sequence selected from the group consisting of SEQ ID NO:18 and SEQ ID NO:19.

~~24.~~32. The recombinant photosynthetic microorganism of Claim ~~19~~25, wherein the dehydrogenase is a D-2-hydroxyacid dehydrogenase.

~~25.~~33. The recombinant photosynthetic microorganism of Claim ~~24~~32, wherein the ~~aldehyde~~ D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least ~~50~~70% identity~~, preferably at least 85% identity~~

to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, and SEQ ID NO:16, ~~and active fragments thereof~~.

34. The recombinant photosynthetic microorganism of Claim 33, wherein the D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least 85% identity to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15 and SEQ ID NO:16.

~~26.~~35. The recombinant photosynthetic microorganism of ~~any one of~~ Claim~~s~~ ~~16-25~~22, wherein the recombinant photosynthetic microorganism is a microalga., ~~preferably a microalga of a species selected from the group consisting of the genera: *Achnanthes*, *Amphiprora*, *Amphora*, *Ankistrodesmus*, *Asteromonas*, *Boekelovia*, *Borodinella*, *Botryococcus*, *Bracteococcus*, *Chaetoceros*, *Carteria*, *Chlamydomonas*, *Chlorococcum*, *Chlorogonium*, *Chlorella*, *Chroomonas*, *Chrysosphaera*, *Cricosphaera*, *Crypthecodinium*, *Cryptomonas*, *Cyclotella*, *Dunaliella*, *Ellipsoidon*, *Emiliania*, *Eremosphaera*, *Ernodesmius*, *Euglena*, *Franceia*, *Fragilaria*, *Gloeothamnion*, *Haematococcus*, *Halocafeteria*, *Hymenomonas*, *Isochrysis*, *Lepocinclis*, *Micractinium*, *Monoraphidium*, *Nannochloris*, *Nannochloropsis*, *Navicula*, *Neochloris*, *Nephrochloris*, *Nephroselmis*, *Nitzschia*, *Ochromonas*, *Oedogonium*, *Oocystis*, *Ostreococcus*, *Pavlova*, *Parachlorella*, *Pascheria*, *Phaeodactylum*, *Phagus*, *Picochlorum*, *Platymonas*, *Pleurochrysis*, *Pleurococcus*, *Prototheca*, *Pseudochlorella*, *Pseudoneochloris*, *Pyramimonas*, *Pyrobotrys*, *Scenedesmus*, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, and *Volvox*.~~

36. The recombinant photosynthetic microorganism of Claim 35, wherein the recombinant photosynthetic microorganism is a species of a genus selected from the group consisting of: *Achnanthes*, *Amphiprora*, *Amphora*, *Ankistrodesmus*, *Asteromonas*, *Boekelovia*, *Borodinella*, *Botryococcus*, *Bracteococcus*, *Chaetoceros*, *Carteria*, *Chlamydomonas*, *Chlorococcum*, *Chlorogonium*, *Chlorella*, *Chroomonas*, *Chrysosphaera*, *Cricosphaera*, *Crypthecodinium*, *Cryptomonas*, *Cyclotella*, *Dunaliella*, *Ellipsoidon*, *Emiliania*, *Eremosphaera*, *Ernodesmius*, *Euglena*, *Franceia*, *Fragilaria*, *Gloeothamnion*, *Haematococcus*, *Halocafeteria*, *Hymenomonas*, *Isochrysis*, *Lepocinclis*, *Micractinium*, *Monoraphidium*, *Nannochloris*, *Nannochloropsis*, *Navicula*, *Neochloris*, *Nephrochloris*, *Nephroselmis*, *Nitzschia*, *Ochromonas*, *Oedogonium*, *Oocystis*, *Ostreococcus*, *Pavlova*, *Parachlorella*, *Pascheria*, *Phaeodactylum*, *Phagus*, *Picochlorum*, *Platymonas*, *Pleurochrysis*, *Pleurococcus*, *Prototheca*, *Pseudochlorella*, *Pseudoneochloris*, *Pyramimonas*, *Pyrobotrys*,

Scenedesmus, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, and *Volvox*.

~~27.~~37. The recombinant photosynthetic microorganism of ~~any one of~~ Claim~~s~~ ~~16-25~~22, wherein the recombinant photosynthetic microorganism is a cyanobacterium., ~~preferably a microalga of a species selected from the group consisting of the genera: *Agmenellum, Anabaena, Anabaenopsis, Anacystis, Aphanizomenon, Arthrospira, Asterocapsa, Borzia, Calothrix, Chamaesiphon, Chlorogloeopsis, Chroococcidiopsis, Chroococcus, Crinalium, Cyanobacterium, Cyanobium, Cyanocystis, Cyanospira, Cyanothece, Cylindrospermopsis, Cylindrospermum, Dactylococcopsis, Dermocarpella, Fischerella, Fremyella, Geitleria, Geitlerinema, Gloeobacter, Gloeocapsa, Gloeothece, Halospirulina, Iyengariella, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Microcystis, Myxosarcina, Nodularia, Nostoc, Nostochopsis, Oscillatoria, Phormidium, Planktothrix, Pleurocapsa, Prochlorococcus, Prochloron, Prochlorothrix, Pseudanabaena, Rivularia, Schizothrix, Scytonema, Spirulina, Stanieria, Starria, Stigonema, Symploca, Synechococcus, Synechocystis, Thermosynechococcus, Tolypothrix, Trichodesmium, Tychonema* and *Xenococcus*.~~

38. The recombinant photosynthetic microorganism of Claim 37, wherein the recombinant photosynthetic microorganism is a species of a genus selected from the group consisting of: *Agmenellum, Anabaena, Anabaenopsis, Anacystis, Aphanizomenon, Arthrospira, Asterocapsa, Borzia, Calothrix, Chamaesiphon, Chlorogloeopsis, Chroococcidiopsis, Chroococcus, Crinalium, Cyanobacterium, Cyanobium, Cyanocystis, Cyanospira, Cyanothece, Cylindrospermopsis, Cylindrospermum, Dactylococcopsis, Dermocarpella, Fischerella, Fremyella, Geitleria, Geitlerinema, Gloeobacter, Gloeocapsa, Gloeothece, Halospirulina, Iyengariella, Leptolyngbya, Limnothrix, Lyngbya, Microcoleus, Microcystis, Myxosarcina, Nodularia, Nostoc, Nostochopsis, Oscillatoria, Phormidium, Planktothrix, Pleurocapsa, Prochlorococcus, Prochloron, Prochlorothrix, Pseudanabaena, Rivularia, Schizothrix, Scytonema, Spirulina, Stanieria, Starria, Stigonema, Symploca, Synechococcus, Synechocystis, Thermosynechococcus, Tolypothrix, Trichodesmium, Tychonema* and *Xenococcus*.

~~28.~~39. An expression cassette comprising a heterologous promoter operably linked to a ~~isolated~~ nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence having at least 65% identity~~, preferably at least 85% identity~~ to SEQ ID NO:29 and a nucleic acid sequence encoding a thioesterase.

40. The expression cassette of Claim 39, wherein the nucleic acid sequence encodes a polypeptide comprising an amino acid sequence having at least 85% identity to SEQ ID NO:29.

41. The method of Claim 1, wherein the thioesterase is an acyl-ACP thioesterase.

42. The recombinant photosynthetic microorganism of Claim 22, wherein the thioesterase is an acyl-ACP thioesterase.