CELL SYSTEMS AND METHODS FOR IMPROVING FATTY ACID SYNTHESIS BY EXPRESSION OF DEHYDROGENASES

REFERENCE TO A SEQUENCE LISTING

[0001] This application contains references to amino acid sequences and/or nucleic acid sequences which have been submitted concurrently herewith as the sequence listing text file "61037527_1.txt", file size 84 KiloBytes (KB), created on 4 December 2012. The aforementioned sequence listing is hereby incorporated by reference in its entirety pursuant to 37 C.F.R. §1.52(e)(ii).

FIELD

[0002] The present invention relates, in some embodiments, to the engineering of a metabolic pathway in a photosynthetic microorganism. Specifically, the invention relates to engineering pathways for the synthesis of fatty acids, fatty acid derivatives, and/or lipids. The present invention also relates to methods, microorganisms, and nucleic acid molecules for producing lipids, such as fatty acid products, in photosynthetic microorganisms, which can be used for a variety of products, including biofuels.

BACKGROUND

[0003] Fossil fuel is a general term for buried combustible geologic deposits of organic materials formed from decayed plants and animals that have been converted to crude oil, coal, natural gas, or heavy oils by exposure to heat and pressure in the earth's crust over hundreds of millions of years. Fossil fuels are a finite, non-renewable resource.

[0004] Increased demand for energy by the global economy has also placed increasing pressure on the cost of hydrocarbons. Aside from energy, many industries, including plastics and chemical manufacturers, rely heavily on the availability of hydrocarbons as a feedstock for their manufacturing processes. Cost-effective alternatives to current sources of supply could help mitigate the upward pressure on energy and these raw material costs. Major efforts to this end are focused on the microbial production of high-energy fuels by cost-effective consolidated bioprocesses. However, some alternatives to fossils fuels production, such as fermentation-based

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 embodiment, the 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 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 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:6,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

amino acid sequence of SEQ ID NO:18 or SEQ ID NO:19, or an active fragment thereof. Alternatively or in addition, the dehydrogenase can be a D-2-hydroxyacid dehydrogenase, and in some examples can be a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence 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 recombinant microorganism can include a non-native gene encoding a 6-phosphogluconate dehydrogenase. The 6-phosphogluconate dehydrogenase in some examples can include an amino acid sequence 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 to SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13, or an active fragment thereof.

[0009] The microorganism that includes the non-native dehydrogenase gene can be a fungus, bacterium, or heterokont, and can be, for example, a photosynthetic microorganism, such as a microalga or cyanobacterium. For example, the microorganism can be a microalga that is a species 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*, *Schizochlamydella*, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetrachorella*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, or *Volvox*. Alternatively, the microorganism can be a cyanobacterium and can be 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*.

[0010] A photosynthetic host microorganism of the 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

production of a lipid can have a higher proliferation rate than a control microorganism identical in all respects to the recombinant microorganism except that it does not include a non-native gene encoding a dehydrogenase. For example, the recombinant microorganism that includes a non-native dehydrogenase gene and a non-native gene encoding a polypeptide for lipid biosynthesis can have a higher proliferation rate during a culture period in which the dehydrogenase gene is expressed and the recombinant microorganism produces a lipid. The recombinant microorganism may be a photosynthetic microorganism, and in particular examples, can have a higher proliferation rate than a control microorganism that does not include or does not express the non-native dehydrogenase gene when cultured under photoautotrophic conditions in which the recombinant microorganism produces at least one lipid, such as, for example, a fatty acid product, which in certain examples may be a fatty acid product not naturally made by the photosynthetic microorganism.

[0013] Also provided herein is a culture comprising a recombinant photosynthetic microorganism in a suitable culture medium, in which the recombinant photosynthetic microorganism includes a non-native gene that encodes a dehydrogenase and a non-native gene encoding a polypeptide that participates in the production of a lipid, in which the culture produces a greater amount of the lipid than is produced by an identical culture of a microorganism identical in all respects except that it lacks the non-native gene encoding the dehydrogenase. Additionally or alternatively, the culture of the microorganism that includes the non-native dehydrogenase gene can reach a higher optical density after three, four, five, or six days of culture than the culture density reached by an identical culture of a microorganism identical in all respects except that it lacks the non-native gene encoding the dehydrogenase. The culture can be a photoautotrophic culture, for example, where the culture medium contains inorganic carbon as substantially the sole carbon source. The culture can produce at least 10% more, at least 25% more, at least 50% more, at least 75% more, at least 100%, at least 200% more, at least 300% more, at least 400% more, at least 500% more, at least 700% more, or at least 800% more of a fatty acid, fatty acid derivative, or triglyceride compared to culture identical in all respects except that it comprises a recombinant microorganism lacking the first non-native gene.

[0014] The recombinant microorganism used in any of the methods herein can include a non-native gene encoding any dehydrogenase as disclosed herein, for example, the dehydrogenase

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 one 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 embodiments, the 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 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 embodiments, the present disclosure relates to a method of producing a fatty acid product comprising culturing a recombinant photosynthetic

microorganism of the 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 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 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 embodiment, the 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.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] **Figure 1** depicts the total free fatty acids produced by engineered *Synechocystis* strains. *Synechocystis* strains expressing the B10 ORF ("dehydrd"; SEQ ID NO:1), the NB8 partial ORF fragment (SEQ ID NO:5), the NB104 ORF ("6-P-de"; SEQ ID NO:9), and NB104 ORF full contig fragment (SEQ ID NO:8), along with Cc1FatB1 acyl-ACP thioesterase gene (SEQ ID NO:20), produced higher levels of free fatty acids as compared to the control strain that contained the CclFatB1 gene alone.

[0027] **Figure 2** depicts optical densities of engineered *Synechocystis* PCC6803 strains at the end of six days of growth. All the strains were induced with 1mM IPTG to express the Cc1FatB1 acyl-ACP thioesterase gene and a dehydrogenase gene. The black bar represents the strain expressing acyl-ACP thioesterase alone. The patterned bars represent strains that contained isolated genes identified as dehydrogenases along with the acyl-ACP thioesterase gene.

[0028] **Figure 3** depicts the redox state of wild type (WT) and engineered *Synechocystis* strains. NADPH/NADP+ ratios are shown for WT *Synechocystis* strain ("6803"), the acyl-ACP thioesterase expressing strain (CclFatB1) and strains co-expressing the CclFatB1 thioesterase gene and a dehydrogenase gene (Cc1FatB1 + B10; Cc1FatBl + NB104). D stands for the number of days in culture.

[0029] **Figure 4** depicts a portion of the pentose phosphate pathway that produces NADPH showing the 6-phosphogluconate dehydrogenase gene.

[0030] **Figure 5** depicts free fatty acid (FFA) production by Synechocystis strains expressing the CcFatB1 acyl-ACP thioesterase gene (black bar), or co-expressing the CclFatBl acyl-ACP thioesterase gene and the *Synechocystis* 6-phosphogluconate dehydrogenase sll0329 gene (SEQ ID NO:12) (patterned bar) six days after inducing expression of the transgenes. Strains were induced at OD_{730}= 5.0.

DETAILED DESCRIPTION

[0031] Photosynthetic organisms synthesize fatty acids for the production of membrane and storage lipids using fixed carbon from CO_2, as well as ATP and NADPH that are also generated from photosynthesis. NADPH can also be generated by the activity of dehydrogenases. The term "dehydrogenase" is used herein to refer to an enzyme that catalyzes the oxidation of a substrate by transferring one or more hydrides (H-) to an acceptor such as NAD+ or NADP+. The invention provides recombinant microorganisms that express at least one non-native gene encoding a dehydrogenase and produce one or more lipids, such as, for example, one or more fatty acids, one or more fatty acid derivatives, and/or one or more glycerolipids (*e.g.*, one or more triglycerides). The recombinant microorganisms in some aspects demonstrate better proliferation rates while producing a lipid than comparable microorganisms that do not express a non-native gene encoding a dehydrogenase, and furthermore cultures of the recombinant microorganisms that express a non-native dehydrogenase gene can produce more lipid than is produced by control cultures of microorganisms that are identical in all respects to the dehydrogenase gene-expressing microorganisms, with the exception that the control microorganisms do not express a non-native dehydrogenase gene. The recombinant microorganisms may be recombinant photosynthetic microorganisms. Also provided are methods for producing a lipid by providing a culture of a microorganism that includes at least one non-native gene encoding a dehydrogenase, in which the culture produces more of the lipid than a culture identical in all respects except that the microorganism does not include a non-native gene encoding a dehydrogenase. The microorganism can be a photosynthetic microorganism and in some examples can be cultured photoautotrophically. The microorganism can additionally include one or more non-native genes encoding a polypeptide that participates in the synthesis of a lipid.

Definitions

[0032] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. In case of conflict, the present application including the definitions will control. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. All publications, patents and other references mentioned herein are

incorporated by reference in their entireties for all purposes as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

[0033] Although methods and materials similar or equivalent to those described herein can be used in practice or testing of the present invention, suitable methods and materials are described below. The materials, methods and examples are illustrative only and are not intended to be limiting. Other features and advantages of the invention will be apparent from the detailed description and from the claims.

[0034] To facilitate an understanding of the present invention, a number of terms and phrases are defined below.

[0035] As used in the present disclosure and claims, the singular forms "a," "an," and "the" include plural forms unless the context clearly dictates otherwise.

[0036] Wherever embodiments are described herein with the language "comprising," otherwise analogous embodiments described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0037] The term "and/or" as used in a phrase such as "A and/or B" herein is intended to include "A and B", "A or B", "A", and "B".

[0038] The term "gene" is used broadly to refer to any segment of a nucleic acid molecule (typically DNA, but optionally RNA) encoding a polypeptide or expressed RNA. Thus, genes include sequences encoding expressed RNA (which can include polypeptide coding sequences or, for example, functional RNAs, such as ribosomal RNAs, tRNAs, antisense RNAs, microRNAs, short hairpin RNAs, ribozymes, *etc.*). Genes may further comprise regulatory sequences required for or affecting their expression, as well as sequences associated with the protein or RNA-encoding sequence in its natural state, such as, for example, intron sequences, 5' or 3' untranslated sequences, *etc.* Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information.

[0039] The term "nucleic acid" or "nucleic acid molecule" refers to, a segment of DNA or RNA (*e.g.*, mRNA), and also includes nucleic acids having modified backbones (*e.g.*, peptide nucleic acids, locked nucleic acids) or modified or non-naturally-occurring nucleobases. The nucleic acid molecules can be double-stranded or single-stranded; a single stranded nucleic acid that comprises a gene or a portion thereof can be a coding (sense) strand or a non-coding (antisense) strand.

[0040] A nucleic acid molecule may be "derived from" an indicated source, which includes the isolation (in whole or in part) of a nucleic acid segment from an indicated source. A nucleic acid molecule may also be derived from an indicated source by, for example, direct cloning, PCR amplification, or artificial synthesis from the indicated polynucleotide source or based on a sequence associated with the indicated polynucleotide source. Genes or nucleic acid molecules derived from a particular source or species also include genes or nucleic acid molecules having sequence modifications with respect to the source nucleic acid molecules. For example, a gene or nucleic acid molecule derived from a source (*e.g.*, a particular referenced gene) can include one or more mutations with respect to the source gene or nucleic acid molecule that are unintended or that are deliberately introduced, and if one or more mutations, including substitutions, deletions, or insertions, are deliberately introduced the sequence alterations can be introduced by random or targeted mutation of cells or nucleic acids, by amplification or other molecular biology techniques, or by chemical synthesis, or any combination thereof. A gene or nucleic acid molecule that is derived from a referenced gene or nucleic acid molecule that encodes a functional RNA or polypeptide can encode a functional RNA or polypeptide having at least 75%, at least 80%, at least 85%, at least 90%, or at least 95%, sequence identity with the referenced or source functional RNA or polypeptide, or to a functional fragment thereof. For example, a gene or nucleic acid molecule that is derived from a referenced gene or nucleic acid molecule that encodes a functional RNA or polypeptide can encode a functional RNA or polypeptide having at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity with the referenced or source functional RNA or polypeptide, or to a functional fragment thereof.

[0041] As used herein, an "isolated" nucleic acid or protein is removed from its natural milieu or the context in which the nucleic acid or protein exists in nature. For example, an isolated protein or nucleic acid molecule is removed from the cell or organism with which it is associated in its native or natural environment. An isolated nucleic acid or protein can be, in some instances, partially or substantially purified, but no particular level of purification is required for isolation. Thus, for example, an isolated nucleic acid molecule can be a nucleic acid sequence that has been excised from the chromosome, genome, or episome that it is integrated into in nature.

[0042] A "purified" nucleic acid molecule or nucleotide sequence, or protein or polypeptide sequence, is substantially free of cellular material and cellular components. The purified nucleic acid molecule or protein may be free of chemicals beyond buffer or solvent, for example. "Substantially free" is not intended to mean that other components beyond the novel nucleic acid molecules are undetectable.

[0043] The terms "naturally-occurring" and "wild-type" refer to a form found in nature. For example, a naturally occurring or wild-type nucleic acid molecule, nucleotide sequence or protein may be present in and isolated from a natural source, and is not intentionally modified by human manipulation.

[0044] As used herein "attenuated" means reduced in amount, degree, intensity, or strength. Attenuated gene expression may refer to a significantly reduced amount and/or rate of transcription of the gene in question, or of translation, folding, or assembly of the encoded protein. As nonlimiting examples, an attenuated gene may be a mutated or disrupted gene (e.g., a gene disrupted by partial or total deletion, or insertional mutation) or having decreased expression due to alteration of gene regulatory sequences.

[0045] "Exogenous nucleic acid molecule" or "exogenous gene" refers to a nucleic acid molecule or gene that has been introduced ("transformed") into a cell. A transformed cell may be referred to as a recombinant cell, into which additional exogenous gene(s) may be introduced. A descendent of a cell transformed with a nucleic acid molecule is also referred to as "transformed" if it has inherited the exogenous nucleic acid molecule. The exogenous gene may be from a different species (and so "heterologous"), or from the same species (and so "homologous"), relative to the cell being transformed. An "endogenous" nucleic acid molecule, gene or protein is a native nucleic acid molecule, gene or protein as it occurs in, or is naturally produced by, the host.

[0046] The term "native" is used herein to refer to nucleic acid sequences or amino acid sequences as they naturally occur in the host. The term "non-native" is used herein to refer to nucleic acid sequences or amino acid sequences that do not occur naturally in the host. A nucleic acid sequence or amino acid sequence that has been removed from a cell, subjected to laboratory manipulation, and introduced or reintroduced into a host cell is considered "non-native." Synthetic or partially synthetic genes introduced into a host cell are "non-native." Non-native

genes further include genes endogenous to the host microorganism operably linked to one or more heterologous regulatory sequences that have been recombined into the host genome.

[0047] A "recombinant" or "engineered" nucleic acid molecule is a nucleic acid molecule that has been altered through human manipulation. As non-limiting examples, a recombinant nucleic acid molecule includes any nucleic acid molecule that: 1) has been partially or fully synthesized or modified *in vitro*, for example, using chemical or enzymatic techniques (*e.g.*, by use of chemical nucleic acid synthesis, or by use of enzymes for the replication, polymerization, digestion (exonucleolytic or endonucleolytic), ligation, reverse transcription, transcription, base modification (including, *e.g.*, methylation), integration or recombination (including homologous and site-specific recombination) of nucleic acid molecules); 2) includes conjoined nucleotide sequences that are not conjoined in nature, 3) has been engineered using molecular cloning techniques such that it lacks one or more nucleotides with respect to the naturally occurring nucleic acid molecule sequence, and/or 4) has been manipulated using molecular cloning techniques such that it has one or more sequence changes or rearrangements with respect to the naturally occurring nucleic acid sequence. As non-limiting examples, a cDNA is a recombinant DNA molecule, as is any nucleic acid molecule that has been generated by in vitro polymerase reaction(s), or to which linkers have been attached, or that has been integrated into a vector, such as a cloning vector or expression vector.

[0048] The term "recombinant protein" as used herein refers to a protein produced by genetic engineering.

[0049] When applied to organisms, the term recombinant, engineered, or genetically engineered refers to organisms that have been manipulated by introduction of a heterologous or exogenous recombinant nucleic acid sequence into the organism, and includes gene knockouts, targeted mutations, and gene replacement, promoter replacement, deletion, or insertion, as well as introduction of transgenes or synthetic genes into the organism. Recombinant or genetically engineered organisms can also be organisms into which constructs for gene "knock down" have been introduced. Such constructs include, but are not limited to, RNAi, microRNA, shRNA, siRNA, antisense, and ribozyme constructs. Also included are organisms whose genomes have been altered by the activity of meganucleases or zinc finger nucleases. An exogenous or recombinant nucleic acid molecule can be integrated into the recombinant/genetically engineered organism's genome or in other instances are not integrated into the recombinant/genetically

engineered organism's genome. As used herein, "recombinant microorganism" or "recombinant host cell" includes progeny or derivatives of the recombinant microorganisms of the invention. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny or derivatives may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[0050] The term "promoter" refers to a nucleic acid sequence capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. A promoter includes the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. A promoter can include a transcription initiation site as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters may contain -10 and -35 prokaryotic promoter consensus sequences. A large number of promoters, including constitutive, inducible and repressible promoters, from a variety of different sources are well known in the art. Representative sources include for example, viral, mammalian, insect, plant, yeast, and bacterial cell types, and suitable promoters from these sources are readily available, or can be made synthetically, based on sequences publicly available on line or, for example, from depositories such as the ATCC as well as other commercial or individual sources. Promoters can be unidirectional (initiate transcription in one direction) or bi-directional (initiate transcription in either direction). A promoter may be a constitutive promoter, a repressible promoter, or an inducible promoter. Non-limiting examples of promoters include, for example, the T7 promoter, the cytomegalovirus (CMV) promoter, the SV40 promoter, and the RSV promoter. Examples of inducible promoters include the lac promoter, the pBAD (araA) promoter, the Tet promoter (U.S. Pat. Nos. 5,464,758 and 5,814,618), and the Ecdysone promoter (No et al., *Proc. Natl. Acad. Sci.* (1996) 93 (8): 3346-3351).

[0051] The term "heterologous" when used in reference to a polynucleotide, gene, nucleic acid, polypeptide, or enzyme refers to a polynucleotide, gene, nucleic acid, polypeptide, or enzyme that is from a source or derived from a source other than the host organism species. In contrast a "homologous" polynucleotide, gene, nucleic acid, polypeptide, or enzyme is used herein to denote a polynucleotide, gene, nucleic acid, polypeptide, or enzyme that is derived from the host organism species. When referring to a gene regulatory sequence or to an auxiliary

nucleic acid sequence used for maintaining or manipulating a gene sequence (*e.g.* a promoter, a 5' untranslated region, 3' untranslated region, poly A addition sequence, intron sequence, splice site, ribosome binding site, internal ribosome entry sequence, genome homology region, recombination site, *etc.*), "heterologous" means that the regulatory sequence or auxiliary sequence is not naturally associated with the gene with which the regulatory or auxiliary nucleic acid sequence is juxtaposed in a construct, genome, chromosome or episome. Thus, a promoter operably linked to a gene to which it is not operably linked to in its natural state (*i.e.* in the genome of a non-genetically engineered organism) is referred to herein as a "heterologous promoter," even though the promoter may be derived from the same species (or, in some cases, the same organism) as the gene to which it is linked.

[0052] As used herein, the term "protein" or "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and refers to a molecule composed of monomers (amino acids) linearly linked by amide bonds (also known as peptide bonds). The term "polypeptide" refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, "protein," "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included within the definition of "polypeptide," and the term "polypeptide" can be used instead of, or interchangeably with any of these terms.

[0053] This application discloses and refers to nucleic acids and polypeptides by identifiers used in long-established and extensively referenced databases maintained by the National Center for Biotechnology Information (NCBI). Accession numbers, commonly provided herein in parenthesis after a gene or species name, are unique identifiers for a sequence record publicly available at the National Center for Biotechnology Information website (ncbi.nlm.nih.gov) maintained by the United States National Institutes of Health. The "GenInfo Identifier" (GI) sequence identification number is specific to a nucleotide or amino acid sequence. If a sequence changes in any way, a new GI number is assigned. A Sequence Revision History tool is available to track the various GI numbers, version numbers, and update dates for sequences that appear in a specific GenBank record. Searching and obtaining nucleic acid or gene sequences or protein sequences based on Accession numbers and GI numbers is well known in the arts of, e.g., cell biology, biochemistry, molecular biology, and molecular genetics.

[0054] As used herein, the terms "percent identity" or "homology" with respect to nucleic acid or polypeptide sequences are defined as the percentage of nucleotide or amino acid residues in the candidate sequence that are identical with the known polypeptides, after aligning the sequences for maximum percent identity and introducing gaps, if necessary, to achieve the maximum percent homology. N-terminal or C-terminal insertion or deletions shall not be construed as affecting homology, and internal deletions and/or insertions into the polypeptide sequence of less than about 30, less than about 20, or less than about 10 amino acid residues shall not be construed as affecting homology.

[0055] Homology or identity at the nucleotide or amino acid sequence level can be determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn, and tblastx (Altschul (1997), *Nucleic Acids Res.* 25, 3389-3402, and Karlin (1990), *Proc. Natl. Acad. Sci. USA* 87, 2264-2268), which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments, with and without gaps, between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified, and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul (1994), *Nature Genetics* 6, 119-129. The search parameters for histogram, descriptions, alignments, expect (*i.e.*, the statistical significance threshold for reporting matches against database sequences), cutoff, matrix, and filter (low complexity) can be at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff (1992), *Proc. Natl. Acad. Sci. USA* 89, 10915-10919), recommended for query sequences over 85 in length (nucleotide bases or amino acids).

[0056] For blastn, designed for comparing nucleotide sequences, the scoring matrix is set by the ratios of M (*i.e.*, the reward score for a pair of matching residues) to N (*i.e.*, the penalty score for mismatching residues), wherein the default values for M and N can be +5 and -4, respectively. Four blastn parameters can be adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings for comparison of amino acid sequences can be: Q=9; R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG

package version 10.0, can use DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty), and the equivalent settings in protein comparisons can be GAP=8 and LEN=2.

[0057] Thus, when referring to the polypeptide or nucleic acid sequences of the present invention, included are sequence identities of at least 65%, 70%, 75%, 80%, or 85%, for example at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or about 100% sequence identity with the full-length polypeptide or nucleic acid sequence, or to fragments thereof comprising a consecutive sequence of at least 50, at least 75, at least 100, at least 125, at least 150 or more amino acid residues of the entire protein; variants of such sequences, *e.g.*, wherein at least one amino acid residue has been inserted N- and/or C-terminal to, and/or within, the disclosed sequence(s) which contain(s) the insertion and substitution. Contemplated variants can additionally or alternately include those containing predetermined mutations by, *e.g.*, homologous recombination or site-directed or PCR mutagenesis, and the corresponding polypeptides or nucleic acids of other species, including, but not limited to, those described herein, the alleles or other naturally occurring variants of the family of polypeptides or nucleic acids which contain an insertion and substitution; and/or derivatives wherein the polypeptide has been covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid which contains the insertion and substitution (for example, a detectable moiety such as an enzyme).

[0058] As used herein, the phrase "conservative amino acid substitution" or "conservative mutation" refers to the replacement of one amino acid by another amino acid with a common property. A functional way to define common properties between individual amino acids is to analyze the normalized frequencies of amino acid changes between corresponding proteins of homologous organisms (Schulz (1979) Principles of Protein Structure, Springer-Verlag). According to such analyses, groups of amino acids can be defined where amino acids within a group exchange preferentially with each other, and therefore resemble each other most in their impact on the overall protein structure (Schulz (1979) Principles of Protein Structure, Springer-Verlag). Examples of amino acid groups defined in this manner can include: a "charged/polar group" including Glu, Asp, Asn, Gln, Lys, Arg, and His; an "aromatic or cyclic group" including Pro, Phe, Tyr, and Trp; and an "aliphatic group" including Gly, Ala, Val, Leu, Ile, Met, Ser, Thr,

and Cys. Within each group, subgroups can also be identified. For example, the group of charged/polar amino acids can be sub-divided into sub-groups including: the "positively-charged sub-group" comprising Lys, Arg and His; the "negatively-charged sub-group" comprising Glu and Asp; and the "polar sub-group" comprising Asn and Gln. In another example, the aromatic or cyclic group can be sub-divided into sub-groups including: the "nitrogen ring sub-group" comprising Pro, His, and Trp; and the "phenyl sub-group" comprising Phe and Tyr. In another further example, the aliphatic group can be sub-divided into sub-groups including: the "large aliphatic non-polar sub-group" comprising Val, Leu, and Ile; the "aliphatic slightly-polar sub-group" comprising Met, Ser, Thr, and Cys; and the "small-residue sub-group" comprising Gly and Ala. Examples of conservative mutations include amino acid substitutions of amino acids within the sub-groups above, such as, but not limited to: Lys for Arg or vice versa, such that a positive charge can be maintained; Glu for Asp or vice versa, such that a negative charge can be maintained; Ser for Thr or vice versa, such that a free -OH can be maintained; and Gln for Asn or vice versa, such that a free -NH2 can be maintained. A "conservative variant" is a polypeptide that includes one or more amino acids that have been substituted to replace one or more amino acids of the reference polypeptide (for example, a polypeptide whose sequence is disclosed in a publication or sequence database, or whose sequence has been determined by nucleic acid sequencing) with an amino acid having common properties, *e.g.*, belonging to the same amino acid group or sub-group as delineated above.

[0059] As used herein, "expression" includes the expression of a gene at least at the level of RNA production, and an "expression product" includes the resultant product, *e.g.*, a polypeptide or functional RNA (e.g., a ribosomal RNA, a tRNA, an antisense RNA, a micro RNA, an shRNA, a ribozyme, etc.), of an expressed gene. The term "increased expression" includes an alteration in gene expression to facilitate increased mRNA production and/or increased polypeptide expression. "Increased production" includes an increase in the amount of polypeptide expression, in the level of the enzymatic activity of a polypeptide, or a combination of both, as compared to the native production or enzymatic activity of the polypeptide.

[0060] The term "secreted" includes movement of polypeptides or fatty acid products produced by the recombinant microorganisms or methods of the invention to the periplasmic space or extracellular milieu. "Increased secretion" includes secretion in excess of the naturally-occurring amount of secretion, *e.g.*, that is at least 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, or

10%, or at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, 1000%, or more, as compared to the naturally-occurring level of secretion.

[0061] Included herein are aspects of engineering a microorganism in which the "insertion," *e.g.*, the addition, integration, incorporation, or introduction of certain nucleic acid molecules or particular polynucleotide sequences within microorganisms or host cells in order to affect the expression of a gene in the microorganism. For example, a microorganism of interest may be engineered by site directed homologous recombination to insert a particular gene of interest with or without an expression control sequence such as a promoter, into a particular genomic locus, or to insert a promoter into a genetic locus of the host microorganism to affect the expression of a particular gene or set of genes at the locus.

[0062] Additional aspects of the present invention include the partial, substantial, or complete deletion, silencing, inactivation, or down-regulation of expression of particular polynucleotide sequences. The genes may be partially, substantially, or completely deleted, silenced, inactivated, or their expression may be down-regulated in order to affect the activity performed by the polypeptide they encode, such as the activity of an enzyme. Genes can be partially, substantially, or completely deleted, silenced, inactivated, or down-regulated by insertion of nucleic acid sequences that disrupt the function and/or expression of the gene (*e.g.*, viral insertion, transposon mutagenesis, meganuclease engineering , homologous recombination, or other methods known in the art). The terms "eliminate," "elimination," and "knockout" can be used interchangeably with the terms "deletion," "partial deletion," "substantial deletion," or "complete deletion." In certain embodiments, a microorganism of interest may be engineered by site directed homologous recombination to knockout a particular gene of interest. In still other embodiments, RNAi or antisense DNA (asDNA) constructs may be used to partially, substantially, or completely silence, inactivate, or down-regulate a particular gene of interest.

[0063] These insertions, deletions, or other modifications of certain nucleic acid molecules or particular polynucleotide sequences may be understood to encompass "genetic modification(s)" or "transformation(s)" such that the resulting strains of the microorganisms or host cells may be understood to be "genetically modified" or "transformed."

[0064] As used herein, "up-regulated" or "up-regulation" includes an increase in expression of a gene or nucleic acid molecule of interest or the activity of an enzyme, *e.g.*, an increase in

gene expression or enzymatic activity as compared to the expression or activity in an otherwise identical gene or enzyme that has not been up-regulated.

[0065] As used herein, "down-regulated" or "down-regulation" includes a decrease in expression of a gene or nucleic acid molecule of interest or the activity of an enzyme, *e.g.*, a decrease in gene expression or enzymatic activity as compared to the expression or activity in an otherwise identical gene or enzyme that has not been down-regulated.

[0066] The term "Pfam" refers to a large collection of protein domains and protein families maintained by the Pfam Consortium and available at several sponsored world wide web sites, including: pfam.sanger.ac.uk/ (Welcome Trust, Sanger Institute); pfam.sbc.su.se/ (Stockholm Bioinformatics Center); pfam.janelia.org/ (Janelia Farm, Howard Hughes Medical Institute); pfam.jouy.inra.fr/ (Institut national de la Recherche Agronomique); and pfam.ccbb.re.kr. The latest release of Pfam is Pfam 26.0 (November 2011) based on the UniProt protein database release 15.6, a composite of Swiss-Prot release 57.6 and TrEMBL release 40.6. Pfam domains and families are identified using multiple sequence alignments and hidden Markov models (HMMs). Pfam-A family or domain assignments, are high quality assignments generated by a curated seed alignment using representative members of a protein family and profile hidden Markov models based on the seed alignment. (Unless otherwise specified, matches of a queried protein to a Pfam domain or family are Pfam-A matches.) All identified sequences belonging to the family are then used to automatically generate a full alignment for the family (Sonnhammer (1998) *Nucleic Acids Research* 26, 320-322; Bateman (2000) Nucleic Acids Research 26, 263-266; Bateman (2004) *Nucleic Acids Research* 32, Database Issue, D138-D141; Finn (2006) *Nucleic Acids Research* Database Issue 34, D247-251; Finn (2010) *Nucleic Acids Research* Database Issue 38, D211-222). By accessing the Pfam database, for example, using any of the above-reference websites, protein sequences can be queried against the HMMs using HMMER homology search software (*e.g.*, HMMER2, HMMER3, or a higher version, hmmer.janelia.org/). Significant matches that identify a queried protein as being in a pfam family (or as having a particular Pfam domain) are those in which the bit score is greater than or equal to the gathering threshold for the Pfam domain. Expectation values (e values) can also be used as a criterion for inclusion of a queried protein in a Pfam or for determining whether a queried protein has a particular Pfam domain, where low e values (much less than 1.0, for example less than 0.1, or less than or equal to 0.01) represent low probabilities that a match is due to chance.

[0067] As used herein, a "long chain length" fatty acid or acyl-ACP is a fatty acid or acyl-ACP having a chain length of greater than 14 carbons and a "medium chain length" fatty acid or acyl-ACP is a fatty acid or acyl-ACP having a chain length of from 8-14 carbons.

[0068] "Substrate preference" refers to the substrate or substrates an enzyme is most active on. For example, different acyl-ACP thioesterases may have different degrees of chain length specificity, sometimes referred to as the enzyme's "preference" for cleaving a particular length of fatty acid from ACP, and thioesterases are typically most active in cleaving a particular chain length fatty acid while having lesser activity in cleaving one or more other chain length fatty acids.

[0069] As used herein, the term "fatty acid product" includes free fatty acids; mono-, di- or triglycerides; fatty aldehydes; fatty alcohols; fatty acid esters (including, but not limited to, wax esters); and hydrocarbons (including, but not limited to, alkanes and alkenes).

[0070] "Propagation rate" or "replicative rate", as used interchangeably herein, is measured commonly in microorganisms by measuring the doubling time of a given culture. Methods for measuring the rate of propagation of microorganisms are well known in the art. For example, optical density (OD) measurements may be taken over periods of time to measure the rate of propagation (increase in the number of cells) or proliferation (increase in cell number as well as increases in cell size and/or cellular contents). Alternatively, the concentration of microorganisms in suspension can be determined by using a hemocytometer or similar apparatus to determine the concentration of cells in a given volume of a culture. By taking multiple data points at various times, the propagation or replicative rate of cells in a culture can be assessed. An increase in culture density over a period of time (for example, as measured by OD) is indicative of propagation and/or proliferation.

Metabolic Pathways for Producing Fatty Acid Products

[0071] The lipids produced by the recombinant microorganisms disclosed herein can be fatty acid products, including free fatty acids and products that are derived from fatty acids and/or incorporate the acyl chains of fatty acids produced by the cell, including, without limitation: mono-, di- or triglycerides; fatty aldehydes; fatty alcohols; fatty acid esters (including, but not limited to, wax esters); and hydrocarbons (including, but not limited to, alkanes and alkenes). The fatty acid biosynthesis pathway, highly conserved in prokaryotes and in the chloroplasts of

eukaryotic algae and higher plants, starts from the central metabolite acetyl-CoA. Fatty acid biosynthesis is initiated by the conversion of acetyl-CoA to malonyl-CoA, catalyzed by acetyl-CoA carboxylase (ACCase). Malonyl-CoA is then converted to malonyl-ACP, catalyzed by malonyl-CoA-ACP transacylase (FabD in *E. coli*). Malonyl-ACP is then converted to acyl-ACP, catalyzed by the enzyme complex fatty acid synthase (FAS). The fatty acid synthase complex initiates the elongation cycle by first condensing malonyl-ACP with acetyl-ACP, catalyzed by a beta-ketoacyl-ACP synthase III (*e.g.*, FabH of *E. coli*). The β-ketoacyl-ACP (3-ketoacyl-ACP) formed by the FabH reaction is reduced to a β-hydroxyacyl-ACP (3-hydroxyacyl-ACP) by 3-ketoacyl-ACP reductase (*e.g.* FabG). The β-hydroxyacyl-ACP is then acted on by a β-hydroxyacyl-ACP dehydratase (*e.g.* FabA, FabZ) to form trans-2-enoyl-ACP, which in turn is reduced by enoyl-ACP reductase (*e.g.* Fab I, Fab K, FabL) to form the 2 carbon-elongated acyl-ACP product. Subsequent cycles are initiated by a beta-ketoacyl-ACP synthase I or II (*e.g.*, FabB or FabF) catalyzed condensation of malonyl-ACP with acyl-ACP. The cycles of condensation, reduction, dehydration, and reduction are repeated, with each cycle adding two carbons from malonyl-ACP, until the acyl chain is transferred to another molecule (*e.g.* glycerol 3-phosphate) by a transacylase or cleaved from ACP by a thioesterase, such as FatA or FatB in chloroplasts, to form free fatty acids.

[0072] Unlike plant chloroplasts, cyanobacteria do not produce free fatty acids, and unlike *E. coli* and other heterotrophic bacteria, cyanobacteria do not produce acyl-CoA (Kaczmarzyk and Fulda (2010) *Plant Physiol.* 152: 1598-1610). Following fatty acid elongation in which the acyl chain is covalently bound to acyl carrier protein, acyl transferases of cyanobacteria transfer the acyl chain to a glycerol backbone to produce membrane lipids.

[0073] To produce free fatty acids in a microorganism, such as, but not limited to, a cyanobacterium, an exogenous or recombinant thioesterase gene, such as but not limited to a gene encoding an acyl-ACP thioesterase, a gene encoding an acyl-CoA thioesterase, or a gene encoding a hydroxybenzoyl thioesterase, can be expressed in the microorganism. To produce fatty acid derivatives such as fatty alcohols, fatty aldehydes, wax esters, alkanes, or alkenes in microorganisms, one or more enzymes to convert acyl-thioester intermediates (e.g., acyl-CoA or acyl-ACP) to the desired end product (*e.g.*, an alcohol, aldehyde, alkane, alkene, or wax ester) may be introduced into the host cell, optionally in combination with an exogenous or recombinant gene encoding a thioesterase and, optionally, an exogenous gene encoding an acyl-

CoA synthetase. For example, if fatty aldehydes and/or alkanes are the desired end product, a gene encoding an aldehyde-forming fatty aldehyde reductase (*e.g.*, aldehyde-forming acyl-CoA reductase, 1.2.1.42 or 1.2.1.50; see also U.S. Patent No. 6,143,538) may be introduced to reduce acyl-CoA to fatty aldehydes; additionally or alternatively, an aldehyde-forming acyl-ACP reductase (*e.g.*, as disclosed in WO 2009/140696 or WO 2011/066137) or a carboxylic acid reductase gene (see, *e.g.*, WO 2010/135624 and WO 2010/042664) may be introduced to reduce free fatty acids to fatty aldehydes. Alternatively or in addition, a gene encoding a fatty alcohol oxidase (*e.g.*, 1.1.3.20) or a fatty alcohol dehydrogenase (*e.g.*, 1.1.1.164) may be introduced to convert fatty alcohols to fatty aldehydes. Fatty aldehydes may optionally be processed further to alkanes with the introduction of a gene encoding a fatty aldehyde decarbonylase (*e.g.*, 4.1.99.5). If fatty alcohols, alkenes and/or wax esters are the desired end product, a gene encoding an alcohol-forming fatty acyl reductase (*e.g.*, an alcohol-forming acyl-CoA reductase, 1.2.1.50) may be introduced into the host cell. Further, a fatty aldehyde reductase gene may be introduced to reduce fatty aldehydes to fatty alcohols. Fatty alcohols may be processed further to alkenes with the introduction of one or more genes encoding a fatty alcohol dehydratase. Fatty acid esters, including wax esters, may be formed by introducing genes encoding polypeptides that catalyze condensation of an alcohol with a fatty acyl thioester, such as acyltransferases and wax synthases.

[0074] In some examples, the conversion of acyl-ACP to fatty alcohol may occur via synthesis of a fatty aldehyde, wherein an acyl reductase (*e.g.*, an aldehyde-forming acyl-CoA reductase or aldehyde-forming acyl-ACP reductase) expressed in the host cell first reduces acyl-ACP to a fatty aldehyde. For example, in certain embodiments, the host cell can be engineered to overexpress an endogenous fatty aldehyde-forming reductase (*e.g.*, by inserting promoter and/or enhancer transcriptional control elements near the fatty aldehyde-forming reductase gene). In other embodiments, the host cell may be engineered to express an exogenous fatty aldehyde-forming reductase. The host cell may further include an exogenous gene that encodes a fatty aldehyde reductase or alcohol dehydrogenase that reduces the fatty aldehyde to a fatty alcohol.

[0075] Wax esters may be formed by introducing a gene encoding a wax ester synthase to catalyze condensation of a fatty alcohol with a fatty acyl thioester. A wax ester synthase can be, for example, an enzyme of the class EC 2.3.1.26 (long chain alcohol O-fatty acyltransferase), EC

2.3.1.20 (diacylglycerol acyltransferase), EC 2.3.1.51 (acyltransferase) , or 2.3.1.75 (wax ester synthase /acyl-CoA diacylglycerol acyltransferase).

[0076] For production of glycerolipids, such as, for example, monoacylglycerides, diacylglycerides, and triacylglycerides ("TAGs"), a recombinant microorganism as disclosed herein that includes a non-native gene encoding a dehydrogenase can further include a non-native gene encoding an enzyme that participates in the production of glycerolipids, including, but not limited to, a glycerolphosphate acyltransferase (GPAT), a lysophosphatidic acid acyltransferase (LPAAT), a phosphatidic acid phosphatase (PAP), or a diacylglycerol O-acyltransferase (DGAT).

Dehydrogenases

[0077] The present invention provides a recombinant microorganism that includes a non-native gene encoding a dehydrogenase and produces at least one fatty acid product. For example, a recombinant microorganism as disclosed herein can be transformed with an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a dehydrogenase. Alternatively or in addition, the recombinant microorganism can include an endogenous nucleic acid sequence encoding a dehydrogenase, in which at least one regulatory sequence has been inserted into the genome of the microorganism to regulate expression of the endogenous dehydrogenase gene. Additionally, the microorganism can be transformed with one or more exogenous genes, and/or can be engineered to overexpress one or more endogenous genes, that participate in the production of a lipid, such as a fatty acid product.

[0078] Dehydrogenases that can be expressed in the recombinant microorganisms disclosed herein include, without limitation, aldehyde dehydrogenases (including aldehyde dehydrogenases (EC 1.2.1.3), succinate-semialdehyde dehydrogenases (EC 1.2.1.16), methylmalonate semialdehyde dehydrogenases (EC 1.2.1.27), lactaldehyde dehydrogenases (EC 1.2.1.22), benzaldehyde dehydrogenases (EC 1.2.1.28), non-phosphorylating glyceraldehyde-3-phosphate dehydrogenases (EC 1.2.1.9), NADP-dependent (phosphorylating) glyceraldehyde-3-phosphate dehydrogenases (EC 1.2.1.13), delta-1-pyrroline-5-carboxylate dehydrogenases (EC 1.5.1.12), acetaldehyde dehydrogenases (EC: 1.5.1.10), and glutamate semialdehyde dehydrogenases (EC: 1.5.1.41)), 2-hydroxyacid dehydrogenases (*e.g.*, isocitrate dehydrogenases, lactate dehydrogenases, malate dehydrogenases, succinate dehydrogenases, alpha ketoglutarate dehydrogenases), D-2-hydroxyacid dehydrogenases *e.g.*, D-2-hydroxyisocaproate

dehydrogenases, formate dehydrogenases, D-glycerate dehydrogenases, vancomycin-resistant protein H, D-2-phosphoglycerate dehydrogenases, and D-lactate dehydrogenases (1.1.1.28)), malic enzymes (1.1.1.40), glucose-6-phosphate dehydrogenases (1.1.1.49), 6-phosphogluconate dehydrogenases (1.1.1.43, 1.1.1.44), glutamate dehydrogenases, isocitrate dehydrogenases, and sorbitol dehydrogenases. In various examples, the dehydrogenase encoded by a non-native gene introduced into or overexpressed in a microorganism of the present invention is not an alcohol dehydrogenase. In further examples, a dehydrogenase encoded by a non-native gene introduced into or overexpressed in a microorganism of the present invention may not be a pyruvate dehydrogenase or a phosphorylating glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12). Assays for the activity of dehydrogenases are well known in the art (*e.g.*, Wynn et al. (1997) *Lipids* 32: 605-610; Graupner et al. (2000) *J. Bacteriol.* 182: 3688-3692; Berrios-Rivera et al. (2002) *Metabolic Engineering* 4: 217-229; Shinoda et al. (2005) *J. Biol. Chem.* 280: 17068-17075; Domenech and Ferrer (2006) *Biochim. Biophys. Acta* 1760: 1667-1674; Lo and Chen (2010) *Mol. Biotechnol* 46: 157-167).

[0079] Of particular interest are dehydrogenases that generate NADPH, although dehydrogenases that produce NADH are also considered for use in the methods and microorganisms of the invention. For example, NADH may be converted to NADPH in cells via the activity of NADPH:NAD+ oxidoreductases (B-specific) sometimes referred to as NADPH-NAD+ transhydrogenases (see, *e.g.*, US 2005/0196866) which may be native to the host cell, or a gene encoding an NADPH-NAD+ transhydrogenases may be introduced into the host microorganism.

[0080] Malic enzyme (EC 1.1.1.40), also known as malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+)) or NADP-malic enzyme, which catalyzes the irreversible decarboxylation of malate to pyruvate while reducing NADP+ to NADPH, is an example of a dehydrogenase that can be produced in a recombinant host cell by expression of a non-native gene. A non-native gene encoding malic enzyme can be derived from any organism, and can be heterologous or homologous with respect to the host microorganism. Nonlimiting examples of a malic enzyme that can be encoded by a non-native gene in a microorganism as disclosed herein include polypeptides that recruit to Pfam PF00390 (malic enzyme, N-terminal domain) with a bit score greater than the gathering cutoff of 19.2, and/or recruit to Pfam PF03949 (malic enzyme NAD binding domain) with a bit score higher than the gathering cutoff of 23.5. A crystal

structure of a malic enzyme has been reported by Yang et al. (*Protein Sci.* 11: 332-341 (2002)). Nonlimiting examples of malic enzymes include those from *Mucor circinelloides* (ABM45933, AAO26053.1), *Thalassiosira pseudonana* (XP_002290550), *Phaeodactylum tricornutum* (XP_002177890), *Ostreococcus lucimarinus* (XP_001420849), *Ricinus communis* (XP_002526507), *Oryza sativa* (NP_001064998), *Arabidopsis thaliana* (AEE36294), *Chlorella variabilis* (EFN53662), *Homo sapiens* (NP_002386), *Chlamydomonas reinhardtii* (XP_001696240), *Synechocystis* sp. PCC 6803 (BAA16663), *Microcystis aeruginosa* (YP_001655800), and *'Nostoc azollae'* (YP_003720944). Without limitation, malic enzymes encoded by a non-native gene in a microorganism as provided herein can be polypeptides with malic enzyme activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to these malic enzymes or others as listed in sequence databases, conservative variants thereof, and N-terminally and/or C-terminally truncated or modified variants thereof. For example, a recombinant microorganism as provided herein can include a non-native gene encoding a polypeptide that includes an amino acid sequence having at least 95% identity to a polypeptide identified as a malic enzyme, or to an active fragment thereof.

[0081] Glucose-6-phosphate dehydrogenase (EC 1.1.1.49) is an NADPH-generating enzyme of the pentose phosphate pathway that can be produced by expression of a non-native gene in a microorganism as provided herein. The gene encoding glucose-6-phosphate can be derived from a plant, animal, or microbe, including a fungus, heterokont, alga, bacterium, or cyanobacterium. For example, the dehydrogenase can be a polypeptide that recruits to Pfam PF00479 "Glucose-6-phosphate dehydrogenase, NAD binding domain" with a bit score greater than the gathering cut-off of 21.7, and/or can recruit to Pfam, PF02781 "Glucose-6-phosphate dehydrogenase, C-terminal domain" with a bit score greater than the gathering cut-off of 19.5. Nonlimiting examples of glucose-6-phosphate dehydrogenases that can be expressed by a microorganism as provided herein include the glucose 6-phosphate dehydrogenase of *Synechocystis* sp. PCC 6803 (BAA17451), *Synechococcus* sp. BL107 (ZP_01468297), *Prochlorococcus marinus* str. AS9601 (YP_001009571), *Lyngbya* sp. PCC 8106 (ZP_01620414), *Thalassiosira pseudonana* CCMP1335 (EED92550), *Micromonas* sp. RCC299 (XP_002508505); *Ostreococcus tauri* (XP_003079573), *Glycine max* (XP_003533032), *Vitis vinifera* (XP_002266930), *Oryza sativa* Japonica Group (AAQ02671), *Mus musculus* (NP_000393; NP_032088), and *Homo sapiens* (NP_000393). Without limitation, glucose-6-phosphate dehydrogenases that can be expressed

from non-native genes in the engineered microorganisms provided herein can be polypeptides with glucose-6-phosphate dehydrogenase activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to these glucose-6-phosphate dehydrogenases or others as listed in sequence databases, including conservative variants thereof, and can be N-terminally and/or C-terminally truncated or modified variants thereof. For example, a recombinant microorganism as provided herein can include a non-native gene encoding a glucose-6-phosphate dehydrogenase having at least 95% identity to a polypeptide identified as a glucose-6-phosphate dehydrogenase, or to an active fragment thereof.

[0082] Another NADPH-producing enzyme of the pentose phosphate pathway is 6-phosphogluconate dehydrogenase. "Phosphogluconate dehydrogenase" or "6-phosphogluconate dehydrogenase" (EC 1.1.1.43 or EC 1.1.1.44) as used herein, refers to an enzyme that catalyzes the decarboxylating reduction of 6-phosphogluconate into ribulose-5-phosphate in the presence of $NADP^+$. As a result of the catalysis, the $NADP^+$ is reduced to NADPH. The invention includes recombinant microorganisms that include a non-native gene encoding a 6-phosphogluconate dehydrogenase, and preferably, at least one additional gene encoding a protein for the production of a lipid. A 6-phosphogluconate dehydrogenase expressed by a recombinant microorganism of the invention can be from a plant, animal, or microbe, including a fungus, heterokont, alga, bacterium, or cyanobacterium. As disclosed herein, expression of non-native genes encoding 6-phosphogluconate dehydrogenase can enhance fatty acid biosynthesis by the host microorganism. Phosphogluconate dehydrogenases that may be useful in the microorganisms and methods disclosed herein include 6-phosphogluconate dehydrogenases that recruit to Pfam PF03446 "NAD binding domain of 6-phosphogluconate dehydrogenase" (gathering cut-off 21.0) and, preferably, recruit to Pfam PF00393 "6-phosphogluconate dehydrogenase, C-terminal domain" (gathering cut-off 20.4). Crystal structures of 6-phosphogluconate dehydrogenases have been published (*e.g.*, Adams *et al.* (1994) *Structure* 2:651-658). Examples of phosphogluconate dehydrogenases that may be encoded by a non-native gene in an engineered microorganism as provided herein include but are not limited to a 6-phosphogluconate dehydrogenase of *Synechocystis* sp. PCC 6803 (BAA10105), *Cyanothece* sp. PCC 7822 (ADN14972), *Nostoc azollae* 0708 (ADI63566), *Synechococcus* sp. PCC 7002 (YP_001733490), *Arabidopsis thaliana* (AED94705), *Glycine max* (BAA22812), *Pinus sylvestris* (ADP03060), *Bombyx mori* (gb DAA21283), *Bos taurus* (DAA21283),

Saccharomyces cerevisiae (AAA53637), *Aspergillus terreus* NIH2624 (EAU33612), *Streptococcus pneumoniae* SP-BS293 (EFL69841), *Escherichia coli* (AAG35237), and variants thereof. Additionally or alternatively, a microorganism as disclosed herein can include a non-native gene encoding a 6-phosphogluconate 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%, or at least 95% amino acid sequence identity to SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:13, or an active fragment thereof. Nonlimiting examples of 6-phosphogluconate dehydrogenases having amino acid sequences with homology to the polypeptide of SEQ ID NO:10 include the 6-phosphogluconate dehydrogenase of *Carnobacterium* sp. AT7 (ZP_02185894), the 6-phosphogluconate dehydrogenase of *Anaerococcus vaginalis* ATCC 51170 (ZP_05473398), the 6-phosphogluconate dehydrogenase of *Enterococcus casseliflavus* (ZP_05646912), and the 6-phosphogluconate dehydrogenase-like protein of *Clostridium beijerinckii* NCIMB 8052 (YP_001309315). Nonlimiting examples of 6-phosphogluconate dehydrogenases having amino acid sequences with homology to the polypeptide of SEQ ID NO:13 include the 6-phosphogluconate dehydrogenase of *Cyanothece* sp. PCC 8801(YP_002372435, *Microcystis aeruginosa* NIES-843 (YP_001656536), *Synechococcus* sp. PCC 7002 (YP_001733490), *Arthrospira platensis* str. Paraca (ZP_06383632), *Nostoc* sp. PCC 7120 (NP_489315), *Oscillatoria* sp. PCC 6506 (ZP_07110168), and *Thermosynechococcus elongatus* BP-1 (NP_681366). Without limitation, 6-phosphogluconate dehydrogenases that can be expressed from non-native genes in the engineered microorganisms provided herein can be polypeptides with phosphogluconate dehydrogenase activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to the above-cited phosphogluconate dehydrogenases or others as listed in publications or sequence databases, including conservative variants of identified phosphogluconate dehydrogenases, and including N-terminally and/or C-terminally truncated or modified variants. In some instances, a nucleic acid molecule useful in the invention can encode a 6-phosphogluconate dehydrogenase that has at least 95% sequence identity to a 6-phosphogluconate dehydrogenase as provided herein or identified in a sequence database or an N-terminally and/or C-terminally truncated variant thereof (for example, a 6-phosphogluconate dehydrogenase that lacks the chloroplast transit peptide of the reference enzyme, or alternatively

has an added chloroplast transit peptide not present in the reference enzyme), a conservative variant thereof, or modified variants thereof.

[0083] As demonstrated in the examples, a non-native gene encoding an aldehyde dehydrogenase can also be expressed in a recombinant microorganism of the invention to improve lipid production by the recombinant microorganism. "Aldehyde dehydrogenase" refers herein to an enzyme that catalyzes the oxidation of aldehydes to carboxylic acids. Aldehyde dehydrogenases useful in the microorganisms and methods disclosed herein include aldehyde dehydrogenases that recruit to Pfam PF00171 "Aldehyde dehydrogenase family" (gathering cut-off 23.0), and include aldehyde dehydrogenases of EC 1.2.1.3, succinate-semialdehyde dehydrogenases (EC 1.2.1.16), methylmalonate semialdehyde dehydrogenases (EC 1.2.1.27), lactaldehyde dehydrogenases (EC 1.2.1.22), benzaldehyde dehydrogenases (EC 1.2.1.28), non-phosphorylating glyceraldehyde-3-phosphate dehydrogenases (EC 1.2.1.9), NADP-dependent glyceraldehyde-3-phosphate dehydrogenases (EC 1.2.1.13), delta-1-pyrroline-5-carboxylate dehydrogenases (EC 1.5.1.12), acetaldehyde dehydrogenases (EC: 1.5.1.10), and glutamate semialdehyde dehydrogenases (EC: 1.5.1.41). The aldehyde substrate can be, for example, acetaldehyde, propionaldehyde, butyraldehyde, valeraldehyde, isovaleraldehyde, benzaldehyde, glyceraldehyde-3-phosphate, or another aldehyde. An example of a crystal structure of an aldehyde dehydrogenase is provided in Di Costanzo *et al.* (2007) *J. Mol. Biol.* 366: 481-493. Aldehyde dehydrogenases useful in the microorganisms and methods of the invention may be aldehyde dehydrogenases that are able to use NADP+ as a cofactor (see, for example, Lo and Chen (2010) *Mol Biotechnol* 46:157-167). Nonlimiting examples of aldehyde dehydrogenases include the aldehyde dehydrogenase of *Bacillus licheniformis* (YP_089937), *Bacillus stearothermophilus* SIC1 (YP_688823), *E. coli* (NP_287888), *Saccharomyces cerevisiae* (NP_015264), *Homo sapiens* (NP_000680), *Mus musculus* (AAB32754), and the NADP-dependent glyceraldehyde-3-phosphate deydrogenases of *Streptococcus mutans* (Q59931), *Zea mays* (NP_001105589), and *Pisum sativum* (P81406). Additionally or alternatively, a microorganism as disclosed herein that includes a non-native gene encoding an aldehyde dehydrogenase can encode a polypeptide 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%, or at least 95% amino acid sequence identity to SEQ ID NO:4, SEQ ID NO:6, or SEQ ID NO:7, or to an active fragment thereof. Examples of aldehyde dehydrogenases

having homology to amino acid sequences of SEQ ID NO:4, SEQ ID NO:6, and SEQ ID NO:7 include aldehyde dehydrogenases from *Bacillus* species, including, without limitation, the aldehyde dehydrogenases of *Bacillus thuringiensis serovar berliner* (ZP_041101108); *Bacillus thuringiensis* IBL 200 (ZP_04070879); *Bacillus thuringiensis* IBL 4222 (ZP_04064201); *Bacillus thuringiensis servovar kurstaki* (ZP_04113863), *Bacillus cereus* ATCC 10876 (ZP_04316482), *Bacillus thuringiensis serovar huazhongensis* (ZP_04083445), *Bacillus cereus* (ZP_03228808), *Bacillus cereus* 172560W (ZP_04305164), *Bacillus cytotoxicus* NVH 391-98 (YP_001374327); *Bacillus megaterium* WSH-002 (AEN89990); *Bacillus mycoides* Rock3-17 (ZP_04156127), *Bacillus cereus* AH621 (ZP_04293977), and *Bacillus thuringiensis* str. Al Hakam (YP_894009). Without limitation, an aldehyde dehydrogenase that can be expressed from a non-native gene in the engineered microorganisms provided herein can be a polypeptide with aldehyde dehydrogenase activity that includes an amino acid sequence having at least 85%, at least 90%, or at least 95% amino acid sequence identity to any of the above-cited aldehyde dehydrogenases or others listed in publications or sequence databases, or active fragments thereof, including conservative variants of identified aldehyde dehydrogenases, and including N-terminally and/or C-terminally truncated or modified variants. In some instances, a nucleic acid molecule useful in the invention can encode an aldehyde dehydrogenase that has at least 95% sequence identity to an aldehyde dehydrogenase as provided herein or identified in a sequence database or an N-terminally and/or C-terminally truncated variant thereof.

[0084] In some instances the aldehyde dehydrogenase encoded by a gene introduced into or overexpressed in the host microorganism may be a methylmalonate semialdehyde dehydrogenase (EC 1.2.1.27). A crystal structure of a methylmalonate semialdehyde dehydrogenase is found in Dubourg et al. (2004) *Acta Crystallogr D. Biol. Crystallogr.* 60: 1435-1437. Nonlimiting examples of methylmalonate semialdehyde dehydrogenases include the methylmalonate semialdehyde dehydrogenases of *Rattus norvegicus* (AAA41638); *Pseudomonas aeruginosa* (AAA25891); *Homo sapiens* (CAB76468); *Geobacillus thermoglucosidasius* C56-YS93 (YP_004588333); *Hanseniella* sp. 'Han2' (ACY45298); *Medicago truncatula* (XP_003608372); *Arabidopsis thaliana* (AEC06286); *Acinetobacter baumannii* 6014059 (ZP_08442960); and *Rhodococcus erythropolis* PR4 (BAH34663). Alternatively or in addition, a microorganism as disclosed herein that includes a non-native gene encoding an aldehyde dehydrogenase can encode a methylmalonate semialdehyde dehydrogenase comprising 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%, or at least 95% amino acid sequence identity to SEQ ID NO:18 or SEQ ID NO:19, or to an active fragment thereof. Nonlimiting examples of methylmalonate semialdehyde dehydrogenases having homology to SEQ ID NO:18 or SEQ ID NO:19 include the methylmalonate semialdehyde dehydrogenase of *Bacillus atrophaeus* 1942 (YP_003975426; ADP34495), *Bacillus licheniformis* ATCC 14580 (YP_081323; AAU25685), *Paenibacillus dendritiformis* C454 (ZP_09676636), *Paenibacillus terrae* HPL-003 (YP_005075546; AET59323), *Bacillus clausii* KSM-K16 (YP_173925; BAD62964), *Listeria monocytogenes* FSL F2-208 (EFR85827), *Listeria marthii* FSL S4-120 (ZP_07869657; EFR88847), and *Alicyclobacillus acidocaldarius* LAA1 (ZP_03495181; EED06125). Without limitation, an aldehyde dehydrogenase encoded by a non-native gene in an engineered microorganism as provided herein can be a polypeptide with methylmalonate semialdehyde dehydrogenase activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to any of these methylmalonate semialdehyde dehydrogenase or others as listed in sequence databases, conservative variants thereof, and N-terminally and/or C-terminally truncated or modified variants thereof. For example, a nucleic acid molecule useful in the invention can encode a methylmalonate semialdehyde dehydrogenase that has at least 95% sequence identity to a polypeptide as cited herein, or to another aldehyde dehydrogenase identified in a publication or sequence databases, or to an active fragment thereof.

[0085] A microorganism as disclosed herein can alternatively or in addition include a non-native gene encoding an aldehyde dehydrogenases that is a non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase (E.C. 1.2.1.9), also referred to as an NADP+-requiring glyceraldehyde-3- phosphate dehydrogenase (non-phosphorylating). A crystal structure of a non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase is provided in Lorentzen *et al.* (2004) *J. Mol. Biol.* 341: 815-828. Nonlimiting examples of a non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase that can be encoded by a recombinant nucleic acid molecule in a microorganism as provided herein include those derived from *Arabidopsis thaliana* (NP_180004), *Chlorella variabilis* (EFN50637), *Glycine max* (XP_003549550), *Brachypodium distachyon* (XP_003574540), *Sorghum bicolor* (XP_002444416), *Zea mays* (ACF84575), *Chlamydomonas reinhardtii* (XP_001753784), *Ostreococcus lucimarinus* (XP_001418445), *Bacillus cereus* (ZP_04196022.1), and *Selaginella moellendorffii* (XP_002981587.1). Without

limitation, a non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase encoded by a non-native gene in an engineered microorganism as provided herein can be polypeptides with non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to any of these non-phosphorylating glyceraldehyde-3- phosphate dehydrogenases or others as listed in sequence databases, including conservative variants thereof, and including N-terminally and/or C-terminally truncated or modified variants thereof. For example, a nucleic acid molecule useful in the invention can encode a non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase that has at least 85% or at least 90% sequence identity to a polypeptide as provided herein or an N-terminally and/or C-terminally truncated or modified variant, or to another non-phosphorylating glyceraldehyde-3- phosphate dehydrogenase identified in sequence listings or databases or to an active fragment thereof. In some instances, a nucleic acid molecule useful in the invention can encode an aldehyde dehydrogenase that has at least 95% sequence identity to a polypeptide as provided herein or identified in a sequence listing or database.

[0086] Yet another type of dehydrogenase that can be produced by expression of a non-native gene in a recombinant microorganism as provided herein is a D-isomer specific 2–hydroxyacid dehydrogenase (a D-2–hydroxyacid dehydrogenase), such as, for example, a D-2-hydroxyisocaproate dehydrogenase, a formate dehydrogenase, a D-glycerate dehydrogenase, a vancomycin-resistant protein H, a D-2-photophoglycerate dehydrogenase, or a D-lactate dehydrogenase. "D-2-hydroxyacid dehydrogenase" as used herein, refers to an enzyme that catalyzes the oxidation of an α-hydroxy carboxylic acid to an α-keto carboxylic acid, *e.g.* a lactate compound to a pyruvate compound. In the process, $NAD(P)^+$ is reduced to yield NAD(P)H. While many D-2-hydroxyacid dehydrogenases prefer NAD+ as a cofactor, others have been found to use NADP+ as a cofactor (Domenech and Ferrer (2006) *Biochim Biophys Acta* 1760: 1667-1674). An example of a crystal structure of a D-2–hydroxyacid dehydrogenases can be found in Dengler et al. (1997) *J. Mol. Biol* 267: 640-660. D-2–hydroxyacid dehydrogenases useful in the microorganisms and methods disclosed herein include D-2–hydroxyacid dehydrogenases that recruit to Pfam PF02826 "D-2-hydroxyacid dehydrogenase family" (gathering cut-off 25.1). Nonlimiting examples of D-2-hydroxyacid dehydrogenases include the D-2–hydroxyacid dehydrogenases of *Haloferax mediterranei* (ABB30004), *Enterococcus faecalis* (AAB05626), *Haloarcula marismortui* ATCC 43049

(AAV47467), *Bacillus* sp. 2 A 57 CT2 (ZP_08008412), *Streptococcus pyogenes* MGAS2096 (ABF36015.1), *Lactobacillus plantarum subsp. plantarum* NC8 (EHS81987.1), *Staphylococcus aureus* subsp. aureus S0385 (CAQ50990.1), *Rhizobium leguminosarum* bv. trifolii WSM2304 (ACI57766.1), *Nostoc punctiforme* ATCC 29133 (YP_001869125), *Micromonas* sp. RCC299 (ACO70365), *Phaeodactylum tricornutum* CCAP 1055/1 (XP_002183675), *Ostreococcus tauri* (XP_003081992), and *Aedes aegypti* (EAT43121), as well as the formate dehydrogenase of *Neurospora crassa* (CAC1825). Alternatively or in addition, a microorganism as disclosed herein that includes a non-native gene encoding a D-2-hydroxyacid dehydrogenase can include a non-native gene encoding a polypeptide 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%, or at least 95% amino acid sequence identity to SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, or SEQ ID NO:16, or to an active fragment thereof. For example, provided herein is a nucleic acid molecule comprising a nucleotide sequence that encodes a polypeptide having dehydrogenase activity that includes an amino acid sequence having at least at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to SEQ ID NO:2 or SEQ ID NO:29, such as, for example, an amino acid sequence having at least 85%, at least 90%, or at least 95% amino acid sequence identity to SEQ ID NO:2 or SEQ ID NO:29. Alternatively, a nucleic acid molecule as provided herein can include a nucleotide sequence that encodes a polypeptide having dehydrogenase activity that includes an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to SEQ ID NO:15 or SEQ ID NO:16.

[0087] Nonlimiting examples of D-2-hydroxyacid dehydrogenases having homology to SEQ ID NO:2 or SEQ ID NO:29 include the D-2-hydroxyacid dehydrogenase of *Polymorphum gilvum* SL003B-26A1 (YP_004302702), *Stappia aggregata* IAM 12614 (ZP_01545666; EAV45595), *Marinomonas* sp. MWYL1 (YP_001342133, ABR72198), *Labrenzia alexandrii* DFL-11 (ZP_05115584, EEE46183); *Delftia acidovorans* SPH-1 (YP_001566649, ABX38264), *Burkholderia* sp. CCGE1001 (YP_004230861; ADX57801), *Rhodobacter sphaeroides* ATCC 17029 (YP_001044959; ABN78187), *Rhodobacter sphaeroides* ATCC 17025 (YP_001168251; ABP70946); *Rhodobacter sphaeroides* WS8N (ZP_08415419; EGJ20215), *Rhodobacter sphaeroides* KD131 (YP_002520541; ACM03468), and *Burkholderia* sp. Ch1-1 (ZP_06839743; EFG72573). Without limitation, a D-2-hydroxyacid dehydrogenase encoded by a non-native

gene in an engineered microorganism as provided herein can be polypeptides with D-2-hydroxyacid dehydrogenase activity having at least 80%, at least 85%, at least 90%, or at least 95% amino acid sequence identity to any of these non-phosphorylating D-2-hydroxyacid dehydrogenases or others as listed in sequence databases, including conservative variants thereof, and N-terminally and/or C-terminally truncated or modified variants thereof. For example, a nucleic acid molecule useful in the invention can encode a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence that has at least 85% or at least 90% sequence identity to SEQ ID NO:2, SEQ ID NO:29, or to a polypeptide cited herein, or that has at least 85% or at least 90% sequence identity to another D-2-hydroxyacid dehydrogenase identified in a publication or sequence database or to an active fragment thereof. In some instances, a nucleic acid molecule useful in the invention can encode a D-2-hydroxyacid dehydrogenase that has at least 95% sequence identity to a polypeptide as provided herein or identified in a sequence database. In some instances, a nucleic acid molecule useful in the invention can encode a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence that has at least 95% sequence identity to SEQ ID NO:2 or SEQ ID NO:29.

[0088] Additional D-isomer specific 2-hydroxyacid dehydrogenases useful in the recombinant microorganisms and methods herein include those having homology to SEQ ID NO:15 or SEQ ID NO:16 such as but not limited to the D-2-hydroxyacid dehydrogenase of *Clostridium beijerinckii* NCIMB 8052 (YP_001309316), *Enterococcus gallinarum* EG2 (ZP_05648199); *Enterococcus casseliflavus* ATCC 12755 (ZP_08145011); the *Carnobacterium* sp. AT7 (ZP_02185893); and *Enterococcus faecium* E1636 (ZP_06695345). Without limitation, a D-2-hydroxyacid dehydrogenase encoded by a non-native gene in an engineered microorganism as provided herein can be polypeptides with D-2-hydroxyacid dehydrogenase activity having at least 85%, at least 90%, or at least 95% amino acid sequence identity to any of these non-phosphorylating D-2-hydroxyacid dehydrogenases or others as listed in publications or sequence databases, including conservative variants thereof and N-terminally and/or C-terminally truncated or modified variants thereof. For example, a nucleic acid molecule useful in the invention can encode a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence that has at least 85% or at least 90% sequence identity to SEQ ID NO:15, SEQ ID NO:16,or to another D-2-hydroxyacid dehydrogenase identified in a sequence listing or database or to an active fragment thereof. In some instances, a nucleic acid molecule useful in the

invention can encode a D-2-hydroxyacid dehydrogenase that has at least 95% sequence identity to a polypeptide as provided herein or identified in a sequence database. In some instances, a nucleic acid molecule useful in the invention can encode a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence that has at least 95% sequence identity to SEQ ID NO:15 or SEQ ID NO:16.

[0089] Alternatively or in addition, an isocitrate dehydrogenase gene can be expressed in a recombinant microorganism as provided herein. Examples of isocitrate dehydrogenases that can be expressed by microorganisms of the invention include, without limitation, the isocitrate dehydrogenase of *Candidatus Regiella insecticola* LSR1 (EFL92794); *Mycobacterium tuberculosis* CDC1551(AAK47786); *Blattabacterium* sp. (*Cryptocercus punctulatus*) str. Cpu (AEU09317); *Treponema azotonutricium* ZAS-9 (AEF80142); *Staphylococcus pseudintermedius* ED99 (ADX76379); *Paenibacillus polymyxa* E681 (ADM69426); *Escherichia coli* IHE3034 (ADE91794); *Acidithiobacillus ferrooxidans* ATCC 23270 (ACK80956); *Coxiella burnetii* RSA 331 (ABX78669); *Burkholderia pseudomallei* 1106a (ABO05966); *Burkholderia mallei* NCTC 10247 (ABO05966); *Burkholderia mallei* NCTC 10229 (ABN02935); *Burkholderia mallei* SAVP1 (ABM52803); *Mycobacterium avium* 104 (ABK66771); and *Aeromonas hydrophila* subsp. hydrophila ATCC 7966 (ABK38368). In some instances, a nucleic acid molecule useful in the invention can encode an isocitrate dehydrogenase that has at least 85%, at least 90%, or at least 95% sequence identity to a polypeptide as provided herein or identified in a sequence database, including conservative variants thereof and N-terminally and/or C-terminally truncated or modified variants thereof.

[0090] A glutamate dehydrogenase that can be encoded by a non-native nucleic acid molecule can include, as nonlimiting examples, the glutamate dehydrogenase of *Chaenocephalus aceratus* (P82264), *Bos Taurus* (NP 872593), *Arabidopsis thaliana* (NP_197318), *Medicago truncatula* (XP_003618972), *Chlorella variabilis* (EFN57943), *Chlamydomonas reinhardtii* (XP_001702270), *Rhodopirellula baltica* SH 1 (NP_867538) *Ktedonobacter racemifer* DSM 44963 (ZP_06967738), or *Roseiflexus* sp. RS-1 (YP_001276062) or a glutamate dehydrogenase that has at least 85%, 90%, or 95% sequence identity to a polypeptide as provided herein or identified in a sequence database, including a conservative variant thereof and/or an N-terminally and/or C-terminally truncated or modified variant thereof.

Microorganisms and Host Cells

[0091] The invention provides a recombinant microorganism that expresses a non-native gene encoding a dehydrogenase, in which the recombinant microorganism produces a lipid, where a culture of the recombinant microorganism expressing the dehydrogenase produces a greater amount of the lipid than does a control culture identical to the culture of the dehydrogenase-expressing microorganism, except that the microorganism of the control culture does not include the non-native gene encoding a dehydrogenase. The recombinant microorganism can further include at least one additional non-native gene for the production of a lipid, such as, for example, a non-native gene encoding an enzyme for the production of fatty acids, fatty acid derivatives, and/or glycerolipids. In some examples, a microorganism that includes a non-native gene encoding a dehydrogenase and a non-native gene encoding a polypeptide that participates in synthesis of a lipid has a higher propagation and/or proliferation rate than does a control microorganism identical in all respects to the microorganism expressing a non-native dehydrogenase gene and a non-native gene encoding a polypeptide that participates in the production of a lipid, except that the control microorganism does not include the non-native gene encoding a dehydrogenase. For example, a culture of a recombinant microorganism as disclosed herein that includes a non-native gene encoding a dehydrogenase and a non-native gene encoding a polypeptide for production of a lipid (*e.g.*, fatty acid product) synthesis can achieve a higher cell density after three, four, five, six, or more than six days in culture than the cell density achieved by a control microorganism identical in all respects to the microorganism expressing a non-native dehydrogenase gene and a non-native gene encoding a polypeptide that participates in the production of a lipid, except that the control microorganism does not include the non-native gene encoding a dehydrogenase. For example, a culture of the recombinant microorganism expressing a non-native dehydrogenase gene and a non-native gene that encodes a polypeptide that participates in the production of a lipid can achieve a higher cell density than a control culture of a microorganism lacking the non-native dehydrogenase gene under culture conditions in which the lipid, *e.g.*, a fatty acid product, is being produced. The fatty acid product may be a lipid not naturally made by the host microorganism (*i.e.*, not made by the host microorganism lacking the non-native gene that participates in the production of the lipid).

[0092] Recombinant microorganisms or host cells of the invention may be of prokaryotic or eukaryotic origin, including, without limitation, fungi, heterokonts, algae, eubacteria,

archaebacteria, green nonsulfur bacteria, purple nonsulfur bacteria, or cyanobacteria. Recombinant host cells can be, but are not limited to, photosynthetic organisms. Photosynthetic organisms include higher plants (*i.e.*, vascular plants), bryophytes, algae, and photosynthetic bacteria. The term "algae" includes cyanobacteria (*Cyanophyceae*), green algae (*Chlorophyceae*), yellow-green algae (*Xanthophyceae*), golden algae (*Chrysophyceae*), brown algae (*Phaeophyceae*), red algae (*Rhodophyceae*), diatoms (*Bacillariophyceae*), and "pico-plankton" (*Prasinophyceae* and *Eustigmatophyceae*). Also included in the term algae are members of the taxonomic classes *Dinophyceae*, *Cryptophyceae*, *Euglenophyceae*, *Glaucophyceae*, and *Prymnesiophyceae*. Microalgae are unicellular or colonial algae that can be seen as single organisms only with the aid of a microscope. Microalgae include both eukaryotic and prokaryotic algae (*e.g.*, cyanobacteria).

[0093] Algae for use in the invention, include without limitation, microalgae, such as but not limited to, *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, Schizochlamydella, Skeletonema, Spyrogyra, Stichococcus, Tetrachlorella, Tetraselmis, Thalassiosira, Viridiella*, or *Volvox* species. For example, the host microorganism can be a diatom, and can be of a genus selected from the group consisting of *Amphora, Chaetoceros, Cyclotella, Fragilaria, Navicula, Phaeodactylum*, or *Thalassiosira*. Alternatively, in some examples the host strain can be a eustigmatophyte, such as a species of *Nannochloropsis* or *Ellipsoidon* or a green alga, such as, but not limited to, a species of *Chlorella, Chlorogonium, Pseudochlorella, Scenedesmus*, or *Tetraselmis*.

[0094] Alternatively, the recombinant microorganism can be a species of cyanobacteria. More than thirty cyanobacterial genomes have been completely sequenced to date, including, for

example, the genomes of various *Acaryochloris, Arthrospira, Cyanobacterium, Cyanothece, Gloeobacter, Microcystis, Nostoc, Prochlorococcus, Synechococcus, Synechocystis*, and *Thermosynechococcus* species, and many cyanobacterial species been manipulated using molecular biological techniques, including for example the cyanobacteria *Leptolyngbya* sp. Strain BL0902, *Anabaena* (*Nostoc*) sp. PCC 7120, *Anabaena variabilis* ATCC 29413, *Nostoc punctiforme* ATCC 29133, *Nostoc sp.* PCC 7422, *Synechocystis* sp. PCC 6803, *Synechococcus elongatus* PCC 7942, *Synechococcus elongatus* PCC 7002, *etc.* (Taton et al. (2012) *PLoS One* Vol.7, Iss. 1 e30910; Ruffing (2011) *Bioengineered Bugs* 2:136-149). The recombinant microorganisms provided herein can be, as non-limiting examples, of any of the following genera of cyanobacteria: *Agmenellum, Anabaena, Anabaenopsis, Anacystis, Aphanizomenon, Arthrospira, Asterocapsa, Borzia, Calothrix, Chamaesiphon, Chroococcus, 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*. For example, the recombinant photosynthetic microorganism can be a *Synechococcus, Synechocystis,* or *Thermosynechococcus* species. Alternatively, the recombinant photosynthetic microorganism can be a *Cyanobium, Cyanothece,* or *Cyanobacterium* species, or further alternatively, the recombinant photosynthetic microorganism can be a *Gloeobacter, Lyngbya, or Leptolyngbya* species.

[0095] The recombinant microorganism can include a non-native gene encoding any dehydrogenase disclosed herein. In some examples, the microorganism expresses a non-native gene encoding an NADPH-producing dehydrogenase, such as, for example, NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating) (EC 1.2.1.9), malic enzyme, isocitrate dehydrogenase, glutamate dehydrogenase, glucose-6-phosphate dehydrogenase, or 6-phosphogluconate dehydrogenase. Alternatively or in addition, the recombinant microorganism can express a gene encoding an aldehyde dehydrogenase, a methylmalonate semialdehyde

dehydrogenase, or a D-2-hydroxyacid dehydrogenase. In particular examples, a recombinant microorganism as provided herein can include a non-native nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide comprising 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%, or at least 85%, for example at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or about 100% sequence identity to the amino acid sequence of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:2, or SEQ ID NO:29, operably linked to a heterologous promoter.

[0096] For example, a recombinant microorganism can include a non-native gene encoding a dehydrogenase of the pentose phosphate pathway, such as a glucose-6-phosphate dehydrogenase or a 6-phosphogluconate dehydrogenase, such as, for example, any disclosed herein. The 6-phosphogluconate dehydrogenase can be derived from any organism, prokaryotic or eukaryotic, and can, for example, be from the same species as the host microorganism, where the non-native gene may be an introduced gene or an endogenous gene that is overexpressed by genetically engineering a promoter operably linked to the endogenous 6-phosphogluconate dehydrogenase gene. Alternatively or in addition, the 6-phosphogluconate dehydrogenase may 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%, or at least 95% sequence identity to SEQ ID NO:10, SEQ ID NO:11 or to an active fragment thereof. For example, the 6-phosphogluconate dehydrogenase can include an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:10 or SEQ ID NO:11 or to an active fragment thereof. Alternatively or in addition, the 6-phosphogluconate dehydrogenase may 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%, or at least 95% sequence identity to SEQ ID NO:13 or to an active fragment thereof. For example, the 6-phosphogluconate dehydrogenase can include an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:13 or to an active fragment thereof. The host microorganism can further include, in addition to a non-native gene encoding 6-phosphogluconate dehydrogenase, at least one additional non-native gene that encodes a

polypeptide that participates in lipid biosynthesis, *e.g.*, synthesis of a fatty acid product. A culture of the recombinant host microorganism that includes a non-native 6-phosphogluconate dehydrogenase gene and a non-native lipid biosynthesis gene can produce a higher amount of a fatty acid product than is produced by a culture of a control microorganism identical in all respects to the recombinant host microorganism, except that the control microorganism does not include a non-native 6-phosphogluconate dehydrogenase gene. Additionally, the recombinant host microorganism that includes a non-native gene encoding a 6-phosphogluconate dehydrogenase and a non-native gene that encodes a polypeptide that participates in synthesis of a fatty acid product can have a higher propagation and/or proliferation rate and/or can achieve a higher cell density than can be achieved by the control microorganism under culture conditions where the fatty acid product is being produced. In particular examples, the lipid produced in a higher amount by a culture of the recombinant microorganism is a fatty acid product that is not produced by the microorganism in the absence of expression of the non-native gene for lipid production.

[0097] In further examples, a recombinant microorganism can include a non-native gene encoding an aldehyde dehydrogenase, including, but not limited to, any disclosed herein. The aldehyde dehydrogenase can be derived from any organism, prokaryotic or eukaryotic, and can, for example, be from the same species as the host microorganism, where the non-native gene may be an introduced gene or an endogenous gene that is overexpressed by genetically engineering a promoter operably linked to the endogenous aldehyde dehydrogenase gene. In various illustrative examples, the aldehyde dehydrogenase may 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% or at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO:4, SEQ ID NO:6 or SEQ ID NO:7, or to an active fragment thereof. For example, the aldehyde dehydrogenase can include an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:4, SEQ ID NO:6, or SEQ ID NO:7. The host microorganism that includes a non-native gene encoding an aldehyde dehydrogenase can further include an additional non-native gene that encodes a polypeptide that participates in lipid biosynthesis, *e.g.*, synthesis of a fatty acid product. A culture of the recombinant host microorganism that includes a non-native aldehyde dehydrogenase gene and a non-native lipid biosynthesis gene can produce a higher amount of a

fatty acid product than is produced by a culture of a control microorganism identical in all respects to the recombinant host microorganism, except that the control microorganism does not include a non-native aldehyde dehydrogenase gene. Additionally, the recombinant host microorganism that includes a non-native gene encoding an aldehyde dehydrogenase and a non-native gene that encodes a polypeptide that participates in synthesis of a fatty acid product can have a higher propagation and/or proliferation rate and/or can achieve a higher cell density than can be achieved by the control microorganism under culture conditions where the fatty acid product is being produced. In particular examples, the lipid produced in a higher amount by the recombinant microorganism is a fatty acid product that is not produced by the microorganism in the absence of expression of the non-native gene for encoding a polypeptide for lipid production.

[0098] For example, the aldehyde dehydrogenase can be a methylmalonate semialdehyde dehydrogenase, and the host microorganism can include a non-native gene encoding a methylmalonate semialdehyde dehydrogenase, such as, but not limited to, any disclosed herein. For example, a methylmalonate semialdehyde dehydrogenase 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%, or at least 95%, identity to SEQ ID NO:18 or SEQ ID NO:19, or to an active fragment thereof. In some examples, the host microorganism can include a non-native gene encoding a methylmalonate semialdehyde dehydrogenase having at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:18 or SEQ ID NO:19.

[0099] In further examples, a recombinant microorganism can include a non-native gene encoding a D-2-hydroxyacid dehydrogenase, such as, but not limited to, any disclosed herein. The D-2-hydroxyacid dehydrogenase can be derived from any organism, prokaryotic or eukaryotic, and can be from the same species as the host microorganism, where the non-native gene may be an introduced gene or an endogenous gene that is overexpressed, for example, by genetically engineering a promoter operably linked to the endogenous D-2-hydroxyacid dehydrogenase gene. In various examples, the microorganism includes a non-native gene encoding a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence 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%, or at least 95% sequence identity to SEQ ID NO:2 or SEQ ID NO:29, or to an active fragment thereof. For example, the D-2-hydroxyacid dehydrogenase can include an

amino acid sequence having at least 85%, at least 90%, or at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:2 or SEQ ID NO:29. In further examples, the microorganism includes a non-native gene encoding a D-2-hydroxyacid dehydrogenase that includes an amino acid sequence 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%, or at least 95% sequence identity to SEQ ID NO:15 or SEQ ID NO:16, or to an active fragment thereof. For example, the D-2-hydroxyacid dehydrogenase can include an amino acid sequence having at least 85%, at least 90%, or at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:15 or SEQ ID NO:16. The host microorganism that includes a non-native gene encoding a D-2-hydroxyacid dehydrogenase can further include an additional non-native gene that encodes a polypeptide that participates in lipid biosynthesis, *e.g.*, synthesis of a fatty acid product. A culture of the recombinant host microorganism that includes a non-native D-2-hydroxyacid dehydrogenase gene and a non-native lipid biosynthesis gene can produce a higher amount of a fatty acid product than is produced by a culture of a control microorganism identical in all respects to the recombinant host microorganism, except that the control microorganism does not include the non-native D-2-hydroxyacid dehydrogenase gene. Additionally, the recombinant host microorganism that includes a non-native gene encoding a D-2-hydroxyacid dehydrogenase and a non-native gene that encodes a polypeptide that participates in synthesis of a fatty acid product can have a higher propagation and/or proliferation rate and/or can achieve a higher cell density than can be achieved by the control microorganism under culture conditions where the fatty acid product is being produced. The lipid produced in a higher amount by the recombinant microorganism may in some examples be a fatty acid product that is not produced by the microorganism in the absence of expression of the non-native gene for encoding a polypeptide for lipid production.

[00100] In particular nonlimiting examples, the recombinant microorganism comprising a non-native gene encoding a dehydrogenase and an additional non-native gene encoding a polypeptide that participates in the production of a fatty acid product not normally produced by the microorganism (*e.g.*, not produced by the species or strain of microorganism used as a host microorganism when not transformed with a non-native gene encoding a polypeptide that participates in the production of a fatty acid product) can be a recombinant photosynthetic microorganism, in which a culture of the recombinant photosynthetic microorganism produces a

greater amount of the fatty acid product than is produced by a control culture identical in all respects except that the recombinant photosynthetic microorganism of the control culture does not include or does not express the non-native gene encoding the dehydrogenase. For example, the host microorganism can be a species of eukaryotic microalgae that does not naturally produce, *e.g.*, free fatty acids, fatty aldehydes, fatty alcohols, fatty acid esters (*e.g.*, fatty acid alkyl esters), or wax esters, where the recombinant host microorganism transformed with a dehydrogenase gene and a gene for production of a fatty acid product is able to produce one or more of a free fatty acid, fatty aldehyde, fatty alcohol, alkane, alkene, fatty acid ester, or wax ester. Alternatively, the host microorganism can be a species of cyanobacteria that does not naturally produce, *e.g.*, a free fatty acid, fatty alcohol, alkane, alkene, fatty acid ester, wax ester, or triglyceride, where the recombinant host microorganism transformed with a dehydrogenase gene and a gene for production of a fatty acid product is able to produce one or more of a free fatty acid, fatty alcohol, alkane, alkene, fatty acid ester, wax ester, or triglyceride.

[00101] Preferably, a culture of the photosynthetic microorganism that includes a non-native gene encoding a dehydrogenase and a non-native gene encoding a polypeptide that participates in the production of a lipid produces a greater amount of a fatty acid product than is produced by a culture of an otherwise identical photosynthetic microorganism that lacks the non-native gene encoding the dehydrogenase. For example, a photoautotrophic culture of the photosynthetic microorganism that includes a non-native gene encoding a dehydrogenase and a non-native gene encoding a polypeptide that participates in the production of a lipid can preferably produce a greater amount of a fatty acid product than is produced by a photoautotrophic culture of an otherwise identical photosynthetic microorganism that lacks the non-native gene encoding the dehydrogenase. Additionally or alternatively, a culture of the recombinant photosynthetic microorganism can achieve a higher cell density while producing a lipid under photoautotrophic conditions, *e.g.*, using inorganic (non-reduced) carbon as the carbon source for production of the fatty acid product.

Genetic Modifications for Production of Fatty Acid Products

[00102] A recombinant microorganism as provided herein can be engineered to produce a lipid, such as, for example, a fatty acid, a fatty acid derivative (*e.g.*, a fatty aldehyde, a fatty alcohol, a fatty acid ester, a wax ester, an alkane, or an alkene), or a glycerolipid (*e.g.*, a triglyceride). For example, the recombinant microorganism can include at least one non-native

gene that encodes one or more of an acyl-ACP thioesterase, an acyl-CoA thioesterase, a hydroxybenzoyl thioesterase, a polypeptide having lipolytic activity, an acyl-ACP reductase, an acyl-CoA reductase, a carboxylic acid reductase, a wax synthase, a decarbonylase, a decarboxylase, a glycerolphosphate acyltransferase (GPAT), a lysophosphatidic acid acyltransferase (LPAAT), a phosphatidic acid phosphatase (PAP), or a diacylglycerol O-acyltransferase (DGAT).

[00103] In various nonlimiting and illustrative examples, a recombinant microorganism that includes a non-native dehydrogenase gene can include, for example, one or more of an acyl-ACP thioesterase, acyl-CoA thioesterase, hydroxybenzoyl thioesterase, and a polypeptide having lipolytic activity for the production of free fatty acids or for the production of fatty aldehydes, fatty alcohols, fatty acid esters, wax esters, alkanes, or alkenes generated from fatty acids. The recombinant microorganism can include, for example, a non-native gene encoding an acyl-ACP thioesterase, such as any disclosed herein, such as, for example, a higher plant FatB thioesterase. In an illustrative example, the microorganism can include a non-native gene encoding a *Cuphea* acyl-ACP thioesterase or a variant thereof, for example, the acyl-ACP thioesterase of SEQ ID NO:21. The recombinant microorganism can be a microalga, for example, a cyanobacterium.

[00104] Alternatively or in addition, a recombinant microorganism that includes a non-native dehydrogenase gene can include a non-native acyl reductase gene for the production of a fatty aldehyde, and optionally, a decarbonylase that converts a fatty aldehyde to an alkane. The aldehyde-forming acyl reductase can be an acyl-ACP reductase or an acyl-CoA reductase. Further alternatively or additionally, a recombinant microorganism that includes a non-native dehydrogenase gene can include an acyl reductase gene for the production of a fatty alcohol, and optionally, a wax synthase that converts a fatty alcohol to a wax ester. The alcohol-forming acyl reductase can be an acyl-ACP reductase or an acyl-CoA reductase. A wax synthase can optionally be a wax synthase that is able to use acyl-ACP as a substrate. The recombinant microorganism can further include an acyl-CoA synthetase, or, in examples where enzymes such as acyl reductases and/or wax synthases or acyltransferases are able to use acyl-ACP as a substrate, may not include a non-native gene encoding an acyl-CoA synthetase. In particular examples, the recombinant microorganism used for the production of a fatty acid derivative is a cyanobacterial species that does not naturally include a gene encoding either of an acyl-CoA

synthetase or an acyl-ACP thioesterase and further does not include an exogenous (*i.e.*, introduced) gene encoding either or both of an acyl-CoA synthetase or an acyl-ACP thioesterase.

[00105] Alternatively or in addition, a recombinant microorganism that includes a non-native dehydrogenase gene can include a non-native gene encoding an acyl transferase, such as, but not limited to, a DGAT, LPAAT, or GPAT, and can optionally additionally or alternatively include a non-native gene encoding a PAP.

[00106] Specifically included for use in the constructs and microorganisms disclosed herein are nucleic acid sequences that encode polypeptides having at least 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, amino acid sequence identity to known or suspected enzymes of a given class, including but not limited to the examples below, where the encoded polypeptides have activity of the enzyme class. For example, a nucleic acid sequence that encodes a thioesterase, lipase, acyl-CoA synthetase, aldehyde forming reductase, alcohol-forming reductase, carboxylic acid reductase, decarbonylase, decarboxylase, wax synthase, acyltransferase, or transporter useful in the microorganisms and methods provided herein can have at least 85%, at least 90%, or at least 95% amino acid sequence identity to an identified thioesterase, lipase, acyl-CoA synthetase, aldehyde forming reductase, alcohol-forming reductase, carboxylic acid reductase, decarbonylase, decarboxylase, wax synthase, or acyltransferase, *e.g.*, a sequence annotated in a database, including but not limited to those disclosed herein.

Thioesterases

[00107] For example, in addition to an expression system for one or more recombinant genes encoding a dehydrogenase, a host microorganism can include a non-native gene encoding a thioesterase. As used herein, the term "thioesterase" is intended to include hydrolases capable of acting on a thioester bond to release fatty acids. Host microorganisms can produce free fatty acids or can convert the fatty acids released by a thioesterase to other products, such as fatty alcohols or wax esters. Thioesterases can correspond to, *e.g.*, Enzyme Commission Number 3.1.2.2, 3.1.2.14, 3.1.2.18, 3.1.2.19, 3.2.1.20, 3.1.2.22, 3.1.2.23, or 3.1.2.27. An exogenous thioesterase expressed in the host microorganism can be, for example, an acyl-ACP thioesterase, an acyl-CoA thioesterase, or a hydroxylbenzoyl thioesterase. For example, a microorganism for the production of free fatty acids in some embodiments can be transformed with a gene encoding an exogenous acyl-ACP thioesterase, such as a gene encoding a polypeptide that when queried

against the Pfam database, provides a match with Pfam PF01643 having a bit score of less than or equal to 20.3 (the gathering cut-off for PF01643). The exogenous acyl-ACP thioesterase gene can encode an acyl-ACP thioesterase from a higher plant species. Genes encoding acyl-ACP thioesterases derived from higher plants can include, without limitation, genes encoding acyl-ACP thioesterases from *Cuphea* species (e.g. *Cuphea carthagenensis*, *Cuphea wrightii* (e.g., GenBank Accession AAC49784), *Cuphea lanceolata* (e.g., GenBank Accession CAA54060), *Cuphea palustris*, (e.g., GenBank Accessions AAC49783; AAC49179); *Cuphea hookeriana* (e.g., GenBank Accessions AAC72882; AAC49269; AAC72881; AAC72883), *Cuphea calophylla* (e.g., GenBank Accession ABB71580) or genes of various *Cuphea* species disclosed in United States patent application publication US 2011/0020883, incorporated by reference herein) or genes from other higher plant species. In further examples, a microorganism used in the methods and cultures disclosed herein can include a gene encoding an acyl-ACP thioesterase from species such as but not limited to, *Arabidopsis* (*e.g.*, GenBank Accessions XP_002885681; NP_172327); *Arachis hypogaea* (*e.g.*, GenBank Accession ABO38556); *Brassica* species (*e.g.*, GenBank Accession CAA52069.1), *Camellia oleifera* (*e.g.*, GenBank Accession ACQ57189); *Cinnamonum camphorum* (*e.g.*, GenBank Accession AAC49151); *Cocos nucifera* (*e.g.*, GenBank Accessions AEM72519; AEM72520; AEM72521); *Glycine max* (*e.g.*, GenBank Accession ABD91726); *Garcinia mangostana* (*e.g.*, GenBank Accession AAB51525); *Gossypium hirsutum* (*e.g.*, GenBank Accession AAD01982); *Helianthus annuus* (*e.g.*, GenBank Accession AAQ08226); *Jatropha curcas* (*e.g.*, GenBank Accession ABU96744); *Macadamia tetraphylla* (*e.g.*, GenBank Accession ADA79524); *Elaeis oleifera* (*e.g.*, GenBank Accession AAM09524); *Elaeis guineensis* (*e.g.*, GenBank Accession AAD42220); *Oryza sativa* (*e.g.*, GenBank Accession BAA83582); *Populus tomentosa* (*e.g.*, GenBank Accession ABC47311); *Umbellularia californica* (*e.g.*, GenBank Accession AAC49001); *Ulmus Americana* (*e.g.*, GenBank Accession AAB71731); and *Zea mays* (*e.g.*, GenBank Accession ACG41291), or any of those disclosed in U.S. Patent No. 5,455,167; U.S. Patent No. 5,654,495; and U.S. Patent No. 5,455,167; and in U.S. Patent Appl. Pub. Nos. 2009/0298143 and 2011/0020883; all incorporated by reference herein in their entireties. Further included are acyl-ACP thioesterases from mosses (Bryophyta), such as, for example, *Physcomitrella patens* (*e.g.*, GenBank Accession XP 001770108). The foregoing examples are not limiting with regard to the types or specific examples of acyl-ACP thioesterase genes that can be used.

[00108] Further included are acyl-ACP thioesterase genes from prokaryotic organisms. Illustrative examples of prokaryotic acyl-ACP thioesterases that may be expressed by a microorganism useful in the methods and cultures provided herein include, but are not limited to acyl-ACP thioesterases from *Desulfovibrio desulfuricans* (*e.g.* Q312L1); *Elusimicrobium minutum* (*e.g.* ACC98705); *Carboxydothermus hydrogenoformans* (*e.g.* YP_359670); *Clostridium thermocellum* (*e.g.* YP_001039461); *Moorella thermoacetica* (*e.g.* YP_431036); *Geobacter metallireducens* (*e.g.* YP_384688); *Salinibacter ruber* (*e.g.* YP_444210); *Microscilla marina* (*e.g.* EAY28464); *Parabacteroides distasonis* (*e.g.* YP_001303423); *Enterococcus faecalis* (*e.g.* ZP_03949391); *Lactobacillus plantarum* (*e.g.* YP_003062170); *Leuconostoc mesenteroides* (*e.g.* YP_817783); *Oenococcus oeni* (*e.g.* ZP_01544069); *Mycobacterium smegmatis* (*e.g.* ABK74560); *Mycobacterium vanbaalenii* (*e.g.* ABM11638); *Rhodococcus erythropolis* (*e.g.* ZP_04385507; *Rhodococcus opacus* (*e.g.* YP_002778825), or any of those disclosed in the co-pending, commonly-assigned patent application No. 13/324,623 entitled "Prokaryotic Acyl-ACP Thioesterases for Producing Fatty Acids in Genetically Engineered Microorganisms", filed on December 13, 2011, which is incorporated herein by reference in its entirety.

[00109] In additional examples, a gene encoding an acyl-CoA thioesterase can be introduced into a host microorganism that includes an exogenous nucleic acid molecule encoding a dehydrogenase. An acyl-CoA thioesterase gene transformed into a microorganism for the production of free fatty acids or fatty acid derivatives can be from a plant, animal, or microbial source. For example, a gene encoding the TesA or TesB thioesterase of *E. coli*, or a variant thereof, for example, an acyl-CoA thioesterase such as not limited to a variant as disclosed in WO 2010/075483, incorporated by reference herein in its entirety, can be introduced into a microorganism. Also included are genes encoding proteins that when queried against the Pfam database of protein families are identified as members of Pfam PF02551 (acyl-CoA thioesterase), where the bit score is equal to or greater than the gathering cut off (20.7).

[00110] Alternately or in addition, the microorganism can include one or more genes encoding an exogenous hydroxybenzoyl thioesterase, for example an exogenous 4-hydroxybenzoyl thioesterase or 4-chlorobenzoate thioesterase. Genes encoding hydroxybenzoyl thioesterases that may be useful in a microorganism for producing free fatty acids can include, for example, those disclosed in the co-pending, commonly-assigned patent application No.

13/324,607 entitled "Genetically Engineered Microorganisms Comprising 4-Hydroxybenzoyl-CoA Thioesterases and Methods of Using Same for Producing Free Fatty Acids and Fatty Acid Derivatives", filed on December 13, 2011, and which is incorporated herein by reference in its entirety, 4-hydroxybenzoyl thioesterases from *Bacillus* species and *Geobacillus* species, as well as 4-hydroxybenzoyl thioesterases of *Acidiphilium, Bartonella, Rhodopseudomonas, Magnetospirillum, Burkholderia, Granulibacter, Rhizobium*, and *Labrenzia* species, or the like, or combinations thereof.

[00111] Acyl-ACP thioesterases typically can be active to some degree on acyl-ACP substrates having a plurality of different acyl chain lengths, but can have higher activity on (*e.g.*, have a substrate preference for) one or more acyl-ACP substrates having particular acyl chain lengths than on other chain length substrates. For example, an acyl-ACP thioesterase may have a substrate preference for one or more of acyl-ACP substrates having acyl chain lengths of 8, 10, 12, 14, 16, 18, 20, 22, and/or 24 carbons. Additionally or alternately, the acyl-ACP thioesterase can hydrolyze one or more acyl-ACP substrates having an acyl chain length from 8 to 18 carbons, for example from 12 to 16 carbons.

Polypeptides having Lipolytic Activity

[00112] Alternatively or in addition to a non-native gene encoding a thioesterase, a recombinant microorganism or host cell of the invention can include one or more non-native genes encoding one or more polypeptides having lipolytic activity, where the polypeptide(s) having lipolytic activity are capable of producing free fatty acids from membrane lipids or storage lipids, *e.g.*, phospholipids, triacylglycerols, diacylglycerols, monoacylglycerols, or the like, or combinations thereof. The polypeptides having lipolytic activity can be, for example, lipases, esterases, cutinases, or amidases. Lipases are enzymes that catalyze the hydrolysis of ester bonds in glycerolipids, including, but not limited to, mono-, di-, and tri-acyl glycerols, as well as combinations thereof, to release free fatty acids and alcohols.

[00113] The use of genes encoding polypeptides having lipolytic activity in microorganisms for the production of free fatty acids is disclosed in commonly-assigned U.S. patent application No. 13/324,653 entitled "Production of Free Fatty Acids and Fatty Acid Derivatives by Recombinant Microorganisms Expressing Polypeptides Having Lipolytic Activity," filed on December 13, 2011, and which is incorporated herein by reference in its entirety. The polypeptide having lipolytic activity can be for example a lipase, *e.g.*, that liberates a fatty acid

from a glycerolipid (including a monoglyceride, a diglyceride, a triglyceride, a phospholipid, a galactolipid, *etc.*) or can be an amidase. For example, the recombinant microorganism can include a non-native gene encoding a lipase, such as but not limited to a lipase that is a member of a Pfam belonging to the AB Hydrolase Pfam clan (CL0028). For example, a non-native gene encoding a polypeptide having lipolytic activity can encode a lipase that includes a LipA domain identified as conserved protein domain COG1075, or is included in the protein family Pfam PF01674 (Lipase 2); a non-native nucleic acid molecule that encodes a lipase that includes a Lipase 3 domain identified as conserved protein domain COG3675, or is included in the protein family Pfam PF01764 (Lipase 3); a non-native nucleic acid molecule that encodes a lipase that is included in the protein family Pfam PF07819 (PGAP1); or a non-native nucleic acid molecule that encodes a polypeptide that is included in any of the protein families Pfam PF03583, Pfam PF00151 (Lipase), Pfam PF00561 (Ab hydrolase 1), Pfam PF02230 (Ab hydrolase 2), Pfam PF07859 (Ab hydrolase 3), Pfam PF08386 (Ab hydrolase 4), Pfam PF12695 (Ab hydrolase 5), Pfam PF12697 (Ab hydrolase 6), Pfam PF12715 (Ab hydrolase 7), Pfam PF04083 (Ab hydro lipase). Further, the recombinant microorganism can include a non-native gene encoding an amidase having lipolytic activity, such as but not limited to an amidase that recruits to Pfam PF01425 (Amidase) with a bit score greater than the gathering cutoff of 20.1 and can catalyze the release of fatty acids from lipids.

[00114] Additionally or alternately contemplated are recombinant microorganisms that are engineered to include gene regulatory sequences that induce or increase expression of an endogenous lipase gene. For example, a microorganism can be engineered such that a heterologous promoter is inserted upstream of a coding region of an endogenous lipase gene. The heterologous promoter can replace an endogenous promoter and/or can be inserted upstream or downstream of the endogenous promoter that regulates expression of the endogenous lipase gene, for example using homologous recombination or site-specific recombination. The heterologous promoter can be a constitutive promoter or an inducible promoter that increases expression of the endogenous lipase gene.

[00115] Additionally but optionally, a recombinant microorganism engineered to include an exogenous gene encoding a thioesterase for the production of fatty acids or fatty acid derivatives can further include an exogenous gene encoding a lysophosphatidic acid acyltransferase (LPAAT), where the LPAAT has a different acyl-ACP substrate preference than the acyl-ACP

substrate preference of the thioesterase. Alternatively, the genetically engineered microorganism, which can be a genetically engineered cyanobacterium, can overexpress an endogenous LPAAT gene having a different substrate preference than the substrate preference of an exogenous thioesterase gene. The engineering of microorganisms such as cyanobacteria to increase fatty acid production by expression of LPAAT genes is disclosed in co-pending and commonly-assigned U.S. patent application 13/404,7171 entitled "Enhanced Production of Fatty Acids and Fatty Acid Derivatives by Recombinant Microorganisms" filed February 24, 2012, and incorporated herein by reference in its entirety.

Acyl-CoA Synthetases

[00116] A recombinant or isolated nucleic acid molecule used in the microorganisms and methods of the invention can optionally comprise a nucleic acid sequence encoding an acyl-CoA synthetase, where the acyl-CoA synthetase may couple a free fatty acid generated by a thioesterase or lipase to coenzyme A to provide acyl-CoA, which is a substrate for many reductases, wax synthases, and acyltransferases that can produce aldehydes, alcohols, wax esters, and glycerolipids using an acyl-CoA substrate. The acyl-CoA synthetase can be, for example, a prokaryotic acyl-CoA synthetase, for example, such as FadD (NP_416319) or FadK of *E. coli* (NP_416216), or their homologs in other bacterial species, including, as nonlimiting examples, the acyl-CoA synthetase of *Vibrio splendidus* (EGU44230) or *Marinobacter adhaerens* HP15 (ADP96803). Additional nonlimiting examples of prokaryotic proteins known to have or suspected of having acyl-CoA synthetase activity include, but are not limited to, *Acinetobacter* sp. ADP1 fadD (YP_045024), *Haemophilus influenza* RdKW20 fadD (NP_438551), *Bacillus halodurans* C-125 BH3103 (NP_243969), *Bacillus subtilis* yhFl (NP_388908), *Pseudomonas fluorescens* Pfo-1 Pfl-4354 (YP_350082), *Comamonas testosteroni* KF-1 EAV15023 (ZP_01520072), *Pseudomonas aeruginosa* fadD1 (NP_251989), *Pseudomonas aeurginosa* PAO1 fadD2 (NP_251990), *Rhizobium etli* CFN42 fadD (YP_468026), *Rhodopseudomo nas palustris* Bis B18 RPC_4074 (YP_533919), *Rasltonia Solanacearum* GM1 1000 fadD1 (NP_520978), *Mycobacterium tuberculosis* H37Rv fadDD35 (NP_217021), *Mycobacterium tuberculosis* H37Rv fadDD22 (NP_217464), and *Stenotrophomon as Maltophilia* R551-3 PRK0059 (ZP_01644857).

[00117] In further examples, the nucleic acid sequence encoding an acyl-CoA synthetase can encode an acyl-CoA synthetase derived from a fungal species, such as, for example, a

Saccharomyces cerevisiae acyl-CoA synthetase (*e.g.*, the medium chain fatty acyl-CoA synthetase Faa2p (NP_010931) or the SCRG_04483 acyl-CoA synthetase (EDV08843) or a *Yarrowia lipolytica* acyl-CoA synthetase (*e.g.*, CAG77892). Additional acyl-CoA synthetase genes that may be used in the constructs and microorganisms disclosed herein include acyl-CoA synthetases of plants, such as, for example, the long chain acyl-CoA synthetase of *Brassica napus* (CAC19877) or the long chain acyl-CoA synthetase of *Arabidopsis thaliana* (AEE74324), or the Yng-I-like acyl-CoA synthetase of *Glycine max* (XP_003524920), and acyl-CoA synthetases of algal species, such as, for example, the long chain acyl-CoA synthetase of *Chlamydomonas reinhardtii* (XP_001693692), or acyl-CoA synthetases of *Nannochloropsis oculata* (*e.g.*, ADP09391), or *Chlorella variabilis* (*e.g.*, EFN56588). Further considered are acyl-CoA synthetases of animal species, including insects (e.g., *Apis mellifera*, for example, the acyl-CoA synthetase family member 2, mitochondrial precursor, NP_001193902) and mammals such as *Mus musculus* (*e.g.*, the "MACS" acyl-CoA synthetase, EDL17174).

[00118] Alternatively, recombinant microorganisms as provided herein may not include an exogenous or overexpressed gene encoding an acyl-CoA synthetase, a thioesterase, and/or a lipase. For example, a recombinant microorganism as provided herein may produce one or more of a fatty aldehyde, fatty alcohol, alkane, alkene, or wax ester without utilizing or generating an acyl-CoA substrate. For example, methods for producing fatty alcohols and wax esters using non-acyl-CoA substrates are provided in the co-pending, commonly-assigned U.S. patent application No. 13/860,417 entitled "Production and Secretion of Fatty Acids and Fatty Acid Derivatives" filed on 27 September 2012 incorporated herein by reference in its entirety, and in the co-pending, commonly-assigned U.S. patent application No. 13/413,426 entitled "Acyl-ACP Wax Ester Synthases ", filed on 6 March 2012 also incorporated herein by reference in its entirety.

Aldehyde-producing Reductases

[00119] For the production of fatty aldehydes, which can optionally be further converted to products such as fatty alcohols, wax esters, or alkanes, a transgenic microorganism as provided herein can include an exogenous gene(s) that encodes an aldehyde-forming reductase, such as, for example, an aldehyde-forming acyl-CoA reductase, an aldehyde-forming acyl-ACP reductase, or a carboxylic acid reductase. Genes or portions of genes that are listed in GenBank and other genetic databases and that are predicted to encode proteins that are homologous to

known acyl-CoA reductases that produce fatty aldehydes, referred to herein as "aldehyde-generating fatty acyl-CoA reductases", can be introduced into various microorganisms in order to test for the production of specific fatty aldehydes or fatty alcohols produced therefrom. Nonlimiting examples of fatty aldehyde-generating acyl-CoA reductases include the Acr1 gene of *Acinetobacter baylyi* (AAC45217.1), the AcrM-1 gene of *Acinetobacter* sp. M-1 (YP 001086217), and the luxC and luxE genes of various photoluminescent bacteria, *e.g*, an *Altermonas*, *Photobacterium*, *Shewanella*, *Vibrio*, or *Xenorhabdus* species. The enzymes encoded by these and other genes identified, for example, by sequence homology or protein domain can be tested to determine their substrates and products using assays know in the art.

[00120] In some examples, the host cell can include a non-native gene encoding an aldehyde-forming acyl-ACP reductase such as but not limited to any of those disclosed in US 2010/0221798 (WO 2009/140696), incorporated by reference herein in its entirety. For example, the recombinant host cell may comprise an aldehyde-forming acyl-ACP reductase that has at least 60%, 70%, 80%, 90% or 95% sequence identity to an aldehyde-forming reductase, *e.g.*, as disclosed in WO 2009/140696 or WO 2011/066137, such as, for example, any of the reductases having the accession numbers AAM82647; AAM82647; BAD78241; ABA22149; BAB76983; ZP_03763674; ACL42791; ZP_01628095; ZP_01619574; YP_001865324; YP_721978; NP_682102; YP_001518341; YP_002371106; ZP_05027136; ZP_03273554; NP_442146; ZP_01728620; ZP_05039135; YP_001802846; NP_926091; YP_001660322; ZP_00516920; CAO90781; ZP_01085337; YP_001227841; ABD96327; NP_897828; YP_001224378; ABD96480; ZP_01123215; ABB92249; ZP_01079773; YP_377636; NP_874926; NP_895058; ABD96274; ABD96442; ZP_01469469; ZP_05045052; YP_001014416; YP_001010913; YP_381056; YP_001550421; NP_892651; YP_001090783; ZP_01472595; YP_293055; ZP_05138243; YP_731192; YP_001483815; YP_001008982; YP_473896; YP_478638; or YP_397030. In some examples the recombinant host cell includes an exogenous gene encoding an aldehyde-forming acyl-ACP reductase, where the aldehyde-forming acyl-ACP reductase can be from a cyanobacterial species, and may be from the same species as the host microorganism, or may be from a different species. Alternatively, a cyanobacterial host can be engineered to overexpress an endogenous acyl-ACP reductase gene.

[00121] Nonlimiting examples of gene encoding carboxylic acid reductases that can be used in the invention include the *Nocardia* CAR gene (AY495697) and homologs thereof, some of which are disclosed in US2010/0105963, incorporated by reference herein in its entirety.

Alcohol-Forming Fatty Acyl Reductases

[00122] For production of a fatty alcohol (that can, optionally, be used as a substrate by a wax ester synthase) a nucleic acid molecule as provided herein can further a sequence encoding a fatty alcohol-forming acyl reductase or "FAR" that can reduce acyl-CoA to a fatty alcohol. FARs have been identified in, *e.g.*, *Euglena* (see, *e.g.*, Teerawanichpan *et al.*, *Lipids* 45:263-273 (2010)), *Arabidopsis* (see, *e.g.*, Rowland *et al.*, *Plant Physiol.* 142:866-877 (2006), Doan *et al.*, *J. Plant Physiol.* 166:787-796 (2009) and Domergue *et al.*, *Plant Physiol.* 153:1539-1554 (2010)), *Artemisia* (see, *e.g.*, Maes *et al.*, *New Phytol.* 189:176-189 (2011)), jojoba (see, *e.g.*, Metz *et al.*, *Plant Physiol.* 122:635-644 (2000)), moth (see, *e.g.*, Lienard *et al.*, *Proc. Natl. Acad. Sci.* 107:10955-10960 (2010)), bee (see, *e.g.*, Teerawanichpan *et al.*, *Insect Biochemistry and Molecular Biology* 40:641-649 (2010)) and mammals (see, *e.g.*, Honsho *et al.*, *J. Biol. Chem.* 285:8537-8542 (2010)). An alcohol-forming fatty acyl reductase useful in microorganisms and methods of the invention can be any alcohol-forming reductase that has activity in the host microorganism.

[00123] Nonlimiting examples of other alcohol-forming fatty acyl reductases that can be used include, but are not limited to, bfar from *Bombyx mori* (BAC79426), jjfar *from Simmondsia chinensis* (AAD38039), an acyl-CoA reductase from *Triticum aestivum* (CAD30694 or CAD30692), mfar1 from *Mus musculus* (NP_081655), mfar2 from *Mus musculus* (NP_848912), hfar from *H. sapiens* (NP_115604), FARXIII from *Ostrinia scapulalis* (ACJ06520), MS2 from *Z. mays* (NP_001151388 or EU970865), or MS2 (NP_187805), FAR4 (NP_001030809 or NP_190040), FAR6 (67633703), CER4 (NP_567936) or Ath (NP567936) from *Arabidopsis thaliana*, *Yev*-pgFAR from *Yponomeuta evonymellus* (GQ907231-GQ907233), *Yro*-pgFAR from *Yponomeuta rorellus* (GQ907234), *Ypa*-pgFAR from *Yponomeuta padellus* (GQ907235), OnuE from *Ostrinia nubilalis* (FJ807735), Has from *Homo sapiens* (AAT42129), *etc.*

[00124] An alcohol-forming fatty acyl reductase useful in microorganisms and methods of the invention can also or alternatively be a prokaryotic alcohol-forming acyl-CoA reductase such as *Marinobacter aquaeolei* VT8 Maqu_2220 (YP_959486), *Marinobacter algicola* DG893

(ZP_01892457); *Hahella chejuensis* KCTC 2396 HCH_05075 (YP_436183); *Oceanobacter sp.* RED65 (ZP_01305629), or *Marinobacter aquaeoli* VT8 2220 Maqu_2507 gene (ABM19582).

[00125] Alcohol-forming reductases that are able to use acyl-ACP as a substrate (and can be used for the production of fatty alcohols and wax esters in recombinant microorganisms that lack an exogenous and/or endogenous acyl-CoA synthetase gene) are disclosed in commonly assigned copending U.S. Patent application 13/860,417 entitled "Production and Secretion of Fatty Acids and Fatty Acid Derivatives" filed on 27 September 2012 which is incorporated herein by reference in its entirety, and in the co-pending, commonly-assigned U.S. patent application No. 13/413,426 entitled "Acyl-ACP Wax Ester Synthases ", filed on March 6, 2012 also incorporated herein by reference in its entirety.

Wax Ester Synthases

[00126] Wax esters are the product of a condensation reaction between a fatty acyl-thioester substrate and a fatty alcohol, catalyzed by a wax ester synthase. Polypeptides having wax ester synthase activity may be polypeptides identified as wax synthases, O-acyltransferases, including membrane-bound O-acyltransferases (MBOATs), diacylglycerol O-acyltransferases (*e.g.*, EC 2.3.1.20), alcohol acyltransferases (AATs, EC 2.3.1.84), long-chain alcohol O-fatty-acyltransferases (*e.g.*, 2.3.1.75). or alcohol synthase/acyl-CoA:diacylglycerol acyltransferases. Some polypeptides identified as diacylglycerol acyltransferases (DGATs) may be found to have wax ester synthase activity. Wax ester synthases have been identified in, *e.g.*, *Acinetobacter* (Ishige *et al.*, *Appl. Environ. Microbiol.* 68:1192-1195 (2002); Kalscheuer and Steinbuchel, *J. Biol. Chem.* 278:8075-8082 (2003); Kalscheuer *et al.*, *Appl. Environ. Microbiol.* 72:1373-1379 (2006)), *Marinobacter* (Holtzapple and Schmidt-Dannert, *J. Bacteriol.* 189:3804-3812 (2007)), *Arabidopsis* (Li *et al.*, *Plant Physiol.* 148:97-107 (2008)), petunia (King *et al.*, *Planta* 226:381-394 (2007)), jojoba (Lardizabal *et al.*, *Plant Physiol.* 122:645-655 (2000), and mammalian species (Cheng and Russell, *J. Biol. Chem.* 279:37798-37807 (2004); Yen *et al.*, *J. Lipid Res.* 46:2388-2397 (2005)).

[00127] Wax ester synthases may be identified using methods known in the art, based on structural domain or sequence similarity to a set of known wax ester synthase/DGAT sequences. As nonlimiting examples, a gene that encodes a polypeptide that recruits to Pfam PF03007 (wax ester synthase like acyl-CoA acyltransferase domain) with a bit score greater than the gathering cutoff of 20.6 and an E value of 0.01 or less or recruits to Pfam PF13813 ("MBOAT_2") with a

bit score greater than the gathering cutoff of 25.0 and an E value of 0.01 or less can be selected for use in the nucleic acid molecules and microorganisms provided herein.

[00128] Wax ester synthesis proteins encoded by nucleic acid molecules provided herein can include, but are not limited to: acyltransferases or wax synthases, fatty acyl transferases, diacylglycerol acyltransferases, acyl-coA wax alcohol acyltransferases, and bifunctional wax ester synthase/acy 1-CoA: diacylglycerol acy transferase selected from a multienzyme complex from *Simmondsia chinensis*, *Acinetobacter* sp. strain ADP1 (formerly *Acinetobacter calcoaceticus* ADP1), *Pseudomonas aeruginosa*, *Fundibacter (Alcanivorax) jadensis*, *Arabidopsis thaliana*, or *Alkaligenes eutrophus*. Wax synthases can also be from a multienzyme complex from *Alkaligenes eutrophus* and other organisms known in the literature to produce wax and fatty acid esters.

[00129] Proteins known or suspected of having wax ester synthase activity that are considered for use in the nucleic acid molecules and transgenic microorganisms provided herein include wax synthases from prokaryotic species, such as but not limited to, *Marinobacter hydrocarbonoclasticus* WS1 (ABO21020), *M. hydrocarbonoclasticus* DSM 8798 WS2 (ABO21021), *M.* sp. ELB 17 (GenBank Accession EBA00388), *M. aquaeolei* Maqu_0168 WS (YP_957462), *M. adhaerens* HP15 WS (ADP99639), *Hahella chejuensis* KCTC 2396 (YP_432512), *Acinetobacter baumannii* wax ester synthase (EGJ63408), *A. calcoaceticus* WS/DGAT (ZP_06058985) *Acinetobacter baylyi* ADP1 wax ester synthase (AAO17391 or Q8GGG1), *Bradyrhizobium japonicum* USDA 110 (NP_769520), *Erythrobacter litoralis* HTCC 2594 (YP_457389), *Rhodococcus* opacus wax ester synthase (BAH53702), *Mycobacterium tuberculosis* wax ester synthase (NP_334638), *M. smegmatis* wax ester synthase (ABK74273), the "WS/DGAT/MGAT" subfamily proteins of *Alcanivorax* species (CAL17252; EDX90960; EDX89052; ZP_05043539; ZP_05041631), wsadpl from *Nocardia farcinica* IFM 10152 (YP_117375), *Photobacterium profundum* SS9 (YP_130413), *Rhodoferax ferrireducens* DSM 15236 (ZP_00691704), and *Salinibacter ruber* DSM 13855 (YP_446603).

[00130] Examples of eukaryotic polypeptides that may be useful as wax synthases include, without limitation, jojoba wax ester synthase JjWS (AF149919), *Euglena gracilis* wax ester synthase (ADI60058), *Arabidiopsis thaliana* WSD1 O-acyltransferase (NP_568547), *Arabidiopsis thaliana* GPAT acyltransferase (NP_174499), the putative long-chain-alcohol O-fatty-acyltransferase 4 of *Arabidiopsis thaliana* (NP_200346) *Murraya koenigii* wax ester

synthase, acyl-CoA wax alcohol acyltransferase 2 from *H. sapiens* (NP_001002254), mWS from *Mus musculus* (Q6E1M8), SAAT from *Fragaria xananas* (AAG13130), the membrane bound O-acyltransferase (MBOAT) of *Zea mays* (NP_001131179), mdAAT2 from *Malus x domestica* (AAS79797), as well as insect wax ester synthases, *etc.*

[00131] Wax ester synthases that are able to use acyl-ACP as a substrate and can be used, for example, for the production of wax esters in recombinant microorganisms that lack either or both of an exogenous or endogenous gene encoding an acyl-CoA synthetase or a thioesterase include those disclosed in commonly assigned, copending U.S. patent No. 13/413,426 entitled "Acyl-ACP Wax Ester Synthases ", filed on March 6, 2012 incorporated herein by reference in its entirety. The wax ester synthases able to use acyl-ACP as a substrate can also have DGAT activity and can be useful in the production of triglycerides in recombinant microorganisms such as but not limited to cyanobacteria that lack acyl-CoA, and/or microorganisms that lack either or both of an exogenous or endogenous gene encoding an acyl-CoA synthetase or a thioesterase.

[00132] Alternatively or in addition to any of the above non-native genes, a recombinant microorganism of the invention can comprise at least one nucleic acid molecule encoding an exogenous fatty acid decarboxylase or an exogenous fatty aldehyde decarbonylase, and additionally but optionally at least one exogenous nucleic acid molecule encoding an exogenous acyl-CoA reductase, carboxylic acid reductase, or acyl-ACP reductase, and can produce an alkane and/or alkene. For example, a recombinant microorganism as provided herein can include an exogenous nucleic acid molecule encoding a decarbonylase, such as as, for example, CER1 of *Arabidopsis thaliana* (NP_171723) or an ortholog of another species, or derivatives thereof, or any of the decarbonylases disclosed in US 20110124071 (WO 2011/062987), incorporated herein in their entireties, which may be expressed along with a non-native gene encoding an aldehyde forming acyl reductase, such as any disclosed hereinabove. Alternatively, the recombinant microorganism as provided herein can include a non-native gene encoding a gene for the production of olefins (alkenes) such as but not limited to any disclosed in US 20100235934 or US 8,110,093, both of which are incorporated herein by reference in their entireties. Alkanes and alkenes produced by the recombinant microorganisms or host cells of the invention can, for example, have chain lengths of 7, 9, 11, 13, 15, 17, 19, 21, and/or 23 carbons, including, for example, chain lengths of 7, 9, 11, 13, 15, and/or 17 carbons, or chain lengths of 7, 9, 11, 13, and/or 15 carbons, or chain lengths of 11, 13, and/or 15 carbons.

[00133] To engineer a microorganism for the production of triglycerides (TAGs), a non-native gene encoding one or more of a glycerol-3-phosphate acyltransferase (hereinafter also referred to as "GPAT"; EC 2.3.1.15), lysophosphatidic acid acyltransferase or "LPAAT", EC 2.3.1.51, phosphatidate phosphatase (PAP, 3-sn-phosphatidate phosphohydrolase), or diacylglycerol acyltransferases (DGATs, E.C. 2.3.1.20) can be introduced into the microorganism. The genes can be from any source, prokaryotic or eukaryotic. Genes belonging to all of these classes of enzymes are known in the art, and references to genes having these activities can be found, for example, in U.S. patent application publications 2007/0184538, US 2010/0159110, and 20100255551, and in commonly assigned, copending U.S. patent application 13/404,7171 entitled "Enhanced Production of Fatty Acids and Fatty Acid Derivatives by Recombinant Microorganisms" filed February 24, 2012, all of which are incorporated herein by reference in their entireties.

[00134] Alternatively or in addition to any of the above modification, a recombinant microorganism of the invention can optionally include an exogenous or recombinant nucleic acid molecule that encodes an enzyme that affects in fatty acid production. For example, a recombinant microorganism as provided herein can include one or more exogenous nucleic acid molecules that encodes a polypeptide that participates in the synthesis of a fatty acid, including, but not limited to, an acetyl-CoA carboxylase, a malonyl CoA: ACP transacylase, or a beta-ketoacyl-ACP synthase, or can be engineered to overexpress an endogenous gene encoding a polypeptide for fatty acid or lipid production.

[00135] Further additionally, the recombinant host cell may optionally be engineered to express an exogenous transmembrane transporter to facilitate secretion of one or more fatty acid products. For example, the recombinant host cell can include a non-native gene encoding an ATP-binding cassette (ABC) transporter or an RND pump. In some embodiments, the transporter is at least 80% identical in sequence to a transporter protein encoded by an *Arabidopsis* genes CER5, WBC11, AtMRPS, AmiS2 and AtPGP1, or fatty acid transporter (FATP) genes from *Saccharomyces*, *Drosophila*, mycobacterial species, or mammalian species.

[00136] The above-described recombinant host cells may be used in any of the methods of producing a fatty acid product as described herein.

Additional Modifications for FFA Production

[00137] A recombinant microorganism can further comprise a modification of an endogenous nucleic acid molecule that encodes, *e.g.*, an acyl-CoA synthetase, acyl-ACP synthetase, acyl CoA dehydrogenase, glycerol-3-phosphate dehydrogenase, acetaldehyde CoA dehydrogenase, pyruvate dehydrogenase, acetate kinase, and the like, and combinations thereof. In certain embodiments, the modification down-regulates the endogenous nucleic acid and includes partial, substantial, or complete deletion, silencing, or inactivation of the nucleic acid or its regulatory elements.

[00138] In some examples, the host microorganism, which may be, for example, a cyanobacterium, can have attenuated expression of an endogenous gene encoding an acyl-ACP synthetase which participates in the recycling of fatty acids into lipids. The endogenous acyl-ACP synthetase gene can be, for example, downregulated by deletion or mutation of the promoter, or the protein-encoding of the gene can be internally deleted or disrupted, for example, by insertional mutagenesis. Alternatively, the entire acyl-ACP synthetase gene can be deleted, for example, by homologous recombination or other genome modification techniques. In yet further alternatives, gene knockdown constructs such as but not limited to ribozyme, antisense, or RNAi constructs can be introduced into the host cell to attenuate expression of the endogenous acyl-ACP synthetase gene.

[00139] Alternatively or in addition, a recombinant microorganism (*e.g.*, a recombinant cuanobacterium) of the invention comprises can be modified such that one or more genes that encode storage carbohydrate and/or polyhydroxyalkanoate (PHA) biosynthesis pathway enzymes are inactivated or down-regulated, and/or such that the enzymes themselves that are operative on such pathways are inhibited. Examples include, but are not limited to, enzymes involved in glycogen, starch, or chrysolaminarin synthesis, including glucan synthases and/or branching enzymes. Other examples include enzymes involved in PHA biosynthesis such as acetoacetyl-CoA synthase and PHA synthase.

[00140] Genes may be targeted specifically by disruption, deletion, generation of antisense sequences, generation of ribozymes, RNAi, meganuclease genome modification, and/or other recombinant approaches. Inactivation of the genes can additionally or alternately be accomplished by random mutation techniques such as exposure to UV and/or chemical mutagens, and the resulting genes and/or enzymes can be screened for mutants with the desired

activity. The proteins themselves can be inhibited by intracellular generation of appropriate antibodies, intracellular generation of peptide inhibitors, or the like, or some combination thereof.

Nucleic Acid Molecules

[00141] The nucleic acid molecules and encoded polypeptides described herein can be used in any of the methods of the invention, and may be included in any of the constructs, vectors, or recombinant microorganisms of the invention. Nucleic acid molecules comprising sequences that encode dehydrogenases are provided for use in host microorganisms and methods for producing fatty acid products, including free fatty acids, fatty aldehydes, fatty alcohols, fatty acid esters, wax esters, alkanes, alkenes, and/or glycerolipids, such as triglycerides. A nucleic acid molecule as disclosed herein can be isolated and/or purified.

[00142] The invention provides isolated nucleic acid molecules that comprise a nucleic acid sequence encoding a dehydrogenase, such as any disclosed herein or any active fragment thereof. For example, a nucleic acid molecule as provided herein can include a nucleic acid sequence encoding an aldehyde dehydrogenase, a 2-hydroxyacid dehydrogenase, a D-2-hydroxyacid dehydrogenase, a glyceride-3-phosophate dehydrogenase (non-phosphorylating), a malic enzyme, a glucose-6-phosphate dehydrogenase, a 6-phosphogluconate dehydrogenase, a glutamate dehydrogenase, an isocitrate dehydrogenase, or a sorbitol dehydrogenase.

[00143] Expression in a host microorganism (such as a recombinant microorganism that expresses a non-native gene encoding a polypeptide that participates in the synthesis of a lipid) of a sequence of a recombinant nucleic acid molecule that encodes a dehydrogenase as described herein can result in a higher production level of a fatty acid product by a culture of the host microorganism than the production level of a culture of a control microorganism, where the control microorganism is cultured under the same conditions and is substantially identical to the microorganism expressing the nucleic acid sequence encoding a dehydrogenase in all respects, with the exception that the control microorganism does not express a non-native nucleic acid sequence that encodes a dehydrogenase. Additionally, a recombinant host microorganism that includes a recombinant nucleic acid molecule or sequence as provided herein that encodes a dehydrogenase can have a higher propagation and/or proliferation rate than a control microorganism that is identical to the host microorganism comprising the non-native nucleic acid molecule encoding a dehydrogenase in all respects, with the exception that the control

microorganism does not include a non-native nucleic acid molecule or sequence that encodes a dehydrogenase. The recombinant host microorganism that includes a recombinant nucleic acid molecule provided herein that includes a sequence encoding a dehydrogenase can have a higher propagation and/or proliferation rate than a control microorganism lacking the non-native nucleic acid molecule encoding a dehydrogenase during a culture period in which the recombinant microorganism is producing a lipid. The recombinant microorganism can be, for example, a photosynthetic microorganism.

[00144] In particular examples, a recombinant nucleic acid molecule as provided herein can encode a 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%, at least 96%, at least 97%, at least 98%, at least 99% identity or 100% identity to the amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13, or an active fragment thereof.

[00145] For example, the invention provides an isolated or recombinant nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence that has at least at least 50%, at least 55%, at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of SEQ ID NO:29, or to a portion thereof, for example, to a functional fragment of the polypeptide of SEQ ID NO:29. For example, a nucleic acid molecule as provided herein can encode a polypeptide that includes an amino acid sequence having at least 85% sequence identity to the amino acid sequence of SEQ ID NO:29, or having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:29, or, for example, having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:29, and can comprise a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:29.

[00146] The invention further provides an isolated or recombinant nucleic acid molecule encoding an dehydrogenase can comprise a nucleic acid sequence that encodes a polypeptide having dehydrogenase activity that includes an amino acid sequence that has at least 50%, at least 55%, at least 60%, at least 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the amino acid sequence of

SEQ ID NO:2, or to a portion thereof, for example, to a functional fragment of the polypeptide. For example, a nucleic acid sequence that encodes a polypeptide having dehydrogenase activity can include an amino acid sequence having at least 85% sequence identity to the amino acid sequence of SEQ ID NO:2, or a functional fragment thereof, or can include an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, or a functional fragment thereof, or, for example, can include an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:2, or a functional fragment thereof, and can comprise a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence that is identical to all or an active fragment of the amino acid sequence of SEQ ID NO:2.

[00147] The invention encompasses variations of the nucleotide sequences of the invention, such as those encoding functional fragments or variants of the polypeptides as described herein. Such variants can be naturally-occurring or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Variations include, but are not limited to, addition, deletion, and substitution of one or more nucleotides which can result in conservative or non-conservative amino acid changes or amino acid additions and deletions. A given nucleic acid sequence may be modified, for example, by chemical synthesis of nucleic acid molecules or portions thereof, DNA amplification methods that introduce random or directed mutations, standard chemical or irradiation mutagenesis and/or artificial evolution (selection) or domain swapping methods to produce modified sequences. Further dehydrogenase ORFs may be derived from a collection of transcripts, such as a cDNA library, and the sequence of the transcript may be unknown. Accelerated evolution methods are described, *e.g.* by Stemmer (1994) *Nature* 370, 389-391, and Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91, 10747-10751. Mutations include but are not limited to codon optimization to enhance expression of the wild-type sequence in transgenic species such as algae or cyanobacteria (*e.g.* Burgess-Brown (2008) *Protein Expr. Purif.* 59, 94-102) and mutations resulting from site-specific mutagenesis that alter the amino acid sequence of the dehydrogenases of the invention. Such alteration in amino acid sequence may increase the biological activity of a dehydrogenase of the invention. For example, the nucleotide sequences of the genes encoding the dehydrogenase proteins of the invention may be mutated so as to increase their biological activity so as to increase fatty acid, fatty acid derivative, or lipid production.

[00148] For example, the invention provides fragments and variants of a dehydrogenase that have increased activity in comparison to the reference polypeptide, and in certain embodiments, the dehydrogenase fragment or variant may have activity that is increased by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, or 1000% in comparison to the activity of the dehydrogenase from which the variant is derived. In certain embodiments, the amount of fatty acid product produced by a culture of a host cell expressing the fragment or variant is at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900% or 1000% of the amount of fatty acid product made by a culture of the host cell expressing the dehydrogenase from which the fragment or variant is derived.

[00149] Additionally or alternatively, the invention provides nucleic acid molecules encoding variants of naturally-occurring dehydrogenase amino acid sequences, such as but not limited to variants of dehydrogenase sequences of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13 or fragments thereof in which at least one amino acid residue has been added or deleted N- and/or C-terminal to, and/or within, the reference sequence. For example, a cellular targeting signal may be added to a protein for directing the protein to a location in the cell, such as the chloroplast.

[00150] The invention also encompasses nucleic acid molecules encoding deletion mutants of a dehydrogenase where one or more amino acids have been deleted from the protein. For example, the encoded polypeptide can lack at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, or 80 amino acids from the N- and/or C-terminus and can have an amino acid sequence at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the corresponding amino acid sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13. In some examples, the deleted sequences may include targeting sequences, for example, at least a portion of a chloroplast transit peptide, at least a portion of a mitochondrial targeting sequence, at least a portion of an endoplasmic reticulum targeting sequence, etc.

[00151] A substitution, insertion or deletion can adversely affect the protein when the altered sequence substantially inhibits a biological function associated with the protein. In certain embodiments, a variant of an dehydrogenase may have activity that is reduced by not more than about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 30%, 40%, or 50%, in comparison to the activity of the dehydrogenase from which the variant is derived (*e.g.*, any of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13, or other dehydrogenases). In some embodiments, the amount of a fatty acid product produced by a culture of the host cell expressing the dehydrogenase variant is not less than about 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80% or 75% of the amount of the fatty acid product produced by a culture of the host cell expressing the dehydrogenase from which the variant is derived (*e.g.*, *e.g.*, any of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13, or other dehydrogenases).

[00152] Thus, the present invention also includes an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence having the amino acid sequence at least 50%, at least 55%, at least 60%, at least 65%, 70%, 75%, 80%, or 85%, for example at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or about 100% sequence identity with the peptide sequence of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13; fragments thereof comprising a consecutive sequence of at least 50, for example at least 75, at least 100, at least 125, at least 150 or more amino acid residues of the entire protein; amino acid sequence variants of such sequences, wherein at least one amino acid residue has been inserted N- and/or C-terminal to, and/or within, the disclosed sequence(s) which contain(s) the insertion and substitution; amino acid sequence variants of the disclosed sequence, and/or their fragments as defined above. The contemplated variants can additionally or alternately include those containing predetermined mutations by, *e.g.* homologous recombination or site-directed or PCR mutagenesis, and the corresponding proteins of other species, including, but not limited to, those described herein, the alleles or other naturally occurring variants of the family of proteins which

contain the insertion and substitution; and/or derivatives wherein the protein has been covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid which contains the insertion and substitution (for example, a detectable moiety such as an enzyme).

[00153] The "nucleic acids" or "nucleic acid molecules" of the invention can be DNA or RNA, for example, mRNA. The nucleic acid molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be the coding, or sense, strand or the non-coding, or antisense, strand. Additionally, chemical or enzymatic alteration of expressed nucleic acids and polypeptides may be performed by standard methods. For example, sequences can be modified by addition of phosphate groups, methyl groups, lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like.

[00154] Additionally, the nucleic acids may encode any dehydrogenase as disclosed herein, or an active fragment thereof, as a fusion protein that includes a polypeptide as disclosed herein or an active fragment thereof. For example, the nucleic acids of the invention include polynucleotide sequences that encode dehydrogenases of the invention or active fragments thereof fused to glutathione-S-transferase (GST), poly-histidine (*e.g.* His_6), poly-HN, poly-lysine, hemagglutinin, HSV-Tag or at least a portion of HIV-Tat.

[00155] The invention described herein also relates to fragments of the isolated nucleic acid molecules described herein encompassing a portion of a nucleotide sequence described herein which is from at least 20 contiguous nucleotides to at least 50 contiguous nucleotides or longer in length. Such fragments may be useful as probes and primers. In particular, primers and probes may selectively hybridize to the nucleic acid molecule encoding the polypeptides described herein. For example, fragments which encode polypeptides that retain activity, as described below, are particularly useful.

[00156] The invention also provides nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to the nucleotide sequences described herein (*e.g.* nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein and encode a dehydrogenase). Hybridization probes include synthetic oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Suitable probes include polypeptide nucleic acids, as described in Nielsen (1991) *Science*, 254, 1497-1500.

[00157] Such nucleic acid molecules can be detected and/or isolated by specific hybridization *e.g.* under high stringency conditions. "Stringency conditions" for hybridization is a term of art that refers to the incubation and wash conditions, *e.g.* conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly complementary, *i.e.* 100%, to the second, or the first and second may share some degree of complementarity, which is less than perfect, *e.g.* 60%, 75%, 85%, 95% or more. For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity.

[00158] "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained in Current Protocols in Molecular Biology (2011) John Wiley & Sons). The exact conditions which determine the stringency of hybridization depend not only on ionic strength, *e.g.* 0.2× SSC, 0.1× SSC of the wash buffers, temperature, *e.g.* 23°C, 42°C, 68°C, etc. and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, high, moderate or low stringency conditions may be determined empirically.

[00159] By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize with the most similar sequences in the sample can be determined.

[00160] Exemplary conditions are described in Krause (1991) *Methods in Enzymology*, 200, 546-556. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each degree (°C) by which the final wash temperature is reduced, while holding SSC concentration constant, allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in Tm. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought. Exemplary high stringency conditions include, but are not limited to, hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1× SSC at

60°C. Example of progressively higher stringency conditions include, after hybridization, washing with 0.2× SSC and 0.1% SDS at about room temperature (low stringency conditions); washing with 0.2× SSC, and 0.1% SDS at about 42°C (moderate stringency conditions); and washing with 0.1× SSC at about 68°C (high stringency conditions). Washing can be carried out using only one of these conditions, *e.g.* high stringency conditions, washing may encompass two or more of the stringency conditions in order of increasing stringency. Optimal conditions will vary, depending on the particular hybridization reaction involved, and can be determined empirically.

[00161] Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used. Hybridizable nucleotide sequences are useful as probes and primers for identification of organisms comprising a nucleic acid of the invention and/or to isolate a nucleic acid of the invention, for example.

[00162] The nucleic acid molecules of the invention can optionally comprise additional non-coding sequences such as non-coding 3' and 5' sequences (including, *e.g.*, regulatory sequences) that may be homologous or heterologous to the dehydrogenase gene. Alternatively or in addition, any of the provided nucleic acid molecules can optionally further comprise an additional nucleic acid sequence of at least 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 700, 800, 900, 1000, or 1500 nucleotides from a photosynthetic organism. The nucleic acid molecules and polypeptides described herein can be used in any of the methods of the invention, and may be included in any of the vectors or recombinant microorganisms of the invention. Nucleic acid molecules comprising sequences that encode dehydrogenases are provided for use in host microorganisms and methods for producing fatty acid products, including free fatty acids, fatty aldehydes, fatty alcohols, fatty acid esters, wax esters, alkanes, alkenes, monoglycerides, diglycerides, and triglycerides.

Nucleic Acid Constructs

[00163] The invention also provides constructs comprising a nucleic acid sequence encoding a dehydrogenase or a polypeptide that participates in the production of a lipid that can further include one or more sequences that regulate or mediate transcription, translation, or integration of nucleotide sequences into a host genome. For example, the invention provides expression constructs that comprise one or more "expression control elements" or sequences that regulate

expression transcription of an operably linked gene, or translation of the transcribed RNA. For example, an expression control element can be a promoter that may be operably linked to the gene of interest (e.g., a dehydrogenase gene) in an expression construct or "expression cassette." The promoter may be regulatable, *e.g.*, inducible.

[00164] In aspects where the nucleic acid construct does not contain a promoter in operable linkage with the nucleic acid sequence encoding the gene of interest (e.g., a dehydrogenase gene) the nucleic acid sequence can be transformed into the cells such that it becomes operably linked to an endogenous promoter by, *e.g.*, homologous recombination, site specific integration, and/or vector integration. In some instances, genomic host sequences included in a nucleic acid construct for mediating homologous recombination into the host genome may include gene regulatory sequences, for example, a promoter sequence, that can regulate expression of an dehydrogenase gene of the nucleic acid construct. In such examples, the transgene(s) of the construct can become operably linked to a promoter that is endogenous to the host microorganism. The endogenous promoter(s) may be regulatable, *e.g.*, inducible.

[00165] A promoter operably linked to a nucleic acid sequence encoding a dehydrogenase may be a promoter that is heterologous with respect to the dehydrogenase gene. In some embodiments, the promoter may be an inducible promoter, *i.e.*, a promoter that mediates transcription of an operably linked gene in response to a particular stimulus. Such promoters may be advantageous, *e.g.*, to minimize any deleterious effects on the growth of the host cell and/or to maximize production of the fatty acid product. An inducible promoter can be responsive to, *e.g.*, light or dark or high or low temperature, and/or can be responsive to specific compounds. The inducible promoter may be, an ara promoter, a lac promoter, a trp promoter, a tet promoter (*e.g.*, U.S. Patent No. 5,851,796), a hybrid promoter that includes a portion of a trp, lac, or tet promoter, a hormone-responsive promoter (*e.g.*, an ecdysone-responsive promoter, such as described in U.S. Patent No. 6,379,945), a metallothionien promoter (*e.g.*, U.S. Patent No. 6,410,828), a pathogenesis-related (PR) promoter that can be responsive to a chemical such as, for example, salicylic acid, ethylene, thiamine, and/or BTH (U.S. Patent No. 5,689,044), or the like, or some combination thereof. An inducible promoter can also be responsive to light or dark (U.S. Patent No. 5,750,385, U.S. Patent No. 5,639,952), metals (*Eukaryotic Cell* 2:995-1002 (2003)) or temperature (U.S. Patent No. 5,447,858; Abe *et al. Plant Cell Physiol.* 49: 625-632 (2008); Shroda *et al. Plant J.* 21: 121-131 (2000)). The foregoing list is exemplary and not

limiting. The promoter sequence can be from any organism, provided that it is functional in the host organism. In certain embodiments, inducible promoters are formed by fusing one or more portions or domains from a known inducible promoter to at least a portion of a different promoter that can operate in the host cell, *e.g.* to confer inducibility on a promoter that operates in the host species.

[00166] For transformation of cyanobacteria, a variety of promoters that function in cyanobacteria can be utilized, including, but not limited to, the ara, lac, tac, and trc promoters, as well as derivatives that are also inducible by the addition of isopropyl β-D-1-thiogalactopyranoside (IPTG) such as the *trcY* or *trcE* promoter. Other promoters that may find use in the invention include promoters that are naturally associated with transposon- or bacterial chromosome-borne antibiotic resistance genes (*e.g.*, neomycin phosphotransferase, chloramphenicol acetyltransferase, spectinomycin adenyltransferase, or the like, or combinations thereof), promoters associated with various heterologous bacterial and native cyanobacterial genes, promoters from viruses and phages, synthetic promoters, or the like, or combinations thereof. For example, the promoter(s) can be selected from prokaryotic promoters from a range of species, including eubacterial and cyanobacterial species, such as, for example, an araC or pBAD promoter, a rha promoter, a Pm promoter, a xylS promoter, a nir promoter, a nar promoter, a pho promoter, a tet promoter, a cys promoter, a metallothionien promoter, an ftf promoter, a gln promoter, a heat shock promoter, a cold-inducible promoter or a viral promoter. The foregoing promoters are exemplary and are not limiting. Promoters isolated from cyanobacteria that can be used can include but are not limited to the following: nrs (nickel-inducible), secA (secretion; controlled by the redox state of the cell), rbc (Rubisco operon), psaAB (PS I reaction center proteins; light regulated), psbA (Dl protein of PSII; light- inducible), and the like, and combinations thereof. In some embodiments, the promoters are regulated by nitrogen compounds, such as, for example, nar, ntc, nir or nrt promoters. In some embodiments, the promoters are regulated by phosphate (e.g., pho or pst promoters) or metals, *e.g.*, the nrs promoter (Liu and Curtis (2009) *Proc Natl Acad Sciences USA* 106: 21550-21554), or the petE promoter (Buikema and Haselkorn (2001) *Proc Natl Acad Sciences USA* 98: 2729-2734)). Inducible promoters, as used in the constructs of the present invention, can use one or more portions or domains of the aforementioned promoters and/or other inducible promoters fused to

at least a portion of a different promoter that can operate in the host organism, *e.g.*, to confer inducibility on a promoter that operates in the host species.

[00167] Likewise, a wide variety of transcriptional terminators can be used for expression vector construction. Examples of possible terminators can include, but are not limited to, psbA, psaAB, rbc, secA, T7 coat protein, and the like, and combinations thereof.

[00168] In some embodiments, an isolated or recombinant nucleic acid molecule of the invention can comprise both a nucleic acid sequence that encodes a dehydrogenase and a nucleic acid sequence that encodes a polypeptide that participates in the synthesis of a lipid, *e.g.*, a thioesterase or other lipid production polypeptide. The nucleic acid sequences encoding the dehydrogenase and the lipid production polypeptide may be, for example, any of the nucleic acid sequences described herein. In certain embodiments, the nucleic acid sequence that encodes a dehydrogenase and the nucleic acid sequence that encodes a polypeptide that participates in the production of a lipid can be operably linked to the same promoter and/or enhancer. For example, in particular embodiments the two genes (encoding an dehydrogenase and, for example, a thioesterase) may be organized as an operon, in which, for example, a promoter sequence is followed, in the 5' to 3' direction, by a thioesterase-encoding sequence (or other polypeptide encoding sequence) and then an dehydrogenase-encoding sequence, or vice versa. In any of the above embodiments of operons that include a dehydrogenase gene and a gene encoding a polypeptide for lipid synthesis, one or more additional regulatory sequences can be included in the isolated nucleic acid molecule, for example, a sequence for enhancing translation can be included upstream of any of the gene-encoding sequences, and/or a transcriptional terminator can optionally be included at or near the 3' end of the synthetic operon.

[00169] In addition to a dehydrogenase gene and a gene encoding a polypeptide that participates in the production of a lipid, one or more additional genes can optionally be included in a synthetic operon as provided herein, where the one or more additional genes may include, for example, one or more additional genes encoding enzymes or proteins of the fatty acid synthesis or a fatty acid synthesis or lipid synthesis pathway and/or one or more genes encoding enzymes or proteins that may enhance fatty acid product synthesis, one or more genes that may enhance photosynthesis or carbon-fixation, and/or one or more reporter genes or selectable markers.

[00170] In some embodiments, the nucleic acid sequence that encodes a dehydrogenase and the nucleic acid sequence that encodes a polypeptide that participates in the production of a lipid can be provided on the same nucleic acid construct where they are operably linked to different promoters and/or transcriptional enhancers. The promoters and enhancers may be, *e.g.*, any of the promoters and transcriptional enhancers described herein.

[00171] In certain embodiments, the vector comprising a nucleic acid sequence encoding a dehydrogenase is designed for transformation into cyanobacteria. In a particular embodiment, the vector permits homologous recombination of the dehydrogenase-encoding sequence with the cyanobacterial genome.

[00172] An isolated nucleic acid molecule of the present invention can include the sequences disclosed herein that encode a dehydrogenase or other polypeptide in a vector, such as, but not limited to, an expression vector. A vector can be a nucleic acid that has been generated via human intervention, including by recombinant means and/or direct chemical synthesis, and can include, for example, one or more of: 1) an origin of replication for propagation of the nucleic acid sequences in one or more hosts (which may or may not include the production host); 2) one or more selectable markers; 3) one or more reporter genes; 4) one or more expression control sequences, such as, but not limited to, promoter sequences, enhancer sequences, terminator sequences, sequence for enhancing translation, *etc.*; and/or 5) one or more sequences for promoting integration of the nucleic acid sequences into a host genome, for example, one or more sequences having homology with one or more nucleotide sequences of the host microorganism. A vector can be an expression vector that includes one or more specified nucleic acid "expression control elements" that permit transcription and/or translation of a particular nucleic acid in a host cell. The vector can be a plasmid, a part of a plasmid, a viral construct, a nucleic acid fragment, or the like, or a combination thereof.

[00173] The vector can be a high copy number vector, a shuttle vector that can replicate in more than one species of cell, an expression vector, an integration vector, or a combination thereof. Typically, the expression vector can include a nucleic acid comprising a gene of interest operably linked to a promoter in an "expression cassette," which can also include, but is not limited to, a transcriptional terminator, a ribosome binding site, a splice site or splicing recognition sequence, an intron, an enhancer, a polyadenylation signal, an internal ribosome entry site, and similar elements. According to some embodiments, the present invention can

involve recombinant microorganisms transformed with an isolated nucleic acid comprising a gene of interest under control of a heterologous promoter. Alternatively, if the vector does not contain a promoter operably linked with an isolated nucleic acid comprising a gene of interest, the isolated nucleic acid can be transformed into the microorganisms or host cells such that it becomes operably linked to an endogenous promoter by homologous recombination, site specific integration, and/or vector integration.

[00174] In some embodiments, the present invention additionally provides recombinant microorganisms or host cells transformed with an isolated nucleic acid comprising a gene of interest that is operably linked to one or more expression control elements. In some instances, it can be advantageous to express the protein at a certain point during the propagation of the recombinant microorganism, *e.g.*, to minimize any deleterious effects on the growth or proliferation of the recombinant microorganism and/or to maximize production of the triglyceride or fatty acid product of interest. In such instances, one or more exogenous genes introduced into the recombinant microorganism or host cell can be operably linked to an inducible promoter, which mediates transcription of an operably linked gene in response to a particular stimulus.

[00175] Transformation vectors can additionally or alternately include a selectable marker, such as, but not limited to, a drug resistance gene, an herbicide resistance gene, a metabolic enzyme and/or factor required for survival of the host (for example, an auxotrophic marker), or the like, or a combination thereof. Transformed cells can be selected based upon the ability to grow in the presence of the antibiotic and/or other selectable marker under conditions in which cells lacking the resistance cassette or auxotrophic marker could not grow. Further, a non-selectable marker may be present on a vector, such as a gene encoding a fluorescent protein or enzyme that generates a detectable reaction product.

Transformation of Microorganisms and Host Cells

[00176] A vector comprising an isolated nucleic acid comprising a gene of interest can be introduced into cyanobacteria via conventional transformation and/or transfection techniques. The terms "transformation," "transfection," "conjugation," and "transduction," as used in the present context, are intended to comprise a multiplicity of methods known to those skilled in the art for the introduction of foreign nucleic acid (for example, exogenous DNA) into a host cell, including calcium phosphate and/or calcium chloride coprecipitation, DEAE-dextran-mediated

transfection, lipofection, natural competence, chemically mediated transfer, electroporation, particle bombardment, or the like, or combinations thereof. Examples of suitable methods for the transformation and/or transfection of host cells, *e.g.*, can be found in Molecular Cloning - A Laboratory Manual (2010), Cold Spring Harbor Laboratory Press.

[00177] Host cells such as plants for use in the invention can be transformed by any feasible means, including, without limitation, the use of *Agrobacterium*, particle gun-mediated transformation, laser-mediated transformation, or electroporation. Algae and photosynthetic bacteria can be transformed by any suitable methods, including, as nonlimiting examples, natural DNA uptake (Chung et al. (1998) *FEMS Microbiol Lett.* 164: 353-361; Frigaard et al. (2004) *Methods Mol. Biol.* 274: 325-40; Zang et al. (2007) *J. Microbiol.* 45: 241-245), conjugation (Wolk et al. (1984) *Proc. Natl. Acad. Sci. USA* 81, 1561-1565), transduction, glass bead transformation (Kindle et al. (1989) *J. Cell Biol.* 109: 2589-601; Feng et al. (2009) *Mol. Biol. Rep.* 36: 1433-9; U.S. Pat. No. 5,661,017), silicon carbide whisker transformation (Dunahay et al. (1997) *Methods Mol. Biol.* (1997) 62: 503-9), biolistics (Dawson et al. (1997) *Curr. Microbiol.* 35: 356-62; Hallmann et al. (1997) *Proc. Natl. Acad. USA* 94: 7469-7474; Jakobiak et al. (2004) *Protist* 155:381-93; Tan et al. (2005) *J. Microbiol.* 43: 361-365; Steinbrenner et al. (2006) *Appl Environ. Microbiol.* 72: 7477-7484; Kroth (2007) *Methods Mol. Biol.* 390: 257-267; U.S. Pat. No. 5,661,017) electroporation (Kjaerulff et al. (1994) *Photosynth. Res.* 41: 277-283; Iwai et al. (2004) *Plant Cell Physiol.* 45: 171-5; Ravindran et al. (2006) *J. Microbiol. Methods* 66: 174-6; Sun et al. (2006) *Gene* 377: 140-149; Wang et al. (2007) *Appl. Microbiol. Biotechnol.* 76: 651-657; Chaurasia et al. (2008) *J. Microbiol. Methods* 73: 133-141; Ludwig et al. (2008) *Appl. Microbiol. Biotechnol.* 78: 729-35), laser-mediated transformation, or incubation with DNA in the presence of or after pre-treatment with any of poly(amidoamine) dendrimers (Pasupathy et al. (2008) *Biotechnol. J.* 3: 1078-82), polyethylene glycol (Ohnuma et al. (2008) *Plant Cell Physiol.* 49: 117-120), cationic lipids (Muradawa et al. (2008) *J. Biosci. Bioeng.* 105: 77-80), dextran, calcium phosphate, or calcium chloride (Mendez-Alvarez et al. (1994) *J. Bacteriol.* 176: 7395-7397), optionally after treatment of the cells with cell wall-degrading enzymes (Perrone et al. (1998) *Mol. Biol. Cell* 9: 3351-3365). Agrobacterium-mediated transformation can also be performed on algal cells, for example after removing or wounding the algal cell wall (e.g., WO 2000/62601; Kumar et al. (2004) *Plant Sci.* 166: 731-738). Biolistic methods are particularly successful for transformation of the chloroplasts of plant and eukaryotic

algal species (see, for example, Ramesh et al. (2004) *Methods Mol. Biol.* 274: 355-307; Doestch et al. (2001) *Curr. Genet.* 39: 49-60; U.S. Pat. No. 7,294,506; WO 2003/091413; WO 2005/005643; and WO 2007/133558, all incorporated herein by reference in their entireties).

Methods of Producing Fatty Acid Products

[00178] The invention encompasses methods of producing a fatty acid product by culturing the recombinant microorganisms as described herein that include a non-native gene encoding a dehydrogenase under conditions in which the dehydrogenase is expressed and at least one fatty acid product is produced. The methods can further comprise isolating at least one fatty acid product. Expression of the non-native gene encoding a dehydrogenase can optionally be induced during the culturing period. Optionally, at least a portion of the fatty acid and/or fatty acid derivative produced by the recombinant microorganisms can be released or secreted into the growth media by the microorganism.

[00179] Also provided herein is a method for producing a lipid comprising culturing a recombinant microorganism that includes a non-native gene encoding a dehydrogenase and at least one non-native gene encoding a polypeptide that participates in the production of a lipid, under conditions in which the non-native gene encoding a dehydrogenase and the at least one gene encoding a polypeptide for the production of a lipid are expressed, to produce a lipid. The methods can further comprise isolating at least one lipid. The lipid can be, for example, a fatty acid product.

[00180] In any of the methods provided herein, the culture of the recombinant microorganism that includes a non-native dehydrogenase gene can produce more of the lipid (*e.g.*, fatty acid product) than is produced by a control culture of control microorganism that is identical in all respects to the culture of the recombinant microorganism that includes a non-native dehydrogenase gene except that the control microorganism does not include the non-native gene encoding the dehydrogenase. In any of the methods provided herein, the recombinant microorganism that includes a non-native dehydrogenase gene have a higher propagation and/or proliferation rate that a control microorganism identical in all respects to the recombinant microorganism that includes a non-native dehydrogenase gene except that the control microorganism does not include the non-native gene encoding the dehydrogenase. For example, the culture of the recombinant microorganism that includes a non-native dehydrogenase gene can achieve a higher cell density that is achieved by the control culture after one, two, three, four,

five, six, or more than six days of culturing. The recombinant microorganism used in the methods can be a photosynthetic microorganism, and the culturing can be under photoautotrophic conditions, where inorganic carbon is substantially the sole source of carbon for proliferation of the culture and production of the lipid.

[00181] In some examples, the lipid (*e.g.*, fatty acid product) that is produced in greater amounts by the recombinant microorganism that includes a non-native dehydrogenase gene and at least one non-native lipid production gene can be a lipid that is not naturally produced by the microorganism, for example, a lipid that is not produced by a microorganism of the same species that lacks the at least one non-native gene that encodes a polypeptide that participates in the production of a lipid, such as a fatty acid product.

[00182] Releasing and secreting, as used herein in the context of products of the invention, are used interchangeably to refer to a process by which active and/or passive transport mechanisms allow products of the invention to cross the cell membrane to exit the cell. Examples of such transport mechanisms can include, but are not limited to, gradient diffusion, facilitated diffusion, active transport, and combinations thereof.

[00183] Culturing refers to the intentional fostering of growth (*e.g.*, increases in cell size, cellular contents, and/or cellular activity) and/or propagation (*e.g.*, increases in cell numbers via mitosis) of one or more cells by use of selected and/or controlled conditions. The combination of both growth and propagation may be termed proliferation. As demonstrated in the examples herein, the expression of a dehydrogenase gene by lipid-producing cells results in increased cell density of the culture with respect to a culture of lipid producing cells that do not include the non-native dehydrogenase gene.

[00184] Non-limiting examples of selected and/or controlled conditions that can be used for culturing the recombinant microorganism can include the use of a defined medium (with known characteristics such as pH, ionic strength, and/or carbon source), specified temperature, oxygen tension, carbon dioxide levels, growth in a bioreactor, or the like, or combinations thereof. In some embodiments, the microorganism or host cell can be grown heterotrophically, using a reduced carbon source, or mixotrophically, using both light and a reduced carbon source. Additionally or alternately, the microorganism or host cell can be cultured phototrophically. When growing phototrophically, the microorganism can advantageously use light as an energy source. An inorganic carbon source, such as CO_2 or bicarbonate, can be used for synthesis of

biomolecules by the microorganism. "Inorganic carbon", as used herein, includes carbon-containing compounds or molecules that cannot be used as a sustainable energy source by an organism. Typically "inorganic carbon" can be in the form of CO_2 (carbon dioxide), carbonic acid, bicarbonate salts, carbonate salts, hydrogen carbonate salts, or the like, or combinations thereof, which cannot be further oxidized for sustainable energy nor used as a source of reducing power by organisms. A microorganism grown photoautotrophically can be grown on a culture medium in which inorganic carbon is substantially the sole source of carbon. For example, in a culture in which inorganic carbon is substantially the sole source of carbon, any organic carbon molecule or compound that may be provided in the culture medium either cannot be taken up and/or metabolized by the cell for energy and/or is not present in an amount sufficient to provide sustainable energy for the growth and proliferation of the cell culture.

[00185] Microorganisms and host cells that can be useful in accordance with the methods of the present invention can be found in various locations and environments throughout the world. The particular growth medium for optimal propagation and generation of lipid and/or other hydrocarbon constituents can vary and may be optimized to promote growth, propagation, or production of a product such as a lipid. In some cases, certain strains of microorganisms may be unable to grow in a particular growth medium because of the presence of some inhibitory component or the absence of some essential nutritional requirement of the particular strain of microorganism or host cell.

[00186] Solid and liquid growth media are generally available from a wide variety of sources, as are instructions for the preparation of particular media suitable for a wide variety of strains of microorganisms. For example, various fresh water and salt water media can include those described in Barsanti (2005) Algae: Anatomy, Biochemistry & Biotechnology, CRC Press for media and methods for culturing algae. Algal media recipes can also be found at the websites of various algal culture collections, including, as nonlimiting examples, the UTEX Culture Collection of Algae (www.sbs.utexas.edu/utex/media.aspx) (visited September 20, 2011); Culture Collection of Algae and Protozoa (www.ccap.ac.uk) (visited September 20, 2011); and Katedra Botaniky (botany.natur.cuni.cz/algo/caup-media.html) (visited September 20, 2011).

[00187] In some embodiments, media used for culturing an organism that produces fatty acids can include an increased concentration of a metal (typically provided as a salt and/or in an ionic form) such as, for example, sodium, potassium, magnesium, calcium, strontium, barium,

beryllium, lead, iron, nickel, cobalt, tin, chromium, aluminum, zinc, copper, or the like, or combinations thereof (particularly multivalent metals, such as magnesium, calcium, and/or iron), with respect to a standard medium formulation, such as, for example, standard BG-11 medium (ATCC Medium 616, Table 5), or a modified medium such as ATCC Medium 854 (BG-11 modified to contain vitamin B12) or ATCC Medium 617 (BG-11 modified for marine cyanobacteria, containing additional NaCl and vitamin B12).

[00188] For example, a medium used for growing microorganisms that produce free fatty acids can include at least 2-fold, for example at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, at least 10-fold, between 2-fold and 10-fold, and/or between 10-fold and 100-fold the amount of metal (*e.g.*, calcium) as compared to a standard medium. The medium used for growing microorganisms that can produce free fatty acids can include, for example, at least 0.5 mM, between about 0.5 mM and about 1 mM, between about 1 mM and about 2 mM, between about 2 mM and about 5 mM, between about 5 mM and about 10 mM, between about 10 mM and about 25 mM, and greater than 25 mM metal (*e.g.*, calcium) in the formulation. For example, by using the excess amount of metal (*e.g.*, calcium) in the medium, at least a portion of the fatty acid(s) can be sequestered as soap precipitates, which may result in decreasing the toxic effects of free fatty acid(s). Addition of metal (*e.g.*, calcium) in the medium can additionally or alternately increase the tolerance of microorganism in media with a relatively high concentration of free fatty acids. Additionally or alternately, fatty acid-producing strains can advantageously be more robust with excess metal (*e.g.*, calcium) content. Although the excess component is described herein as a metal, it is contemplated that the component can more generally be described as a carboxylate counterion source, for example a soap-forming counterion source, a metal ion source (noted as "metal" herein), a multivalent (*i.e.*, having a valence of +2 or higher) counterion source, a divalent counterion source, or some combination thereof. Other details regarding this metal/carboxylate counterion source are described in the co-pending, commonly-assigned U.S. Patent Application No. 13/324,636, entitled "Culturing a Microorganism in a Medium with an Elevated Level of a Carboxylate Counterion Source", filed on December 13, 2011.

[00189] The culture methods can include inducing expression of one or both of a dehydrogenase gene as described and a gene encoding a protein that participates in the production of fatty acid products and triglycerides, and/or regulating metabolic pathway in the

microorganism. Inducing expression can include adding a nutrient or compound to the culture, removing one or more components from the culture medium, increasing or decreasing light and/or temperature, and/or other manipulations that promote expression of the gene of interest. Such manipulations can largely depend on the nature of the (heterologous) promoter operably linked to the gene of interest.

[00190] In some embodiments of the present invention, the recombinant microorganisms or host cells can be cultured in a bioreactor. "Bioreactor" refers to an enclosure or partial enclosure in which cells are cultured, optionally in suspension and, when suspended, preferably in an aqueous liquid. The bioreactor can be used to culture microalgal cells through the various phases of their physiological cycle. Bioreactors can offer many advantages for use in heterotrophic growth and propagation methods. To produce biomass for use as food, microorganisms or host cells are preferably fermented in large quantities in liquid, such as in suspension cultures as an example. Bioreactors such as steel fermentors can accommodate very large culture volumes (40,000 liter and greater capacity bioreactors can be used in various embodiments of the invention). Bioreactors can also typically allow for the control of one or more culture conditions such as temperature, pH, oxygen tension, carbon dioxide levels, and the like, as well as combinations thereof. Bioreactors can typically be configurable, for example, using ports attached to tubing, to allow gaseous components, such as CO_2, CO_2-enriched air, oxygen, and/or nitrogen, to be contacted with (*e.g.*, bubbled through) a liquid culture. Other culture parameters, such as the pH of the culture media, the identity and/or concentration of trace elements and/or nutrients, the identity and/or concentration of other media constituents, or the like, or combinations thereof, can typically be more readily manipulated using a bioreactor.

[00191] Microorganisms and host cells can additionally or alternately be cultured in a bioreactor equipped with an artificial light source, a "photobioreactor", and/or can have one or more walls that is transparent enough to light, including sunlight, to enable, facilitate, and/or maintain acceptable microorganism growth and proliferation. For production of fatty acid products or triglycerides, photosynthetic microorganisms or host cells can additionally or alternately be cultured in shake flasks, test tubes, vials, microtiter dishes, petri dishes, or the like, or combinations thereof.

[00192] Additionally or alternately, recombinant photosynthetic microorganisms or host cells may be grown in ponds, canals, sea-based growth containers, trenches, raceways, channels, or

the like, or combinations thereof. As with standard bioreactors, a source of inorganic carbon (such as, but not limited to, CO_2, bicarbonate, carbonate salts, and the like), including, but not limited to, air, CO_2-enriched air, flue gas, or the like, or combinations thereof, can be supplied to the culture. When supplying flue gas and/or other sources of inorganic that may contain CO in addition to CO_2, it may be necessary to pre-treat such sources such that the CO level introduced into the (photo)bioreactor do not constitute a dangerous and/or lethal dose with respect to the growth, proliferation, and/or survival of the microorganisms.

[00193] The methods include culturing a recombinant microorganism, such as a photosynthetic microorganism, such as, for example, a microalga or cyanobacterium, that includes a non-native gene encoding a dehydrogenase as described herein to produce at least one fatty acid product, in which the method results in production by the culture of at least or about 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 110%, 120%, 130%, 140%, 150%, 160%, 170%, 180%, 190%, 200%, 300%, 400%, 500%, 600%, 700%, 800%, 900%, or 1000% more than the amount of the fatty acid product produced by a culture of an otherwise identical microorganism not including the non-native gene encoding the dehydrogenase, cultured under identical conditions. Additionally or alternately, the methods include producing at least 100 mg, at least 110 mg, at least 120 mg, at least 130 mg, at least 140 mg, at least 150 mg, at least 160 mg, at least 170 mg, at least 180 mg, at least 190 mg, at least 200 mg, at least 210 mg, at least 220 mg, at least 230 mg, at least 240 mg, at least 250 mg, at least 260 mg, at least 270 mg, at least 280 mg, at least 290 mg, at least 300 mg, at least 310 mg, at least 320 mg, at least 330 mg, at least 340 mg, at least 350 mg, at least 360 mg, at least 370 mg, at least 380 mg, at least 390 mg, at least 400 mg, at least 450 mg, at least 500 mg, at least 550 mg, at least 600 mg, at least 650 mg, at least 700 mg, at least 750 mg, at least 800 mg, at least 850 mg, at least 900 mg, at least 950 mg, per liter of culture of a fatty acid product by culturing the recombinant microorganisms described herein. Although many times the goal can be to produce and/or recover as much fatty acid product as possible, in some instances the amount of the fatty acid product produced and/or recovered by the method described herein can be limited to about 2 g or less per liter of culture, for example, 1.5 g or less per liter of culture, 1 g or less per liter of culture, 800 mg or less per liter of culture 600 mg or less per liter of culture, for example about 550 mg or less per liter of culture, or about 500 mg or less per liter of culture.

[00194] Fatty acid products can be recovered from culture by recovery means known to those of ordinary skill in the art, such as by whole culture extraction, for example, using organic solvents. In some cases, recovery of fatty acid products can be enhanced by homogenization of the cells. For example, lipids such as fatty acids, fatty acid derivatives, and/or triglycerides can be isolated from algae by extraction of the algae with a solvent at elevated temperature and/or pressure, as described in the co-pending, commonly-assigned U.S. patent application No. 13/407,817 entitled "Solvent Extraction of Products from Algae ", filed on February 29, 2012, which is incorporated herein by reference in its entirety.

[00195] When fatty acid products are sufficiently released or secreted from the microorganisms into the culture medium, the recovery method can be adapted to efficiently recover only the released fatty acid products, only the fatty acid products produced and stored within the microorganisms, or both the produced and released fatty acid products. Fatty acid products secreted/released into the culture medium by the recombinant microorganisms described above can be recovered in a variety of ways. A straightforward isolation method, *e.g.*, by partition using immiscible solvents, may be employed. Additionally or alternately, particulate adsorbents can be employed. These can include lipophilic particulates and/or ion exchange resins, depending on the design of the recovery method. They may be circulating in the separated medium and then collected, and/or the medium may be passed over a fixed bed column, for example a chromatographic column, containing these particulates. The fatty acid products can then be eluted from the particulate adsorbents, *e.g.*, by the use of an appropriate solvent. In such circumstances, one isolation method can include carrying out evaporation of the solvent, followed by further processing of the isolated fatty acid products, to yield chemicals and/or fuels that can be used for a variety of commercial purposes.

[00196] In some examples, the level of a fatty acid product, for example a C8-C24 fatty acid, a C10-C22 fatty acid, or a C12-C18 fatty acid, such as, for example, at least one of a C12, C14, C16, and/or a C18 fatty acid, can be increased in the culture with respect to a culture of an otherwise identical microorganism or host cell, but lacking the non-native dehydrogenase gene. The invention further includes compositions that include free fatty acids, fatty acid derivatives, or glycerolipids produced by the methods of the invention.

[00197] Additionally or alternatively, the present invention can include one or more of the following embodiments:

[00198] Embodiment 1. A recombinant microorganism comprising a first non-native nucleic acid molecule comprising a nucleotide sequence encoding a dehydrogenase and at least a second non-native nucleic acid molecule comprising a sequence encoding a polypeptide that participates in lipid biosynthesis; wherein a culture of the recombinant microorganism produces a greater amount of a lipid than is produced by a control culture of a microorganism identical in all respects to the recombinant microorganism that includes the first and second non-native nucleotide sequences, except that the control microorganism does not include the first non-native nucleotide sequence encoding a dehydrogenase, wherein the recombinant microorganism has a higher propagation and/or proliferation rate than the control microorganism under conditions in which the lipid is produced.

[0199] Embodiment 2. A recombinant microorganism according to Embodiment 1, wherein the dehydrogenase is selected from the group consisting of an aldehyde dehydrogenase, acetaldehyde dehydrogenase, alcohol dehydrogenase, glutamate dehydrogenase, glyceraldehyde 3-phosphate dehydrogenase, 2-hydroxyacid dehydrogenase, isocitrate dehydrogenase, lactate dehydrogenase, malate dehydrogenase, methylmalonate semialdehyde dehydrogenase, succinate dehydrogenase, pyruvate dehydrogenase, alpha ketoglutarate dehydrogenase, D-2-hydroxyacid dehydrogenase, D-2-hydroxyisocaproate dehydrogenase, formate dehydrogenase, D-glycerate dehydrogenase, vancomycin-resistant protein H, D-2-photophoglycerate dehydrogenase, D-lactate dehydrogenase, glucose-6-phosphate dehydrogenase, 6-phosphogluconate dehydrogenase, and a sorbitol dehydrogenase, and/or

the dehydrogenase comprises an amino acid sequence having at least 50% identity to SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:18, or SEQ ID NO:19, SEQ ID NO:2, SEQ ID NO:29, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:10, SEQ ID NO:11, or SEQ ID NO:13.

[0200] Embodiment 3. A recombinant microorganism according to Embodiment 1 or 2, wherein the polypeptide that participates in lipid biosynthesis is selected from the group consisting of: an acyl-ACP thioesterase, an acyl-CoA thioesterase, a 4-hydroxybenzoyl-thioesterase, a polypeptide having lipolytic activity, an aldehyde-forming acyl-CoA reductase, an aldehyde-forming acyl-ACP reductase, a carboxylic acid reductase, an alcohol-forming acyl-CoA reductase, an alcohol-forming acyl-ACP reductase, a wax synthase, a decarbonylase, a decarboxylase, a GPAT, an LPAAT, a PAP, and a DGAT; further optionally wherein the lipid is a fatty acid product selected from the group consisting of: a free fatty acid, a fatty aldehyde, a

fatty alcohol, an alkane, an alkene, a fatty acid ester, a wax ester, a monoacylglyceride, a diacylglyceride, and a triacylglyceride.

[0201] Embodiment 4. A recombinant microorganism according to any of the previous Embodiments wherein the first non-native nucleic acid molecule comprises:

a nucleotide sequence encoding an aldehyde 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 between 95% and 100% identity to SEQ ID NO.:4, SEQ ID NO.:6, or SEQ ID NO.:7;

a nucleotide sequence encoding 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 between 95% and 100% identity to SEQ ID NO:18 or SEQ ID NO:19;

a nucleotide sequence encoding a D-2-hydroxyacid 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 between 95% and 100% identity to SEQ ID NO:2 or SEQ ID NO:29;

a nucleotide sequence encoding a D-2-hydroxyacid 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 between 95% and 100% identity to SEQ ID NO:15 or SEQ ID NO:16.

a nucleotide sequence encoding a phosophogluconate 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 between 95% and 100% identity to SEQ ID NO:10 or SEQ ID NO:11; or

a nucleotide sequence encoding a phosophogluconate 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 between 95% and 100% identity to SEQ ID NO:13.

[0202] Embodiment 5. A recombinant microorganism according to any of the previous Embodiments, wherein a culture of the recombinant microorganism that includes a first non-native nucleic acid molecule encoding a dehydrogenase and a second non-native nucleic acid

molecule encoding a polypeptide that participates in the production of a lipid produces a greater amount of a lipid than is produced by a control culture of a microorganism identical in all respects to the recombinant microorganism that includes the first non-native nucleotide and the second non-native nucleotide sequence, except that the control microorganism does not include the first non-native nucleotide sequence encoding a dehydrogenase;

wherein the lipid is a fatty acid product not produced by a microorganism of the same species or strain as the recombinant microorganism that does not include the second non-native nucleic acid molecule.

[0203] Embodiment 6. A recombinant microorganism according to any of the previous Embodiments wherein the recombinant microorganism is a photosynthetic microorganism.

[0204] Embodiment 7. A recombinant microorganism according to any of the previous Embodiments, wherein the photosynthetic microorganism is a cyanobacterium, optionally 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*; or the photosynthetic microorganism is a microalga, optionally 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*, *Schizochlamydella*, *Skeletonema*, *Spyrogyra*, *Stichococcus*, *Tetrachlorella*, *Tetraselmis*, *Thalassiosira*, *Viridiella*, and *Volvox*.

[0205] Embodiment 8. A recombinant photosynthetic microorganism according to Embodiment 6 or 7, wherein the expression of the first nucleic acid molecule encoding the dehydrogenase increases the intracellular ratio of NADPH to NADP+ relative to the ratio of NADPH to NADP+ in an otherwise identical microorganism that lacks the first nucleic acid, for example wherein intracellular NADPH/NADP+ ratio about 5% higher, about 10% higher, about 20% higher, about 30% higher, about 40% higher, about 60% higher, about 80% higher, about 100% higher, about 150% higher, about 200% higher, about 300% higher, about 500% higher, about 700% higher, about 900% higher, about 1000% higher, or about 2000% higher than an otherwise identical microorganism lacking the first nucleic acid.

[0206] Embodiment 9. A recombinant photosynthetic microorganism according to any one of Embodiments 6–8, wherein a culture of the recombinant microorganism produces about 1% more, about 5% more, about 10% more, about 20% more, about 30% more, about 40% more, about 50% more, about 60% more, about 70% more, about 80% more, about 90% more, about 100% more, about 200% more, about 500% more, about 700% more, about 1000% more, or about 2000% more of a fatty acid product compared to a culture of an otherwise identical microorganism lacking said first nucleic acid.

[0207] Embodiment 10. A recombinant photosynthetic microorganism of any one of Embodiments 6–9, wherein the recombinant photosynthetic microorganism has a replicative rate about 5% higher, about 10% higher, about 20% higher, about 30% higher, about 40% higher, about 60% higher, about 80% higher, about 100% higher, about 150% higher, about 200% higher, 400% higher, about 600% higher, about 800% higher, about 1000% higher, or at least 2000% higher than an otherwise identical photosynthetic microorganism lacking said first non-native nucleic acid molecule.

[0208] Embodiment 11. A method of producing a lipid comprising culturing a recombinant microorganism according to any one of the preceding Embodiments in a suitable culture medium for a sufficient amount of time to produce a lipid, optionally wherein the lipid is a fatty acid product selected from the group consisting of a free fatty acid, a fatty aldehyde, a fatty alcohol,

an alkane, an alkene, a fatty acid ester, a wax ester, a monoacylglyceride, a diacylglyceride, and a triacylglyceride.

[0209] Embodiment 12. A method according to Embodiment 11, wherein the recombinant *microorganism is a photosynthetic microorganism and the recombinant photosynthetic* microorganism is cultured photoautotrophically.

[0210] Embodiment 13. A method according to Embodiment 11 or 12, wherein the method includes inducing expression of one or both of the nucleic acid encoding the dehydrogenase and the nucleic acid sequence encoding a polypeptide that participates in the production of a lipid.

[0211] Embodiment 14. A method according to any of Embodiments 11–13, wherein the method further comprises recovering the lipid from the culture.

[0212] Embodiment 15. A method of increasing the growth and/or proliferation rate of a microorganism that produces a lipid, wherein 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 growth and/or proliferation of the microorganism, wherein the growth 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.

[0213] Embodiment 16. A method according to any of Embodiments 11–15, wherein the culture reaches a higher optical density after three, four, five, or six days of culture than the culture density reached by an identical culture of a microorganism identical in all respects except that it lacks the non-native gene encoding the dehydrogenase.

[0214] Embodiment 17. A cell culture comprising a recombinant microorganism of any one of Embodiments 1–10, optionally wherein the recombinant microorganism is a photosynthetic recombinant microorganism and the culture does not include a substantial amount of a reduced carbon source.

[0215] Embodiment 18. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide 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%, or at least 95% identity to SEQ ID NO:2 or SEQ ID NO:29.

EXAMPLES

Example 1

[0216] Screens were designed for identification of genes encoding proteins that were able to enhance fatty acid production by microbes. The Nile Blue screen used an *E. coli* Top 10 strain that carried an N-terminally truncated version of the CclFatB1 acyl-ACP thioesterase from *Cuphea carthagenensis* (nucleotide sequence codon-optimized for *Synechocystis*, SEQ ID NO:20, amino acid sequence SEQ ID NO:21; see US 2011/0020883, incorporated by reference herein) as the background for transformation of a metagenomic library containing DNA fragments from an environmental sample removed from a shipping channel in Laguna Madre, Texas. A plate-based assay was used to identify recombinant *E. coli* colonies producing free fatty acids on a solid media that contained 10 μg/mL Nile Blue A (Alfa Aesar, Ward Hill, MA #A17174). Nile blue stains fatty acids blue. Colonies were examined by visual inspection for staining by positioning plates on a standard light box. Colonies displaying a high level of Nile Blue A staining over background controls that expressed the CclFatB1 thioesterase but did not include library fragments were selected, grown up, and further screened to determine the amount of total non-esterified free fatty acid (FFA) using a free fatty acid Detection kit (#SFA-1, Zenbio, Inc, Research Triangle Park, NC).

[0217] The free fatty acid content of *E. coli* clones exhibiting elevated free fatty acid levels over background controls in the Nile Blue plate assay and subsequently by assay with the free fatty acid detection kit were analyzed further by gas chromatography (GC) with flame ionization detection (GC-FID). Two hundred isolates showing elevated free fatty acid levels in GC-FID analysis over background controls were selected and the nucleotide sequences of the clones were determined. The cloned fragments in these isolates contained from one to at least five open reading frames (potential genes) each, based on bioinformatic analysis of their sequences. Following DNA sequencing and removal of redundant clones, sequences were analyzed again to identify recurring protein domains. Clones denoted "NB" were isolated from the Nile Blue assay. A separate genetic assay for detecting enhanced biosynthesis of fatty acids using a metagenomic library made from isolation of DNA from water samples taken from ponds at Pacific Aquafarms located North of the Salton Sea in southern California was also performed resulting in the isolation of clone B10 (Table 1).

[0218] Several clones were identified as having open reading frames encoding polypeptides containing dehydrogenase domains (Table 1). Clones B10 and NB106 were identified as including sequences encoding D-isomer specific 2-hydroxyacid dehydrogenases; NB8 and NB112 were identified as encoding aldehyde dehydrogenases; and NB104 was identified as encoding a 6-phosphogluconate dehydrogenase. Thus, genes encoding three distinct types of dehydrogenase were identified in the cloned fragments isolated in the functional screens.

Table 1: Clones selected from Assays.

Library hit	**Pfam**	**Pfam Annotation, Closest BLAST hit**
B10	PF02826	D-isomer specific 2-hydroxyacid dehydrogenase (NAD binding domain) *Polymorphum gilvum* SL003B-26A1 YP_004302702
NB106	PF00389	D-isomer specific 2-hydroxyacid dehydrogenase (catalytic domain) *Enterococcus faecalis* ZP_05597403
NB8	PF00171	Aldehyde dehydrogenase ywdH *Bacillus thuringiensis serovar berliner* ZP_04101108
NB112	PF00171	Methylmalonate semialdehyde dehydrogenase *Bacillus amyloliquefaciens* YP_001423238
NB104	PF000393	6-phosphogluconate dehydrogenase *Enterococcus faecalis* TX4248 ZP_07551842

[0219] The B10 insert included an open reading frame (ORF) (SEQ ID NO:1) encoding a polypeptide (SEQ ID NO:2) that was identified as belonging to Pfam 02826 ("D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain", gathering cutoff, 25.1) with a bit score of 159.3 and an e value of 4.2 e-47. The B10 ORF encodes a polypeptide having an amino acid sequence that is 64% identical to the D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding protein of *Polymorphum gilvum* SL003B-26A1 (Gene ID: 328542593; accession YP_004302702); 57% identical to the D-isomer specific 2-hydroxyacid dehydrogenase of

Labrenzia alexandrii DFL-11 (Gene ID: 254503433; accession ZP_05115584); 56% identical to the 2-hydroxyacid dehydrogenase of *Stappia aggregata* IAM126114 (Gene ID: 118438963; accession ZP_01545666); and 55% identical to the D-isomer specific 2-hydroxyacid dehydrogenase (NAD-binding) of *Marinomonas* sp. MWYL1 (Gene ID: 5367846; accession YP_001342133). The first twelve amino acids of the B10 ORF (SEQ ID NO:2) were upstream of a methionine that is the first amino acid of the *Polymorphum gilvum* D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding protein, thus these amino acids may not be part of the native protein encoded by the B10 ORF: the encoded polypeptide is likely to comprise amino acids 13-326 of SEQ ID NO:2. SEQ ID NO:29 represents amino acids 13-326 of SEQ ID NO:2.

[0220] The NB106 insert included an open reading frame (SEQ ID NO:14) that encoded a polypeptide (SEQ ID NO:15) identical to amino acids 1-137 of as the D-isomer specific 2-hydroxyacid dehydrogenase of *Enterococcus faecalis* (ZP_05597403; SEQ ID NO:16) This polypeptide sequence recruited to Pfam PF00389 ("D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain", gathering cutoff, 24.6) with a bit score of 57.6 and an e value of 7.8 e-16. Additional D-isomer specific 2-hydroxyacid dehydrogenases having homology to the polypeptide encoded by the NB106 ORF (SEQ ID NO:14) include the D-isomer specific 2-hydroxyacid dehydrogenase of *Enterococcus gallinarum* EG2 (ZP_05648199; EEV31532) (79% identity); the D-isomer specific 2-hydroxyacid dehydrogenase of *Enterococcus casseliflavus* ATCC 12755 (ZP_08145011; EGC69912) (78% identity); the D-isomer specific 2-hydroxyacid dehydrogenase of *Carnobacterium* sp. AT7 (ZP_02185893; EDP67348) (72% identity); the D-isomer specific 2-hydroxyacid dehydrogenase of *Enterococcus faecium* E1636 (ZP_06695345; EFF23321) (78% identity); the 2-hydroxyacid dehydrogenase of *Pediococcus acidilactici* 7_4 (ZP_06196181; EFA27324) (63% identity); the 2-hydroxyacid dehydrogenase of *Lactobacillus brevis* ATCC 367 (YP_794343; ABJ63312) (63% identity); the 2-hydroxyacid dehydrogenase of *Lactobacillus coleohominis* 101-4-CHN (ZP_05553013; EEU30233) (64% identity); and the D-isomer specific 2-hydroxyacid dehydrogenase of *Clostridium beijerinckii* NCIMB 8052 (YP_001309316.1 GI:150017062) (75% identity).

[0221] The NB8 insert included an ORF (SEQ ID NO:3) encoding a polypeptide (SEQ ID NO:4) that was identified as belonging to Pfam 00171 ("aldehyde dehydrogenase", gathering cutoff, 23.0) with a bit score of 280.5 and an e value of 1.4 e-83. The ORF, which begins at the 5'-most end of the insert, has at least 99% identity to amino acids 95-455 of a *Bacillus*

thuringiensis serovar thuringiensis aldehyde reductase (Gene ID: 118438963; accession ZP_01432004; SEQ ID NO:7). NB8 appears to encode a truncated *Bacillus* aldehyde reductase, as the ORF is missing amino acids homologous to the N-terminal-most 90-100 amino acids of the *Bacillus thuringiensis aldehyde reductase* (SEQ ID NO:7). Further, due to a cloning error that was not realized when the expression experiments were performed, only a subportion of this ORF was cloned into the integration vector for expression in *Synechocystis*. Amino acids N-terminal to amino acid 95 and C-terminal of amino acid 347 of SEQ ID NO:7 (the *Bacillus* aldehyde dehydrogenase) therefore do not appear to be required for activity, as expression of the NB8 partial ORF (SEQ ID NO:5), which encodes a polypeptide (SEQ ID NO:6) that lacks 94 amino acids of the N-terminal and 108 amino acids of the C-terminal of the *Bacillus* aldehyde dehydrogenase, demonstrated effects on proliferation and fatty acid productivity (see Example 2). Other *Bacillus* aldehyde dehydrogenases including amino acid sequences having sequence homology to SEQ ID NO:4 include the ywdH aldehyde dehydrogenase of *Bacillus thuringiensis serovar berliner* (Gene ID: 228938499; accession ZP_041501108) (99% identity); the ywdH aldehyde dehydrogenase of *Bacillus thuringiensis* IBL 200 (Gene ID: 228907013; accession ZP_04070879) (98% identity); the aldehyde dehydrogenase (NAD) family protein of *Bacillus thuringiensis* IBL 4222 (Gene ID: 228899962; accession ZP_04064201) (98% identity); the aldehyde dehydrogenase ywdH of *Bacillus thuringiensis servovar kurstaki* (Gene ID: 228951764; ZP_04113863) (98% identity), the aldehyde dehydrogenase ywdH of *Bacillus cereus* ATCC 10876 (Gene ID: 229189465; ZP_04316482) (98% identity), the aldehyde dehydrogenase ywdH of *Bacillus thuringiensis serovar huazhongensis* (Gene ID: 228920096; ZP_04083445) (98% identity), the aldehyde dehydrogenase (NAD) family protein of *Bacillus cereus* (Gene ID: 206967852; ZP_03228808) (98% identity), and the aldehyde dehydrogenase ywdH of *Bacillus cereus* 172560W (Gene ID: 229177791; ZP_04305164) (97% identity). Aldehyde dehydrogenases that include amino acid sequences having at least 50% identity to SEQ ID NO:4 include the aldehyde dehydrogenase of *Bacillus cytotoxicus* NVH 391-98 (Gene ID: 5344056; YP_001374327) (82% identity); the aldehyde dehydrogenase of *Bacillus megaterium* WSH-002 (Gene ID: 345444973; gb AEN89990) (62% identity); aldehyde dehydrogenase ywdH of *Bacillus mycoides* Rock3-17 (Gene ID: 228996488 ZP_04156127) (81% identity), aldehyde dehydrogenase ywdH [*Bacillus cereus* AH621 (gi 229166217;

ZP_04293977) (89% identity), and the aldehyde dehydrogenase (NAD(P)+) of *Bacillus thuringiensis* str. Al Hakam (gi 118476858; YP_894009) (90% identity).

[0222] The NB112 insert included an open reading frame (SEQ ID NO:17) that encoded a portion of a polypeptide (SEQ ID NO:18) having 98% identity to the methylmalonate semialdehyde dehydrogenase of *Bacillus amyloliquefaciens* (YP_001423238; SEQ ID NO:19). This polypeptide sequence recruited to Pfam PF00171 ("aldehyde dehydrogenase", gathering cutoff, 23.0) with a bit score of 203.7 and an e value of 3 e-60. Additional methylmalonate semialdehyde dehydrogenases having homology to the polypeptide encoded by the NB112 ORF (SEQ ID NO:18) include the methylmalonate semialdehyde dehydrogenase of *Bacillus atrophaeus* 1942 (YP_003975426; ADP34495) (92% identity); the methylmalonate-semialdehyde dehydrogenase of *Bacillus licheniformis* ATCC 14580 (YP_081323; gi 52082532) (89% identity); the methylmalonate-semialdehyde dehydrogenase *Paenibacillus dendritiformis* C454 (ZP_09676636) (84% identity); the methylmalonate-semialdehyde dehydrogenase of *Paenibacillus terrae* HPL-003 (YP_005075546; AET59323) (83% identity); the methylmalonate-semialdehyde dehydrogenase of *Bacillus clausii* KSM-K16 (YP_173925; BAD62964) (80% identity); the methylmalonate-semialdehyde dehydrogenase of *Listeria monocytogenes* FSL F2-208 (EFR85827) (79% identity); the methylmalonate-semialdehyde dehydrogenase of *Listeria marthii* FSL S4-120 (ZP_07869657; EFR88847) (79% identity); and the methylmalonate-semialdehyde dehydrogenase of *Alicyclobacillus acidocaldarius* LAA1 (ZP_03495181; EED06125) (70% identity).

[0223] The NB104 insert (SEQ ID NO:8) included an open reading frame (SEQ ID NO:9) that encoded a polypeptide (SEQ ID NO:10) identified as a portion of a 6-phosphogluconate dehydrogenase of *Enterococcus faecalis* (*e.g.*, ZP_0521253; SEQ ID NO:11). This polypeptide sequence recruited to Pfam 00393 ("phosphogluconate dehydrogenase", gathering cutoff, 20.4) with a bit score of 55.4 and an e value of 4.4 e-15. The NB104 open reading frame encodes a polypeptide having 100% identity to amino acids 13-311 of the *Enterococcus faecalis* 6-phosphogluconate dehydrogenase (SEQ ID NO:11). Additional 6-phosphogluconate dehydrogenases having homology to the polypeptide encoded by the NB104 ORF (SEQ ID NO:10) include the 6-phosphogluconate dehydrogenase of *Carnobacterium* sp. AT7 (Gene ID: 163791487; ZP_02185894; 56% identity), the 6-phosphogluconate dehydrogenase of *Anaerococcus vaginalis* ATCC 51170 (Gene ID: 256546044; ZP_05473398; 51% identity), the

6-phosphogluconate dehydrogenase of *Enterococcus casseliflavus* (Gene ID: 257867259; ZP_05646912; 51% identity), and the 6-phosphogluconate dehydrogenase-like protein of *Clostridium beijerinckii* NCIMB 8052 (Gene ID: 150017061; YP_001309315; 49% identity).

Example 2

[0224] Cloned DNA fragments of several of the sequenced clones, including NB8, NB104, and B10 strain (under the control of the IPTG-inducible trcY promoter (SEQ ID NO:22)), were subsequently transformed into a *Synechocystis* PCC 6803 that included an integrated Cc1FatB1 acyl-ACP thioesterase gene at a different locus.

[0225] The N-terminally truncated Cc1FatB1 acyl-ACP thioesterase gene (SEQ ID NO:20) was cloned into *Synechocystis* integration vector YC28 (SEQ ID NO:23) which included a P15A origin of replication for E. coli, "RS1 up" (SEQ ID NO:24) and "RS1 down" (SEQ ID NO:25) fragments for homologous recombination in *Synechocystis* 6803, a lacIQ repressor for the IPTG-inducible trcE driven *Cuphea* Cc1FatB1 thioesterase gene and a kanamycin resistance marker for selection. DNA source material for PCR amplification of segments of the vector came from *Synechocystis* genomic DNA, a pUC-19 vector, a pACYC-184 vector, and a vector containing a synthesized *Cuphea* Cc1FatB1 gene (DNA2.0, Menlo Park).

[0226] Expression vectors were also constructed for overexpressing the fragments identified as having sequences encoding dehydrogenases (or portions thereof) by the functional screen described in Example 1. The B10 ORF (SEQ ID NO:1), the NB104 contig fragment (SEQ ID NO:8), and the NB104 ORF (SEQ ID NO:9), were independently amplified from the "contig" clones identified in the library screen using primers which contained around 15 bp of sequence homologous with cyanobacterial integration vector pSGI-YC63 (SEQ ID NO:28). An NB8 partial ORF fragment (SEQ ID NO:5) was also cloned in the pSGI-YC63 integration vector. pSGI-YC63 contained a spectinomycin marker for selection, homologous "RS2 up" (SEQ ID NO:26) and "RS2 down" (SEQ ID NO:27) arms for integration in the RS2 site of *Synechocystis*, the lacIQ repressor to regulate the trcY promoter (SEQ ID NO:22), and a pUC origin of replication for *E.coli* propagation.

[0227] To introduce the Cc1FatB1 acyl-ACP thioesterase gene construct and the dehydrogenase ORF constructs into cyanobacteria, *Synechocystis* sp. PCC 6803 cells were cultured in BG-11 media, which does not include a substantial amount of a reduced carbon

source, to an OD (730 nm) of about 0.7-0.9. About 10 mL of the culture was spun down at approximately 2000 g for 15 minutes, and the cell pellet was resuspended in 1 mL fresh BG-11 media. An aliquot of 300 μL of cells was transformed with about 100 ng of integration vector. The cells were incubated under lights (80 μE) for about 6 hours, then spread onto Minipore filters and placed on top of BG-11 agar plates containing no antibiotics. The plates were incubated at about 30°C under about 80 μE of light for about 24 hours. The filters were then transferred onto fresh BG-11 1.5% agar plates with 20 μg/mL kanamycin and cultured for 7 days. Colonies of *Synechocystis* sp. PCC 6803 were picked and patched onto new agar plates. The putative dehydrogenase-encoding constructs for integration into the *Synechocystis* genome were transformed into Cc1FatB1-transformed strains using the same procedure, except that antibiotic selection included 20 μg/mL spectinomycin in addition to 20 μg/mL kanamycin.

[0228] Cultures that included the Cc1FatB1 acyl-ACP thioesterase gene and a dehydrogenase-encoding open reading frame were grown at about 60 uE of light with constant shaking and 1% CO_2. OD at the time of induction was 0.6. Cultures were induced with 1mM IPTG. The strains were grown in 4mL glass vials with an initial volume of 1.5mL. At the end of 6 days, the entire vial with about 1 mL of culture remaining in the vial (due to evaporative loss) was submitted for gas chromatography. A strain with the CcFatB1 thioesterase gene (under the control of the TrcY promoter) integrated into the RS2 site of 6803 but not carrying an exogenous dehydrogenase gene served as the control.

[0229] Free fatty acids were analyzed by gas chromatography (GC) with flame ionization detection (GC-FID). 1mL cultures in 4mL vials capped with PTFE (polytetrafluoroethylene)-lined caps (National Scientific) were submitted to Analytical for analysis. Eighty four microliters of an internal standard (I.S.) set that included the free fatty acids C9:0, C13:0, and C17:0, each at a concentration of 600 μg/ml, in hexane, were added to the culture sample, followed by 83 microliters of 50% H_2SO_4, 167 microliters of 5M NaCl, and 1.4 milliliters of hexane. The final concentration of each I.S. was 50 μg/ml relative to sample volume. The fatty acids for making the I.S. set were purchased from Fluka or Nu-Chek Prep, Inc. Three I.S.'s were used given the variable response of the free fatty acids. C8:0 and C10:0 were calibrated w/ C9:0 I.S.; C12:0 and C14:0 used the C13:0 I.S.; and the remaining C16:0 through C18:2 cis9,12 used the C17:0 I.S. Post reagent and I.S. addition, the cultures were vortexed on a multi-tube vortexer at 2,500 rpm for 30 min. The vials were finally centrifuged for 3 min. at 2500 rpm to provide

good separation between organic and aqueous phases. The hexane layers were sampled by a Gerstel MPS2L Autosampler. Fatty acid samples were analyzed on an Agilent model 7890A gas chromatograph equipped with an FID (flame ionization detector) that included a J&W Scientific DB-FFAP capillary column (10 m length, 0.10 mm internal diameter, 0.10 μm film thickness). The GC oven was programmed as follows: 120°C for 0.1 min., then heated at 40°C/min. to 240°C (hold 3 minutes). The injector temperature was kept at 250°C, and a 40:1 split 1.0 μl injection was used. Hydrogen was used as a carrier gas at a flow rate of 0.5999 ml/min. The FID was set to 320C. The analytes were identified by comparison of retention times to individually injected standards. The calibration range for the analytes was 2.5 μg/ml to 200 μg/ml for C8:0-C16:1 fatty acids and 0.625 μg/ml to 50 μg/ml for C18:0-C18:2 fatty acids. The limit of quantitation for each analyte was the lowest concentration listed in the calibration range except C18:0, C18:1 cis9 (1.25ug/mL) and C18:2 cis9,12 (2.5ug/mL). Spiking and recovery experiments into whole cell culture showed that the extraction method recovered consistently within a range of 85%-115% for each analyte in this sample batch run except C16:1 cis9 (74%), C18:1 cis9 (63%), and C18:2 cis9,12 (64%) .

[0230] The total amount of free fatty acid produced by these engineered *Synechocystis* strains is provided in Figure 1. It can be seen that *Synechocystis* strains expressing the B10 ORF ("dehydrd"; SEQ ID NO:1), the NB8 partial ORF fragment (SEQ ID NO:5), the NB104 ORF ("6-P-de"; SEQ ID NO:9), and NB104 ORF full contig fragment (SEQ ID NO:8) along with CclFatB1 thioesterase encoding sequence (SEQ ID NO:20) produced higher levels of free fatty acids as compared to the control strain that contained the CclFatB1 thioesterase gene alone. Figure 2 demonstrates that in this experiment strains that included a CclFatB1 thioesterase and a dehydrogenase gene obtained from the screen were able to achieve culture that were four to five-fold higher than the cell density of the strain that expressed CclFatB1 thioesterase, but lacked a dehydrogenase gene.

Example 3

[0231] To further investigate the effects of expressing genes that enhanced fatty acid production, *Synechocystis* strains engineered to express the B10 (2-hydroxyacid dehydrogenase NAD-binding domain protein) gene and the NB104 (6-phosphogluconate dehydrogenase) gene together with a CclFatB1 acyl-ACP thioesterase gene were assessed for their ability to alter the

redox state of the cells. As a control, the Cc1FatB1 gene integrated at the RS2 site integration vector pSGI-YC63 (1A/YC63) was expressed in independent *Synechocystis* 6803 strains that did not have an additional dehydrogenase gene. *Synechocystis* 6803 having no transgenes ("6803") was included as a further control. Cells were grown under constant light at 60 uE with shaking, and induced with the addition of 1mM IPTG at an OD_{730} of 0.5 to express the thioesterase and, where present, the putative dehydrogenase. Samples were collected every 24 hours for three days.

[0232] To determine the redox state of the *Synechocystis* strains engineered with the dehydrogenase genes and the control strains, enzymatic assays were performed to determine NADPH/NADP+ ratios on samples taken at 1, 2, and 3 days post induction. An NADP/NADPH Quantitation Kit (BioVision, Inc., Mountain View, CA) was used for this purpose. The enzymes in the assay kit specifically recognize NADP+/NADPH in an enzyme cycling reaction. For the assay, approximately 1.5 x 107 cells for each time point were lysed in 1 ml of NADPH extraction buffer provided with the assay kit. The cells were subjected to 2 freeze/thaw cycles in liquid nitrogen and 4 rounds of bead beating. The lysate was then centrifuged and the supernatant was filtered over a 10K cutoff column. All photosynthetic pigments and enzymes that might consume NADPH were retained on the filter membrane. The filtrate consisted of only small metabolites and was used in the NADPH assay. The assay kit enabled the measurement of total NADP (NADP+ plus NADPH) and NADPH. The NADPH / NADP+ ratio was determined by subtracting the amount of NADPH from the total NADP to provide the amount of NADP+, and then to divide the amount of NADPH by the calculated amount of NADP+.

[0233] Assay results are summarized in Figure 3. Figure 3 shows the ratio of NADPH to NADP+ on successive days of the experiment. In the control strain, wild-type *Synechocystis* PCC 6803, NADPH declines with respect to NADP+ with each additional day in culture. The strain expressing an exogenous acyl-ACP thioesterase, Cc1FatB1, shows a marked decline in the ratio of NADPH to NADP+ when compared with the wild-type cells. This was expected as the fatty acid biosynthesis process is known to require extensive reducing power. Addition of a dehydrogenase gene to a strain expressing a foreign acyl-ACP thioesterase, however, increased the ratio of NADPH to NADP+, with the NB104 (6-phosphogluconate dehydrogenase) gene having a greater effect on the NADPH/NADP+ ratio than the B10 (2- hydroxyacid dehydrogenase NAD-binding domain protein) gene in this experiment. While the ratio of

NADPH to NADP+ is not restored to wild type levels, it is at least 2-fold higher than the strains expressing the acyl ACP thioesterase alone.

[0234] Expression of the B10 ORF or the NB104 ORF in *Synechocystis* 6803 along with CclFatB1 thioesterase therefore increased the NADPH/NADP+ ratio of cells (Figure 3), allowed for higher proliferation rates of strains as measured by culture density at six days (Figure 2), and also led to higher production of free fatty acids of all chain lengths (Figure 1). The NB104 ORF encodes a portion of a 6-phosphogluconate dehydrogenase, an enzyme of the pentose phosphate pathway (Figure 4). This pathway produces 5C sugars, used in nucleotide and nucleic acids biosynthesis, from 6C sugars. The pentose phosphate pathway helps in generation of reducing equivalents in the form of NADPH which is use for reductive biosynthesis reactions within the cells such as fatty acid biosynthesis.

Example 4

[0235] The NB104 ORF from a metagenomic library encoded a portion of an *Enterococcus* 6-phosphogluconate dehydrogenase. Overexpression of the 6-phosphogluconate dehydrogenase enzyme gene (SEQ ID NO:12) from *Synechocystis* sp. PCC 6803 was also tested to determine if it would exert the same effect as the *Enterococcus*-derived 6-phosphogluconate dehydrogenase gene. The *Synechocystis* 6-phosophogluconate dehydrogenase gene sll0239 (Accession BAA10105; GI:1001479; SEQ ID NO:12) was therefore cloned into a YC63 construct in which it was placed under the control of the trcY promoter and integrated into the RS2 site of a *Synechocystis* strain expressing the CclFatB1 acyl-ACP thioesterase gene regulated by the trcE promoter (SEQ ID NO:30) and integrated at the RS1 site. The resulting strain was tested for fatty acid production along with a control *Synechocystis* sp. PCC 6803 strain that only expressed the acyl-ACP thioesterase gene from a trcY promoter (integrated at the RS2 site). In this experiment, strains were induced after they had reached a high density to attain greater levels of free fatty acid production. Briefly, 5.0 OD equivalent cells were spun down and resuspended in fresh BG11 media containing 1mM IPTG and appropriate antibiotics. The final culture volume was 1.5m1. These strains were grown in a 4mL glass vial with constant shaking, a light intensity of 60uE and 1% CO_2. In this example, in which cells were induced at a relatively high density and cultured for 6 days under induction, expression of the homologous *Synechocystis*

dehydrogenase gene also increased the amount of free fatty acids (Figure 5). Fatty acid analysis of the samples was performed as in Example 2.

[0236] The native *Synechocystis* 6-phosphogluconate dehydrogenase enzyme increased the FFA by at least two-fold as compared to strains expressing the CclFatB1 thioesterase alone (Figure 5). The patterned bar represents the native *Synechocystis* 6803 6-phosphogluconate dehydrogenase enzyme cloned in *Synechocystis* along with CclFatB1. We therefore conclude that overexpression of an NADPH producing dehydrogenase such as 6-phosphogluconate dehydrogenase in organisms, including photosynthetic microorganisms cultured photoautotrophically (without a reduced carbon source supporting growth or proliferation of the culture), improves the proliferation rate and also enhances the overall yield of free fatty acid by the culture.

[0237] The Summary and Abstract sections may set forth one or more but not all exemplary embodiments of the present invention as contemplated by the inventor(s), and thus, are not intended to limit the present invention and the appended claims in any way.

[0238] The foregoing description of the specific embodiments will reveal the general nature of the invention that others can, by applying knowledge within the skill of the art, readily modify and/or adapt for various applications such specific embodiments, without undue experimentation and without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein, and the breadth and scope of the present invention should not be limited by any of the above-described exemplary embodiments.

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 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.

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 70% sequence identity to SEQ ID NO:4.

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.

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

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

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.

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

11. The method of Claim 10, wherein the D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least 70% 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.

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.

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

14. The method of Claim 13, wherein the 6-phosphogluconate dehydrogenase comprises an amino acid sequence having at least 70% 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.

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.

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

17. The method of Claim 1, wherein the recombinant photosynthetic microorganism is a microalga.

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*.

19. The method of Claim 1, wherein the recombinant photosynthetic microorganism is a cyanobacterium.

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*.

21. The method of Claim 1, wherein the recombinant photosynthetic microorganism is cultured photoautotrophically.

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 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.

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

24. The recombinant photosynthetic microorganism of either Claim 22, wherein the dehydrogenase is an NADP-dependent dehydrogenase.

25. The recombinant photosynthetic microorganism of Claim 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.

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

27. The recombinant photosynthetic microorganism of Claim 26, wherein the aldehyde dehydrogenase comprises an amino acid sequence having at least 70% identity to SEQ ID NO:4.

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.

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

30. The recombinant photosynthetic microorganism of Claim 29, wherein the methylmalonate semialdehyde dehydrogenase comprises an amino acid sequence having at least 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NO:18 and SEQ ID NO:19.

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.

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

33. The recombinant photosynthetic microorganism of Claim 32, wherein the D-2-hydroxyacid dehydrogenase comprises an amino acid sequence having at least 70% 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.

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.

35. The recombinant photosynthetic microorganism of Claim 22, wherein the recombinant photosynthetic microorganism is a microalga.

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*.

37. The recombinant photosynthetic microorganism of Claim 22, wherein the recombinant photosynthetic microorganism is a cyanobacterium.

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*.

39. 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.

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.