[0006] The burning of fossil fuels by humans is the largest source of emissions of carbon dioxide, which is one of the greenhouse gases that allows radiative forcing and contributes to global warming. In the United States, more than 90% of greenhouse gas emissions come from the combustion of fossil fuels. In addition, other air pollutants, such as nitrogen oxides, sulfur dioxide, volatile organic compounds (VOCs), and heavy metals are produced.

[0007] Human activity raises levels of greenhouse gases primarily by releasing carbon dioxide from fossil fuel combustion, but other gases, e.g., methane, are not negligible. The concentrations of several greenhouse gases have increased over time due to human activities, such as burning of fossil fuels and deforestation leading to higher carbon dioxide concentrations. According to the global warming hypothesis, greenhouse gases from industry and agriculture have played a major role in the recently observed global warming.

[0008] 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.

SUMMARY OF THE INVENTION

[0008a] In a first aspect, the present invention refers to a method of producing fuel, comprising:

(a) culturing a population of microalgae in the presence of a fixed carbon source, wherein:

(i) the microalgae express an exogenous sucrose invertase;

(ii) the microalgae accumulate at least 10% of their dry cell weight as lipid; and

(ii) the fixed carbon source is selected from the group consisting of sugar cane juice, sugar cane, sugar beet, molasses, or other sucrose-containing feedstock;

(b) isolating lipid components from the cultured microalgae; and

(c) subjecting the isolated lipid components to one or more chemical reactions to generate fatty acid esters and/or alkanes,

whereby fuel is produced.

[0008b] In a second aspect, the present invention refers to a composition of alkanes or fatty acid esters made according to the method of the present invention.

[0008c] In a third aspect, the present invention refers to a microalgal cell containing at least 10% of its dry cell weight as lipid, and comprising an exogenous gene encoding a sucrose invertase enzyme.

[0008d] In a fourth aspect, the present invention refers to a lipid produced by a microalgal cell of the present invention.

[0008e] In a fifth aspect, the present invention refers to a method of producing a lipid, comprising:

(a) culturing a population of microalgae comprising an exogenous gene encoding a sucrose invertase in a culture medium comprising a fixed carbon source until the microalgae accumulate 10% or more of their dry cell weight as lipid; and

(b) separating the lipid from the microalgae.

[0008f] In a sixth aspect, the present invention refers to a lipid produced by the method of the present invention.

[0009] In one ~~aspect~~example, the present ~~invention~~disclosure is directed to ~~The invention provides~~ a microbe, which in various ~~embodiments~~examples can comprise a microalgae cell, an oleaginous yeast, or a fungus containing an exogenous gene that encodes a protein selected from the group consisting of a lipase, sucrose transporter, sucrose invertase, fructokinase, polysaccharide-degrading enzyme, a fatty acyl-ACP thioesterase, a fatty acyl-CoA/aldehyde reductase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty aldehyde decarbonylase, and an acyl carrier protein (ACP). The microbe (e.g., microalgae cell) can, for example, be selected from Table 1. In particular ~~embodiments~~examples, the cell is a species of the genus *Chlorella*, such as, e.g., *Chlorella fusca, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella kessleri, Chlorella vulgaris, Chlorella saccharophila, Chlorella sorokiniana* or *Chlorella ellipsoidea*. In other ~~embodiments~~examples, the microbe is an oleaginous yeast selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica*. In still other ~~embodiments~~examples, the microbe is a fungus selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella*

alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum, a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*. In other ~~embodiments~~examples, the ~~invention~~disclosure includes expression of hydrocarbon modification enzymes in bacterial hosts such as *E. Coli* and *Bacill*a method of producing renewable diesel. In one ~~embodiment~~example, the method comprises (a) culturing a population of microorganisms in the presence of a fixed carbon source, wherein (i) the microorganisms accumulate at least 10% of their dry cell weight as lipid, and (ii) the fixed carbon source is selected from the group consisting of glycerol, depolymerized cellulosic material, sucrose, molasses, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing, (b) isolating lipid components from the cultured microorganisms, and (c) subjecting the isolated lipid components to one or more chemical reactions to generate straight chain alkanes, whereby renewable diesel is produced.

[0010] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a composition of liquid hydrocarbons made according to the method described directly above, wherein the composition conforms to the specifications of ASTM D975.

[0011] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of producing jet fuel. In one ~~embodiment~~example, the method comprises (a) culturing a population of microorganisms in the presence of a fixed carbon source, wherein (i) the microorganisms accumulate at least 10% of their dry cell weight as lipid, and (ii) the fixed carbon source is selected from the group consisting of glycerol, depolymerized cellulosic material, sucrose, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing, (b) isolating lipid components from the cultured microorganisms, (c) subjecting the isolated lipid components to one or more chemical reactions to generate straight chain alkanes, (d) cracking the straight chain alkanes, whereby jet fuel is produced.

[0012] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a composition of liquid hydrocarbons produced according to the method described directly above, wherein the composition conforms to the specifications of ASTM D1655.

[0013] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microalgae or yeast cell that has been genetically engineered and/or selected to express a lipid pathway enzyme at an altered level compared to a wild-type cell of the same species. In some cases, the cell

produces more lipid compared to the wild-type cell when both cells are grown under the same conditions. In some cases, the cell has been genetically engineered and/or selected to express a lipid pathway enzyme at a higher level than the wild-type cell. In some cases, the lipid pathway enzyme is selected from the group consisting of pyruvate dehydrogenase, acetyl-CoA carboxylase, acyl carrier protein, and glycerol-3 phosphate acyltransferase. In some cases, the cell has been genetically engineered and/or selected to express a lipid pathway enzyme at a lower level than the wild-type cell. In at least one ~~embodiment~~example in which the cell expresses the lipid pathway enzyme at a lower level, the lipid pathway enzyme comprises citrate synthase.

[0014] In some ~~embodiments~~examples, the microalgae or yeast cell described above has been genetically engineered and/or selected to express a global regulator of fatty acid synthesis at an altered level compared to the wild-type cell, whereby the expression levels of a plurality of fatty acid synthetic genes are altered compared to the wild-type cell. In some cases, the lipid pathway enzyme comprises an enzyme that modifies a fatty acid. In some cases, the lipid pathway enzyme is selected from a stearoyl-ACP desaturase and a glycerolipid desaturase.

[0015] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to an oil-producing microbe containing one or more exogenous genes, wherein the exogenous genes encode protein(s) selected from the group consisting of a fatty acyl-ACP thioesterase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty acyl-CoA/aldehyde reductase, a fatty aldehyde decarbonylase, and an acyl carrier protein. In some cases, the microbe is *Chlorella protothecoides, Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea,* or *Chlorella sp.* In other cases, the microbe is another species as described herein. In one ~~embodiment~~example, the exogenous gene is in operable linkage with a promoter, which is inducible or repressible in response to a stimulus. In some cases, the stimulus is selected from the group consisting of an exogenously provided small molecule, heat, cold, and light. In some cases, the exogenous gene is expressed in a cellular compartment. In some ~~embodiments~~examples, the cellular compartment is selected from the group consisting of a chloroplast and a mitochondrion.

[0016] In one ~~embodiment~~example, the exogenous gene encodes a fatty acid acyl-ACP thioesterase. In some cases, the thioesterase encoded by the exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an acyl carrier protein (ACP). In some cases, the thioesterase encoded by the exogenous gene catalyzes the cleavage of a 10 to 14-carbon fatty acid from an

ACP. In one ~~embodiment~~example, the thioesterase encoded by the exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from an ACP.

[0017] In one ~~embodiment~~example, the exogenous gene encodes a fatty acyl-CoA/aldehyde reductase. In some cases, the reductase encoded by the exogenous gene catalyzes the reduction of a 20 to 30-carbon fatty acyl-CoA to a corresponding primary alcohol. In some cases, the reductase encoded by the exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol. In some cases, the reductase encoded by the exogenous gene catalyzes the reduction of a 10 to 14-carbon fatty acyl-CoA to a corresponding primary alcohol. In one ~~embodiment~~example, the reductase encoded by the exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol.

[0018] In one ~~embodiment~~example, the exogenous gene encodes a fatty acyl-CoA reductase. In some cases, the reductase encoded by the exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde. In one ~~embodiment~~example, the reductase encoded by the exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanal.

[0019] In at least one ~~embodiment~~example, the microbe of the ~~invention~~disclosure further contains one or more exogenous sucrose utilization genes.

[0020] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microbe containing two exogenous genes, wherein a first exogenous gene encodes a fatty acyl-ACP thioesterase and a second exogenous gene encodes a protein selected from the group consisting of a fatty acyl-CoA reductase, a fatty acyl-CoA/aldehyde reductase, and an acyl carrier protein. In some cases, the microbe is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*. In other cases, the microbe is another species as described herein. In some cases, the two exogenous genes are each in operable linkage with a promoter, which is inducible in response to a stimulus. In some cases, each promoter is inducible in response to an identical stimulus.

[0021] In one ~~embodiment~~example, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an ACP. In some ~~embodiments~~examples, the second exogenous gene encodes a fatty acyl-CoA/aldehyde reductase which catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol. In some cases, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 10 to 14-carbon fatty acid from an ACP, and the reductase encoded by the second exogenous gene catalyzes

the reduction of a 10 to 14-carbon fatty acyl-CoA to the corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length. In one ~~embodiment~~example, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from an ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol. In some ~~embodiments~~examples, the the second exogenous gene encodes a fatty acyl-CoA reductase which catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde.

[0022] In some ~~embodiments~~examples, the second exogenous gene encodes a fatty acyl-CoA reductase, and the microbe further contains a third exogenous gene encoding a fatty aldehyde decarbonylase. In some cases, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an ACP, the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding fatty aldehyde, and the decarbonylase encoded by the third exogenous gene catalyzes the conversion of an 8 to 18-carbon fatty aldehyde to a corresponding alkane, wherein the thioesterase, the reductase, and the decarbonylase act on the same carbon chain length.

[0023] In some ~~embodiments~~examples, the second exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

[0024] In some ~~embodiments~~examples, the second exogenous gene encodes an acyl carrier protein, and the microbe further contains a third exogenous gene encoding a protein selected from the group consisting of a fatty acyl-CoA reductase and a fatty acyl-CoA/aldehyde reductase. In some cases, the third exogenous gene encodes a fatty acyl-CoA reductase, and the microbe further contains a fourth exogenous gene encoding a fatty aldehyde decarbonylase.

[0025] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of producing a molecule in a microbe population. In one ~~embodiment~~example, the method comprises culturing a population of microbes in a culture medium, wherein the microbes contain (i) a first exogenous gene encoding a fatty acyl-ACP thioesterase, and (ii) a second exogenous gene encoding a fatty acyl-CoA/aldehyde reductase, and the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP), the fatty acyl-ACP thioesterase catalyzes the cleavage of the fatty acid from the ACP to yield, through further processing, a fatty acyl-CoA, and the fatty acyl-CoA/aldehyde reductase catalyzes the reduction of the acyl-CoA to an alcohol.

[0026] In one ~~embodiment~~example of the method of producing a molecule in a microbe population, the microbe is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.* or *Chlorella protothecoides*. In other cases, the microbe is another species of microorganism as described herein. In some cases, the culture medium contains glycerol. In one ~~embodiment~~example, the glycerol is a byproduct of a transesterification process. In some cases, the culture medium contains glycerol and at least one other fixed carbon source. In one ~~embodiment~~example, the at least one other fixed carbon source is sucrose. In some cases, all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation. In some cases, the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation. In some culture methods of the ~~invention~~disclosure, glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time, the at least one other fixed carbon source is provided at the end of the first period of time, and the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

[0027] In some ~~embodiments~~examples, the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus. In some cases, the method further comprises providing the first stimulus, and incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an alcohol. In some cases, the method further comprises extracting the alcohol from aqueous biomass comprising the culture medium and the microbes.

[0028] In some ~~embodiments~~examples, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length. In some cases, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 10 to 14-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 10 to 14-carbon fatty acyl-CoA to a corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length. In one ~~embodiment~~example, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol. In some cases, the microbes further contain a third

exogenous gene encoding an acyl carrier protein. In some ~~embodiments~~examples, the third exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

[0029] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of producing a lipid molecule in a microbe population. In one ~~embodiment~~example, the method comprises culturing a population of microbes in a culture medium, wherein the microbes contain (i) a first exogenous gene encoding a fatty acyl-ACP thioesterase, and (ii) a second exogenous gene encoding a fatty acyl-CoA reductase, and wherein the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP), the fatty acyl-ACP thioesterase catalyzes the cleavage of the fatty acid from the ACP to yield, through further processing, a fatty acyl-CoA, and the fatty acyl-CoA reductase catalyzes the reduction of the acyl-CoA to an aldehyde. In some cases, the microbe is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*. In other cases, the microbe is another species of microorganism as described herein.

[0030] In some ~~embodiments~~examples, the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus, and the method further comprises providing the first stimulus, and incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an aldehyde. In one ~~embodiment~~example, the method further comprises extracting the aldehyde from aqueous biomass comprising the culture medium and the population of microbes.

[0031] In some ~~embodiments~~examples, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde, wherein the thioesterase and the reductase act on the same carbon chain length. In some cases, the microbes further contain a third exogenous gene encoding a fatty aldehyde decarbonylase that catalyzes the conversion of the aldehyde to an alkane.

[0032] In some cases, the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus, and the method further comprises providing the first stimulus, and incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an alkane. In some cases, the method further comprises

extracting the alkane from aqueous biomass comprising culture medium and the microbe population.

[0033] In some cases, the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde, and the decarbonylase encoded by the third exogenous gene catalyzes the conversion of an 8 to 18-carbon aldehyde to a corresponding alkane, wherein the thioesterase, the reductase, and the decarbonylase act on the same carbon chain length. In some ~~embodiments~~examples, the microbes further contain a third exogenous gene encoding an acyl carrier protein. In some cases, the third exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase. In some cases, the microbes further contain a fourth exogenous gene encoding a fatty aldehyde decarbonylase that catalyzes the conversion of the aldehyde to an alkane.

[0034] In some methods, the culture medium contains glycerol. In one ~~embodiment~~example, the glycerol is a byproduct of a transesterification process. In some cases, the culture medium contains glycerol and at least one other fixed carbon source. In one ~~embodiment~~example, the at least one other fixed carbon source is sucrose. In some cases, all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation. In some cases, the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation. In one ~~embodiment~~example, glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time, the at least one other fixed carbon source is provided at the end of the first period of time, and the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

[0035] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of producing a fatty acid molecule having a specified carbon chain length in a microbe population. In one ~~embodiment~~example, the method comprises culturing a population of lipid-producing microbes in a culture medium, wherein the microbes contain an exogenous gene encoding a fatty acyl-ACP thioesterase having an activity specific to a carbon chain length, and wherein the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP) and the thioesterase catalyzes the cleavage of the fatty acid from the ACP when the fatty acid has been synthesized to the specific carbon chain length. In some cases, the microbe is *Chlorella minutissima, Chlorella*

emersonii, *Chlorella sorokiniana*, *Chlorella ellipsoidea*, *Chlorella sp.*, or *Chlorella protothecoides*. In other cases, the microbe is another species of microorganism as described herein.

[0036] In some ~~embodiments~~examples, the exogenous gene is in operable linkage with a promoter that is inducible in response to a first stimulus, and the method further comprises providing the first stimulus, and incubating the population of microbes for a period of time in the presence of the first stimulus. In some cases, the method further comprises extracting the fatty acid from aqueous biomass comprising culture medium and the microbe population.

[0037] In some cases, the microbes further contain a second exogenous gene encoding an acyl carrier protein. In some ~~embodiments~~examples, the second exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase. In one ~~embodiment~~example, the acyl-ACP thioesterase catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP.

[0038] In some cases, the culture medium contains glycerol. In one ~~embodiment~~example, the glycerol is a byproduct of a transesterification process. In some ~~embodiments~~examples, the culture medium contains glycerol and at least one other fixed carbon source. In one ~~embodiment~~example, the at least one other carbon source is sucrose. In some cases, all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation. In some cases, the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation. In one ~~embodiment~~example, glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time, the at least one other fixed carbon source is provided at the end of the first period of time, and the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

[0039] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microalgae cell containing an exogenous gene, wherein the exogenous gene encodes a protein selected from the group consisting of a lipase, a sucrose transporter, a sucrose invertase, a fructokinase, or a polysaccharide-degrading enzyme. In some cases, the cell is *Chlorella minutissima*, *Chlorella emersonii*, *Chlorella sorokiniana*, *Chlorella ellipsoidea*, *Chlorella sp.*, or *Chlorella protothecoides*. In other cases, the cell is another species of microalgae as described herein.

[0040] In some cases, the exogenous gene is in operable linkage with a promoter. In some cases, the promoter is inducible or repressible in response to a stimulus. In various

~~embodiments~~examples, the stimulus is selected from the group consisting of an exogenously provided small molecule, heat, cold, and light. In some cases, the exogenous gene is expressed in a cellular compartment. In some ~~embodiments~~examples, the cellular compartment is selected from the group consisting of a chloroplast and a mitochondrion.

[0041] In some cases, the gene encodes a lipase that has at least 70% amino acid identity with a lipase selected from Table 9. In one ~~embodiment~~example, the lipase is novozym-435. In one ~~embodiment~~example, the polysaccharide-degrading enzyme is endogenous to a *Chlorella* virus.

[0042] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microalgae cell containing two exogenous genes, wherein a first exogenous gene encodes a lipase and a second exogenous gene encodes a polysaccharide-degrading enzyme. In some cases, the exogenous genes are each in operable linkage with a promoter. In some cases, the exogenous genes are each in operable linkage with promoters that are inducible in response to a stimulus. In some cases, the exogenous genes are each in operable linkage with promoters that are inducible in response to the same stimulus. In some cases, the exogenous genes are each in operable linkage with a promoter that is inducible in response to at least one stimulus that does not induce the other promoter.

[0043] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of manufacturing a lipid molecule in a microbe. In one ~~embodiment~~example, the method comprises (a) culturing the microbe for a first period of time sufficient to increase the cell density, wherein the microbe contains (i) an exogenous gene encoding a lipase, and/or (ii) an exogenous gene encoding a polysaccharide-degrading enzyme,wherein the exogenous gene(s) are in operable linkage with a promoter that is inducible in response to a stimulus, (b) providing the stimulus, and (c) incubating the microbe for a second period of time in the presence of the stimulus.

[0044] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of manufacturing a lipid molecule in a microbe. In one ~~embodiment~~example, the method comprises (a) culturing a lipid-producing microbe for a first period of time sufficient to increase the cell density, (b) providing a virus capable of infecting and lysing the microbe when in direct contact with the microbe, and (c) incubating the microbe for a second period of time to produce lysed aqueous biomass. In one ~~embodiment~~example, the method further compries extracting lipid molecules from the lysed aqueous biomass.

[0045] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microalgae cell containing an exogenous gene, wherein the exogenous gene encodes a cofactor for a lipid pathway enzyme or encodes a protein that participates in the synthesis of the cofactor.

[0046] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of culturing a lipid-producing microbe. In one ~~embodiment~~example, the method comprises culturing the microbe in the presence of a sufficient amount of one or more cofactor(s) for a lipid pathway enzyme to increase microbial lipid yield over microbial lipid yield in the absence of said one or more cofactors. In some cases, the one or more cofactors is a vitamin required by one or more lipid pathway enzymes. In one ~~embodiment~~example, the one or more cofactors is biotin. In some cases, the one or more cofactors is/are provided by including in the culture a microbe that has been genetically engineered to produce the one or more cofactors.

[0047] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of fermenting a microorganism, which comprises providing a mixture comprising glucose and xylose as an energy source to the microorganism. In one ~~embodiment~~example, the mixture further comprises lignin. In one ~~embodiment~~example, the mixture further comprises at least one species of furfural. In some cases, the mixture is depolymerized cellulosic material. In some cases, the mixture further comprises as least one sucrose utilization enzyme. In one ~~embodiment~~example, the mixture comprises a sucrose invertase.

[0048] In some cases, the microorganism is selected from the group consisting of *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana, Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis,* and *Pseudochlorella aquatica.* In other cases, the microorganism is another species of microorganism as described herein. In some cases, the microorganism has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme.

[0049] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of culturing a microalgae, which comprises culturing the microalgae in a culture medium including a feedstock comprising at least one carbon substrate selected from the group consisting of a cellulosic material, a 5-carbon sugar, a 6-carbon sugar, and acetate. In some cases, the carbon substrate is glucose and the microalgae is of a genus selected from the group

consisting of *Chlorella, Parachlorella, Pseudochlorella, Bracteococcus, Prototheca* and *Scenedesmus*. In some cases, the carbon substrate is xylose and the microalgae is of a genus selected from the group consisting of *Chlorella, Pseudochlorella,* and *Prototheca*. In some cases, the carbon substrate is sucrose and the microalgae is of a genus selected from the group consisting of *Chlorella,* and *Bracteococcus*. In some cases, the carbon substrate is fructose and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella, Prototheca,* and *Scenedesmus*. In some cases, the carbon substrate is arabinose and the microalgae is *Chlorella sp.* In some cases, the carbon substrate is mannose and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella, Bracteococcus, Prototheca,* and *Scenedesmus*. In some cases, the carbon substrate is galactose and the microalgae is of a genus selected from the group consisting of *Bracteococcus, Parachlorella, , Chlorella, Pseudochlorella, Bracteococcus,* and *Prototheca*. In some cases, the carbon substrate is acetate and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella,* and *Prototheca*.

[0050] In one ~~embodiment~~example, the culture medium further includes at least one sucrose utilization enzyme. In some cases, the microalgae has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme. In some cases, the culture medium includes a sucrose invertase.

[0051] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of culturing microalgae comprising placing a plurality of microalgae cells in the presence of depolymerized cellulosic material. In some cases, the microalgae are cultured in the presence of an additional fixed carbon source selected from the group consisting of glycerol, sucrose, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing. In one ~~embodiment~~example, the microalgae are cultured in the presence of at least one sucrose utilization enzyme.

[0052] In some cases, the microalgae is selected from a species of the genus *Bracteococcus,* a species of the genus *Chlorella,* a species of the genus *Parachlorella,* a species of the genus *Prototheca,* or a species of the genus *Pseudochlorella*. In some cases, the microalgae is selected from *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana,*

Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis, and *Pseudochlorella aquatica*. In other cases, the microalgae is another species of microalgae as described herein.

[0053] In some ~~embodiments~~examples, the microalgae has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme. In one ~~embodiment~~example, the at least one sucrose utilization enzyme is a sucrose invertase. In some cases, the at least one lipid modification enzyme is selected from a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, and a glycerol-3 phosphate acyltransferase. In some cases, the at least one hydrocarbon modification enzyme is selected from a fatty acyl-ACP thioesterase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty acyl-CoA/aldehyde reductase, a fatty aldehyde decarbonylase, and an acyl carrier protein.

[0054] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of culturing a lipid-producing microbe, the method comprising culturing the microbe in the presence of acetic acid and the absence of a fixed nitrogen source. In some cases, the microbe is cultured in the presence of a sufficient amount of acetic acid to increase microbial lipid yield over microbial lipid yield in the absence of acetic acid, wherein culture conditions are otherwise the same between the two cultures.

[0055] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microbial culture containing a population of microorganisms and a culture medium comprising glucose, xylose, and a molecule selected from the group consisting of lignin and a species of furfural. In some cases, the microorganisms are selected from *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana, Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis,* and *Pseudochlorella aquatica*. In other cases, the microorganisms are another species of microorganism as described herein.

[0056] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of cultivating microalgae. In one ~~embodiment~~example, the method comprises (a) providing a microalgae cell capable of performing heterotrophic growth, (b) placing the microalgae cell in growth media, wherein the growth media comprises depolymerized cellulosic material, and (c) incubating the microalgae for a period of time sufficient to allow the cell to grow.

[0057] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of biodiesel manufacturing. In one ~~embodiment~~example, the method comprises (a) culturing a lipid-producing microorganism in a first microbial culture, (b) recovering lipid from the biomass produced by the first microbial culture, (c) subjecting the lipid to transesterification to produce fatty acid ester(s) and glycerol, and (d) adding the glycerol to a second microbial culture. In some cases, the first and second microbial cultures are cultures of the same species of microorganism. In some cases, the second microbial culture comprises microorganisms selected from the group consisting of *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.*, and *Chlorella sorokiniana*. In other cases, the second microbial culture comprises another species of microorganism as described herein.

[0058] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of fermentation comprising culturing a microorganism in the presence of glycerol and at least one other fixed carbon source. In some cases, the glycerol and the at least one other fixed carbon source are provided to the microorganism simultaneously at a predetermined ratio. In some cases, all of the glycerol and the at least one other fixed carbon source are provided to the microorganism at the beginning of the fermentation. In some cases, all of the glycerol and the at least one other fixed carbon source are fed to the microorganism at a predetermined rate over the course of the fermentation. In one ~~embodiment~~example of the method, glycerol is provided to the microorganism in the absence of the at least one other fixed carbon source for a first period of time, the at least one other fixed carbon source is provided at the end of the first period of time, and the microorganism is cultured for a second period of time in the presence of the at least one other fixed carbon source. In one ~~embodiment~~example, the at least one other fixed carbon source is fed to the microorganism at a predetermined rate during the second period of time. In some cases, all of the at least one other fixed carbon source is provided to the microorganism at the end of the first period of time. In one ~~embodiment~~example of the method, the at least one other fixed carbon source is provided to the microorganism in the absence of glycerol for a first period of time, glycerol is provided at the end of the first period of time, and the microorganism is cultured for a second period of time in the presence of glycerol. In one ~~embodiment~~example, the glycerol is a byproduct of a transesterification process. In one ~~embodiment~~example, the glycerol is acidulated. In another ~~embodiment~~example, the glycerol is non-acidulated. In some cases, the at least one other fixed carbon source is glucose. In some

cases, the at least one other fixed carbon source is depolymerized cellulosic material. In one ~~embodiment~~example, the at least one other fixed carbon source is sucrose.

[0059] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a fermentor comprising a population of microorganisms, glycerol, and at least one sugar selected from the group consisting of xylose, glucose, and sucrose. In one ~~embodiment~~example, the glycerol is a byproduct of a lipid transesterification process. In some cases, the microorganisms are selected from the group consisting of *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.,* and *Chlorella sorokiniana.* In other cases, the microorganisms are another species as described herein.

[0060] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a method of fermenting a microorganism. In one ~~embodiment~~example, the method comprises providing byproduct glycerol from a transesterification process as a sole source of fixed carbon energy. In one ~~embodiment~~example, no light energy is provided to the microorganism. In another ~~embodiment~~example, light energy is provided to the microorganism. In some cases, the microorganism is selected from *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.,* and *Chlorella sorokiniana.* In other cases, the microorganism is another species as described herein.

[0061] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microorganism containing an exogenous sucrose utilization gene. In one ~~embodiment~~example, the gene encodes a sucrose transporter. In one ~~embodiment~~example, the gene encodes a sucrose invertase. In one ~~embodiment~~example, the gene encodes a fructokinase. In some cases, the microorganism is a species selected from the group consisting of *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*. In other cases, the microorganism is another species as described herein.

[0062] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a cell of the species *Chlorella protothecoides, Chlorella emersonii, or Chlorella minutissima* wherein the cell contains an exogenous gene. In some cases, the exogenous gene encodes a protein selected from the group consisting of a sucrose transporter, a sucrose invertase, a lipid modification enzyme, a hydrocarbon modification enzyme and a fructokinase. In some ~~embodiments~~examples, the protein is a sucrose invertase secreted into the extracellular space. In some ~~embodiments~~examples, the protein is a sucrose invertase targeted to the cytoplasm.

[0063] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microbial culture containing a population of microorganisms, and a culture medium comprising (i) sucrose and (ii) a sucrose invertase enzyme.

[0064] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microbial culture containing a population of microorganisms, and a culture medium comprising (i) molasses and (ii) a sucrose invertase enzyme.

[0065] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a microbial culture containing a population of microorganisms, and a culture medium comprising (i) sucrose, (ii) lignin, and (iii) a sucrose invertase enzyme.

[0066] In the various microbial cultures described above, the microorganisms contain at least one exogenous sucrose utilization gene. In some ~~embodiments~~examples, the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase. In one ~~embodiment~~example, the sucrose invertase enzyme is a secrectable sucrose invertase enzyme encoded by an exogenous sucrose invertase gene expressed by the population of microorganisms. In some cases, the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme or a hydrocarbon modification enzyme.

[0067] In another ~~aspect~~example, the present ~~invention~~disclosure is directed to a nucleic acid comprising a cDNA encoding a sucrose utilization gene, and a cDNA encoding a protein conferring resistance to the antibiotic hygromycin or the antibiotic G418.

[0068] In ~~embodiments~~examples of the various methods, compositions, cells, microorganisms, microbes, microbial cultures, fermentors, and the like, described above, the microorganism or microbe can be a microalgae, an oleaginous yeast, a fungus, or a bacterium, unless otherwise specified. In some cases, the microorganism is selected from the group consisting of the microalgae listed in Table 1. In some cases, the microorganism is a species of the genus *Chlorella*. In some cases, the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella*

protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis*. In some cases, the microorganism is an oleaginous yeast selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica*. In some cases, the microorganism is a fungus selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

[0069] In the various ~~embodiments~~examples described above, the microorganism can contain at least one exogenous sucrose utilization gene. In some cases, the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

[0070] In the various ~~embodiments~~examples described above, the microorganism can contain at least one exogenous gene encoding a lipid pathway enzyme. In some cases, the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

[0071] In the various ~~embodiments~~examples described above, the microorganism can contain at least one exogenous gene encoding a hydrocarbon modification enzyme. In some cases, the hydrocarbon modification enzyme is selected from the group consisting of a fatty acyl-ACP thioesterase, a fatty acyl-CoA/aldehyde reductase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty aldehyde decarbonylase, and/or an acyl carrier protein.

[0072] Any two or more of the various ~~embodiments~~examples described above can be combined together to produce additional ~~embodiments~~examples encompassed within the scope of the present ~~invention~~disclosure.

WHAT IS CLAIMED IS:

1. A method of producing renewable diesel, comprising:

(a) culturing a population of microorganisms in the presence of a fixed carbon source, wherein:

(i) the microorganisms accumulate at least 10% of their dry cell weight as lipid; and

(ii) the fixed carbon source is selected from the group consisting of glycerol, depolymerized cellulosic material, sucrose, molasses, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing;

(b) isolating lipid components from the cultured microorganisms; and

(c) subjecting the isolated lipid components to one or more chemical reactions to generate straight chain alkanes,

whereby renewable diesel is produced.

2. The method of claim 1, wherein the microorganism is a microalgae.

3. The method of claim 2, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

4. The method of claim 3, wherein the microorganism is a species of the genus *Chlorella*.

5. The method of claim 4, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis,*

Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

6. The method of claim 1, wherein the microorganism is an oleaginous yeast.

7. The method of claim 6, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

8. The method of claim 1, wherein the microorganism is a fungus.

9. The method of claim 8, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

10. The method of claim 1, wherein the microorganism contains at least one exogenous sucrose utilization gene.

11. The method of claim 10, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

12. The method of claim 1, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

13. The method of claim 12, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

14. A method of producing jet fuel, comprising:

(a) culturing a population of microorganisms in the presence of a fixed carbon source, wherein:

(i) the microorganisms accumulate at least 10% of their dry cell weight as lipid; and

(ii) the fixed carbon source is selected from the group consisting of glycerol, depolymerized cellulosic material, sucrose, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing;

(b) isolating lipid components from the cultured microorganisms; and

(c) subjecting the isolated lipid components to one or more chemical reactions to generate straight chain alkanes,

whereby jet fuel is produced.

15. The method of claim 14, wherein the microorganism is a microalgae.

16. The method of claim 15, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

17. The method of claim 16, wherein the microorganism is a species of the genus *Chlorella*.

18. The method of claim 17, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis*.

19. The method of claim 14, wherein the microorganism is an oleaginous yeast.

20. The method of claim 19, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

21. The method of claim 14, wherein the microorganism is a fungus.

22. The method of claim 21, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo,* a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

23. The method of claim 14, wherein the microorganism contains at least one exogenous sucrose utilization gene.

24. The method of claim 23, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

25. The method of claim 14, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

26. The method of claim 25, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

27. A composition of liquid hydrocarbons made according to the method of claim 1, wherein the composition conforms to the specifications of ASTM D975.

28. The composition of claim 27, wherein the microorganism is a microalgae.

29. The composition of claim 28, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

30. The composition of claim 29, wherein the microorganism is a species of the genus *Chlorella*.

31. The composition of claim 30, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella reguläris, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis*.

32. The composition of claim 27, wherein the microorganism is an oleaginous yeast.

33. The composition of claim 32, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica*.

34. The composition of claim 27, wherein the microorganism is a fungus.

35. The composition of claim 34, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

36. The composition of claim 27, wherein the microorganism contains at least one exogenous sucrose utilization gene.

37. The composition of claim 36, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

38. The composition of claim 27, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

39. The composition of claim 38, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

40. A composition of liquid hydrocarbons produced according to the method of claim 14, wherein the composition conforms to the specifications of ASTM D1655.

41. The composition of claim 40, wherein the microorganism is a microalgae.

42. The composition of claim 41, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

43. The composition of claim 42, wherein the microorganism is a species of the genus *Chlorella*.

44. The composition of claim 43, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella*

saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

45. The composition of claim 40, wherein the microorganism is an oleaginous yeast.

46. The composition of claim 45, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

47. The composition of claim 40, wherein the microorganism is a fungus.

48. The composition of claim 47, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

49. The composition of claim 40, wherein the microorganism contains at least one exogenous sucrose utilization gene.

50. The composition of claim 49, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

51. The composition of claim 40, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

52. The composition of claim 51, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

53. A microalgae or yeast cell that has been genetically engineered and/or selected to express a lipid pathway enzyme at an altered level compared to a wild-type cell of the same species.

54. The cell of claim 53, wherein the cell produces more lipid compared to the wild-type cell when both cells are grown under the same conditions.

55. The cell of claim 53, wherein the cell has been genetically engineered and/or selected to express a lipid pathway enzyme at a higher level than the wild-type cell.

56. The cell of claim 55, wherein the lipid pathway enzyme is selected from the group consisting of pyruvate dehydrogenase, acetyl-CoA carboxylase, acyl carrier protein, and glycerol-3 phosphate acyltransferase.

57. The cell of claim 53, wherein the cell has been genetically engineered and/or selected to express a lipid pathway enzyme at a lower level than the wild-type cell.

58. The cell of claim 57, wherein the lipid pathway enzyme comprises citrate synthase.

59. The cell of claim 53, wherein the cell has been genetically engineered and/or selected to express a global regulator of fatty acid synthesis at an altered level compared to the wild-type cell, whereby the expression levels of a plurality of fatty acid synthetic genes are altered compared to the wild-type cell.

60. The cell of claim 53, wherein the lipid pathway enzyme comprises an enzyme that modifies a fatty acid.

61. The cell of claim 60, wherein the lipid pathway enzyme is selected from a stearoyl-ACP desaturase and a glycerolipid desaturase.

62. The cell of claim 53, wherein the cell is a microalgae species selected from Table 1.

63. The microalgae cell of claim 62, wherein the microalgae is of the genus *Chlorella*.

64. The microalgae cell of claim 63, wherein the microalgae is of the species selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis*.

65. An oil-producing microbe containing one or more exogenous genes, wherein the exogenous genes encode protein(s) selected from the group consisting of a fatty acyl-ACP thioesterase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty acyl-CoA/aldehyde reductase, a fatty aldehyde decarbonylase, and an acyl carrier protein.

66. The microbe of claim 65, wherein the microbe is a microalgae.

67. The microbe of claim 65, wherein the microbe is an oleaginous yeast.

68. The microbe of claim 67, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

69. The microbe of claim 65, wherein the microbe is a fungus.

70. The microbe of claim 69, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus*

terreus, Pennicillium iilacinum, a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

71. The microbe of claim 65, wherein the microbe is selected from the group consisting of the microorganisms listed in Table 1.

72. The microbe of claim 71, wherein the microbe is a species of the genus *Chlorella*.

73. The microbe of claim 72, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis*.

74. The microbe of claim 73, wherein the species is *Chlorella protothecoides, Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea,* or *Chlorella sp.*

75. The microbe of claim 65, wherein the exogenous gene is in operable linkage with a promoter, which is inducible or repressible in response to a stimulus.

76. The microbe of claim 75, wherein the stimulus is selected from the group consisting of an exogenously provided small molecule, heat, cold, and light.

77. The microbe of claim 65, wherein the exogenous gene is expressed in a cellular compartment.

78. The microbe of claim 77, wherein the cellular compartment is selected from the group consisting of a chloroplast and a mitochondrion.

79. The microbe of claim 65, wherein the exogenous gene encodes a fatty acid acyl-ACP thioesterase.

80. The microbe of claim 79, wherein the thioesterase encoded by the exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an acyl carrier protein (ACP).

81. The microbe of claim 80, wherein the thioesterase encoded by the exogenous gene catalyzes the cleavage of a 10 to 14-carbon fatty acid from an ACP.

82. The microbe of claim 81, wherein the thioesterase encoded by the exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from an ACP.

83. The microbe of claim 65, wherein the exogenous gene encodes a fatty acyl-CoA/aldehyde reductase.

84. The microbe of claim 83, wherein the reductase encoded by the exogenous gene catalyzes the reduction of a 20 to 30-carbon fatty acyl-CoA to a corresponding primary alcohol.

85. The microbe of claim 83, wherein the reductase encoded by the exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol.

86. The microbe of claim 85, wherein the reductase encoded by the exogenous gene catalyzes the reduction of a 10 to 14-carbon fatty acyl-CoA to a corresponding primary alcohol.

87. The microbe of claim 86, wherein the reductase encoded by the exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol.

88. The microbe of claim 65, wherein the exogenous gene encodes a fatty acyl-CoA reductase.

89. The microbe of claim 88, wherein the reductase encoded by the exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde.

90. The microbe of claim 89, wherein the reductase encoded by the exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanal.

91. The microbe of claim 65, wherein the microbe further contains one or more exogenous sucrose utilization genes.

92. A microbe containing two exogenous genes, wherein a first exogenous gene encodes a fatty acyl-ACP thioesterase and a second exogenous gene encodes a protein selected from the group consisting of a fatty acyl-CoA reductase, a fatty acyl-CoA/aldehyde reductase, and an acyl carrier protein.

93. The microbe of claim 92, wherein the microbe is a microalgae.

94. The microbe of claim 92, wherein the microbe is an oleaginous yeast.

95. The microbe of claim 94, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

96. The microbe of claim 92, wherein the microbe is a fungus.

97. The microbe of claim 96, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Penniciltium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

98. The microbe of claim 92, wherein the microbe is selected from the group consisting of the microorganisms listed in Table 1.

99. The microbe of claim 98, wherein the microbe is a species of the genus *Chlorella*.

100. The microbe of claim 99, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis*.

101. The microbe of claim 100, wherein the species is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*.

102. The microbe of claim 92, wherein the two exogenous genes are each in operable linkage with a promoter, which is inducible in response to a stimulus.

103. The microbe of claim 102, wherein each promoter is inducible in response to an identical stimulus.

104. The microbe of claim 92, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an ACP.

105. The microbe of claim 104, wherein the second exogenous gene encodes a fatty acyl-CoA/aldehyde reductase which catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol.

106. The microbe of claim 105, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 10 to 14-carbon fatty acid from an ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of a 10 to 14-carbon fatty acyl-CoA to the corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length.

107. The microbe of claim 106, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from an ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol.

108. The microbe of claim 104, wherein the second exogenous gene encodes a fatty acyl-CoA reductase which catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde.

109. The microbe of claim 92, wherein the second exogenous gene encodes a fatty acyl-CoA reductase, and the microbe further contains a third exogenous gene encoding a fatty aldehyde decarbonylase.

110. The microbe of claim 109, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from an ACP, the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding fatty aldehyde, and the decarbonylase encoded by the third exogenous gene catalyzes the conversion of an 8 to 18-carbon fatty aldehyde to a corresponding alkane, wherein the thioesterase, the reductase, and the decarbonylase act on the same carbon chain length.

111. The microbe of claim 92, wherein the microbe further contains one or more exogenous sucrose utilization genes.

112. The microbe of claim 92, wherein the second exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

113. The microbe of claim 92, wherein the second exogenous gene encodes an acyl carrier protein, and the microbe further contains a third exogenous gene encoding a

protein selected from the group consisting of a fatty acyl-CoA reductase and a fatty acyl-CoA/aldehyde reductase.

114. The microbe of claim 113, wherein the third exogenous gene encodes a fatty acyl-CoA reductase, and the microbe further contains a fourth exogenous gene encoding a fatty aldehyde decarbonylase.

115. A method of producing a molecule in a microbe population, the method comprising culturing a population of microbes in a culture medium, wherein the microbes contain:

(i) a first exogenous gene encoding a fatty acyl-ACP thioesterase, and

(ii) a second exogenous gene encoding a fatty acyl-CoA/aldehyde reductase; and

wherein the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP), the fatty acyl-ACP thioesterase catalyzes the cleavage of the fatty acid from the ACP to yield, through further processing, a fatty acyl-CoA, and the fatty acyl-CoA/aldehyde reductase catalyzes the reduction of the acyl-CoA to an alcohol.

116. The method of claim 115, wherein the microbe is a microalgae.

117. The method of claim 115, wherein the microbe is an oleaginous yeast.

118. The method of claim 117, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica*.

119. The method of claim 115, wherein the microbe is a fungus.

120. The method of claim 119, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Penniciilium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

121. The method of claim 115, wherein the microbe is selected from the group consisting of the microorganisms listed in Table 1.

122. The method of claim 121, wherein the microbe is a species of the genus *Chlorella*.

123. The method of claim 122, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis*.

124. The method of claim 123, wherein the species is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.* or *Chlorella protothecoides*.

125. The method of claim 115, wherein the culture medium contains glycerol.

126. The method of claim 125, wherein the glycerol is a byproduct of a transesterification process.

127. The method of claim 125, wherein the culture medium contains glycerol and at least one other fixed carbon source.

128. The method of claim 127, wherein the at least one other fixed carbon source is sucrose.

129. The method of claim 127, wherein all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation.

130. The method of claim 127, wherein the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation.

131. The method of claim 127, wherein:

(a) glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time;

(b) the at least one other fixed carbon source is provided at the end of the first period of time; and

(c) the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

132. The method of claim 115, wherein the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus, and wherein the method further comprises:

providing the first stimulus; and

incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an alcohol.

133. The method of claim 132, further comprising extracting the alcohol from aqueous biomass.

134. The method of claim 115, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length.

135. The method of claim 134, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 10 to 14-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 10 to 14-carbon fatty acyl-CoA to a corresponding primary alcohol, wherein the thioesterase and the reductase act on the same carbon chain length.

136. The method of claim 135, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of a 12-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of a 12-carbon fatty acyl-CoA to dodecanol.

137. The method of claim 115, wherein the microbes further contain a third exogenous gene encoding an acyl carrier protein.

138. The method of claim 137, wherein the third exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

139. A method of producing a lipid molecule in a microbe population, the method comprising culturing a population of microbes in a culture medium, wherein the microbes contain:

(i) a first exogenous gene encoding a fatty acyl-ACP thioesterase, and

(ii) a second exogenous gene encoding a fatty acyl-CoA reductase; and

wherein the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP), the fatty acyl-ACP thioesterase catalyzes the cleavage of the fatty acid from the ACP to yield, through further processing, a fatty acyl-CoA, and the fatty acyl-CoA reductase catalyzes the reduction of the acyl-CoA to an aldehyde.

140. The method of claim 139, wherein the microbe is a microalgae.

141. The method of claim 139, wherein the microbe is an oleaginous yeast.

142. The method of claim 139, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

143. The method of claim 139, wherein the microbe is a fungus.

144. The method of claim 143, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

145. The method of claim 139, wherein the microbe is selected from the group consisting of the microorganisms listed in Table 1.

146. The method of claim 145, wherein the microbe is a species of the genus *Chlorella*.

147. The method of claim 146, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis*.

148. The method of claim 147, wherein the species is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*.

149. The method of claim 139, wherein the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus, and wherein the method further comprises:

providing the first stimulus; and

incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an aldehyde.

150. The method of claim 149, further comprising extracting the aldehyde from aqueous biomass.

151. The method of claim 139, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, and the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde, wherein the thioesterase and the reductase act on the same carbon chain length.

152. The method of claim 139, wherein the microbes further contain a third exogenous gene encoding a fatty aldehyde decarbonylase that catalyzes the conversion of the aldehyde to an alkane.

153. The method of claim 152, wherein the exogenous genes are in operable linkage with a promoter that is inducible in response to a first stimulus, and wherein the method further comprises:

providing the first stimulus; and

incubating the population of microbes for a first period of time in the presence of the first stimulus to produce an alkane.

154. The method of claim 153, further comprising extracting the alkane from aqueous biomass.

155. The method of claim 152, wherein the thioesterase encoded by the first exogenous gene catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP, the reductase encoded by the second exogenous gene catalyzes the reduction of an 8 to 18-carbon fatty acyl-CoA to a corresponding aldehyde, and the decarbonylase encoded by the third exogenous gene catalyzes the conversion of an 8 to 18-carbon aldehyde to a corresponding alkane, wherein the thioesterase, the reductase, and the decarbonylase act on the same carbon chain length.

156. The method of claim 139, wherein the microbes further contain a third exogenous gene encoding an acyl carrier protein.

157. The method of claim 156, wherein the third exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

158. The method of claim 156, wherein the microbes further contain a fourth exogenous gene encoding a fatty aldehyde decarbonylase that catalyzes the conversion of the aldehyde to an alkane.

159. The method of claim 139, wherein the culture medium contains glycerol.

160. The method of claim 159, wherein the glycerol is a byproduct of a transesterification process.

161. The method of claim 159, wherein the culture medium contains glycerol and at least one other fixed carbon source.

162. The method of claim 161, wherein the at least one other fixed carbon source is sucrose.

163. The method of claim 161, wherein all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation.

164. The method of claim 161, wherein the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation.

165. The method of claim 161, wherein:

(a) glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time;

(b) the at least one other fixed carbon source is provided at the end of the first period of time; and

(c) the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

166. A method of producing a fatty acid molecule having a specified carbon chain length in a microbe population, the method comprising culturing a population of lipid-producing microbes in a culture medium, wherein the microbes contain an exogenous gene encoding a fatty acyl-ACP thioesterase having an activity specific to a carbon chain length, and wherein the microbes synthesize a fatty acid linked to an acyl carrier protein (ACP) and the thioesterase catalyzes the cleavage of the fatty acid from the ACP when the fatty acid has been synthesized to the specific carbon chain length.

167. The method of claim 166, wherein the microbe is a microalgae.

168. The method of claim 166, wherein the microbe is an oleaginous yeast.

169. The method of claim 168, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

170. The method of claim 166, wherein the microbe is a fungus.

171. The method of claim 170, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

172. The method of claim 166, wherein the microbe is selected from the group consisting of the microorganisms listed in Table 1.

173. The method of claim 172, wherein the microbe is a species of the genus *Chlorella.*

174. The method of claim 173, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila,*

Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and Chlorella zofingiensis.

175. The method of claim 174, wherein the species is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides.*

176. The method of claim 166, wherein the exogenous gene is in operable linkage with a promoter that is inducible in response to a first stimulus, and wherein the method further comprises:

providing the first stimulus; and

incubating the population of microbes for a period of time in the presence of the first stimulus.

177. The method of claim 176, further comprising extracting the fatty acid from the aqueous biomass.

178. The method of claim 166, wherein the microbes further contain a second exogenous gene encoding an acyl carrier protein.

179. The method of claim 178, wherein the second exogenous gene encodes an acyl carrier protein that is naturally co-expressed with the fatty acyl-ACP thioesterase.

180. The method of claim 166, wherein the acyl-ACP thioesterase catalyzes the cleavage of an 8 to 18-carbon fatty acid from the ACP.

181. The method of claim 166, wherein the culture medium contains glycerol.

182. The method of claim 181, wherein the glycerol is a byproduct of a transesterification process.

183. The method of claim 181, wherein the culture medium contains glycerol and at least one other fixed carbon source.

184. The method of claim 183, wherein the at least one other carbon source is sucrose.

185. The method of claim 183, wherein all of the glycerol and all of the at least one other fixed carbon source are provided to the microbes at the beginning of fermentation.

186. The method of claim 183, wherein the glycerol and the at least one other fixed carbon source are fed to the microbes at a predetermined rate over the course of fermentation.

187. The method of claim 183, wherein:

(a) glycerol is provided to the microbes in the absence of the at least one other fixed carbon source for a first period of time;

(b) the at least one other fixed carbon source is provided at the end of the first period of time; and

(c) the microbes are cultured for a second period of time in the presence of the at least one other fixed carbon source.

188. A microalgae cell containing an exogenous gene, wherein the exogenous gene encodes a protein selected from the group consisting of a lipase, a sucrose transporter, a sucrose invertase, a fructokinase, or a polysaccharide-degrading enzyme.

189. The microalgae cell of claim 188, wherein the cell is selected from the microorganisms in Table 1.

190. The microalgae cell of claim 189, wherein the cell is a species of the genus *Chlorella*.

191. The microalgae cell of claim 190, wherein the species is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis,*

Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

192. The microalgae cell of claim 191, wherein the cell is *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides.*

193. The microalgae cell of claim 188, wherein the exogenous gene is in operable linkage with a promoter.

194. The microalgae cell of claim 193, wherein the promoter is inducible or repressible in response to a stimulus.

195. The microalgae cell of claim 194, wherein the stimulus is selected from the group consisting of an exogenously provided small molecule, heat, cold, and light.

196. The microalgae cell of claim 188, wherein the exogenous gene is expressed in a cellular compartment.

197. The microalgae cell of claim 196, wherein the cellular compartment is selected from the group consisting of a chloroplast and a mitochondrion.

198. The microalgae cell of claim 188, wherein the gene encodes a lipase that has at least 70% amino acid identity with a lipase selected from Table 9.

199. The microalgae cell of claim 198, wherein the lipase is novozym-435.

200. The microalgae cell of claim 188, wherein the gene encodes a polysaccharide-degrading enzyme.

201. The microalgae cell of claim 200, wherein the polysaccharide-degrading enzyme is endogenous to a *Chlorella* virus.

202. A microalgae cell containing two exogenous genes, wherein a first exogenous gene encodes a lipase and a second exogenous gene encodes a polysaccharide-degrading enzyme.

203. The microalgae cell of claim 202, wherein the exogenous genes are each in operable linkage with a promoter.

204. The microalgae cell of claim 203, wherein the exogenous genes are each in operable linkage with promoters that are inducible in response to a stimulus.

205. The microalgae cell of claim 204, wherein the exogenous genes are each in operable linkage with promoters that are inducible in response to the same stimulus.

206. The microalgae cell of claim 204, wherein the exogenous genes are each in operable linkage with a promoter that is inducible in response to at least one stimulus that does not induce the other promoter.

207. A method of manufacturing a lipid molecule in a microbe, the method comprising:

(a) culturing the microbe for a first period of time sufficient to increase the cell density, wherein the microbe contains:

(i) an exogenous gene encoding a lipase; and/or

(ii) an exogenous gene encoding a polysaccharide-degrading enzyme;

wherein the exogenous gene(s) are in operable linkage with a promoter that is inducible in response to a stimulus;

(b) providing the stimulus; and

(c) incubating the microbe for a second period of time in the presence of the stimulus.

208. A method of manufacturing a lipid molecule in a microbe, the method comprising:

(a) culturing a lipid-producing microbe for a first period of time sufficient to increase the cell density;

(b) providing a virus capable of infecting and lysing the microbe when in direct contact with the microbe; and

(c) incubating the microbe for a second period of time to produce lysed aqueous biomass.

209. The method of claim 208, further comprising the step of extracting lipid molecules from the lysed aqueous biomass.

210. A microalgae cell containing an exogenous gene, wherein the exogenous gene encodes a cofactor for a lipid pathway enzyme or encodes a protein that participates in the synthesis of the cofactor.

211. A method of culturing a lipid-producing microbe, the method comprising culturing the microbe in the presence of a sufficient amount of one or more cofactor(s) for a lipid pathway enzyme to increase microbial lipid yield over microbial lipid yield in the absence of said one or more cofactors.

212. The method of claim 211, wherein said one or more cofactors is a vitamin required by one or more lipid pathway enzymes.

213. The method of claim 211, wherein said one or more cofactors is biotin.

214. The method of claim 211, wherein said one or more cofactors is/are provided by including in the culture a microbe that has been genetically engineered to produce said one or more cofactors.

215. A method of fermenting a microorganism comprising providing a mixture comprising glucose and xylose as an energy source to the microorganism.

216. The method of claim 215, wherein the mixture further comprises lignin.

217. The method of claim 215, wherein the mixture further comprises at least one species of furfural.

218. The method of claim 215, wherein the mixture is depolymerized cellulosic material.

219. The method of claim 215, wherein the microorganism is a microalgae.

220. The method of claim 219, wherein the microalgae is selected from Table 1.

221. The method of claim 220, wherein the microalgae is a species of the genus *Chlorella*.

222. The method of claim 221, wherein the microalgae is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis*.

223. The method of claim 220, wherein the microalgae is selected from the group consisting of *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana, Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis,* and *Pseudochlorella aquatica*.

224. The method of claim 215, wherein the microorganism is an oleaginous yeast.

225. The method of claim 224, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

226. The method of claim 215, wherein the microorganism is a fungus.

227. The method of claim 226, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

228. The method of claim 215, wherein the mixture further comprises at least one sucrose utilization enzyme.

229. The method of claim 228, wherein the microorganism is of the genus *Chlorella.*

230. The method of claim 215, wherein the microorganism has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme.

231. The method of claim 228, wherein the mixture comprises a sucrose invertase.

232. A method of culturing a microalgae comprising culturing the microalgae in a culture medium including a feedstock comprising at least one carbon substrate selected from the group consisting of a cellulosic material, a 5-carbon sugar, a 6-carbon sugar, and acetate.

233. The method of claim 232, wherein the carbon substrate is glucose and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella, Pseudochlorella, Bracteococcus, Prototheca* and *Scenedesmus*.

234. The method of claim 232, wherein the carbon substrate is xylose and the microalgae is of a genus selected from the group consisting of *Chlorella, Pseudochlorella,* and *Prototheca.*

235. The method of claim 232, wherein the carbon substrate is sucrose and the microalgae is of a genus selected from the group consisting of *Chlorella,* and *Bracteococcus.*

236. The method of claim 232, wherein the carbon substrate is fructose and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella, Prototheca,* and *Scenedesmus.*

237. The method of claim 232, wherein the carbon substrate is arabinose and the microalgae is *Chlorella sp.*

238. The method of claim 232, wherein the carbon substrate is mannose and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella, Bracteococcus, Prototheca,* and *Scenedesmus.*

239. The method of claim 232, wherein the carbon substrate is galactose and the microalgae is of a genus selected from the group consisting of *Bracteococcus, Parachlorella, , Chlorella, Pseudochlorella, Bracteococcus,* and *Prototheca.*

240. The method of claim 232, wherein the carbon substrate is acetate and the microalgae is of a genus selected from the group consisting of *Chlorella, Parachlorella,* and *Prototheca.*

241. The method of claim 232, wherein the culture medium further includes at least one sucrose utilization enzyme.

242. The method of claim 241, wherein the microalgae is of the genus *Chlorella.*

243. The method of claim 242, wherein the microalgae has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme.

244. The method of claim 241, wherein the culture medium includes a sucrose invertase.

245. The method of claim 232, wherein the microalgae is selected from Table 1.

246. A method of culturing microalgae comprising placing a plurality of microalgae cells in the presence of depolymerized cellulosic material.

247. The method of claim 246, wherein the microalgae are cultured in the presence of an additional fixed carbon source selected from the group consisting of glycerol, sucrose, glucose, arabinose, galactose, xylose, fructose, arabinose, mannose, acetate, and any combination of the foregoing.

248. The method of claim 246, wherein the microalgae is selected from a species of the genus *Bracteococcus,* a species of the genus *Chlorella,* a species of the genus *Parachlorella,* a species of the genus *Prototheca,* or a species of the genus *Pseudochlorella.*

249. The method of claim 248, wherein the microalgae is selected from *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana, Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis,* and *Pseudochlorella aquatica.*

250. The method of claim 246, wherein the microalgae are cultured in the presence of at least sucrose utilization enzyme.

251. The method of claim 250, wherein the microalgae is of the genus *Chlorella.*

252. The method of claim 246, wherein the microalgae has been genetically engineered to express an exogenous gene encoding at least one lipid modification enzyme, hydrocarbon modification enzyme, or sucrose utilization enzyme.

253. The method of claim 250, wherein the at least one sucrose utilization enzyme is a sucrose invertase.

254. The method of claim 252, wherein the at least one lipid modification enzyme is selected from a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, and a glycerol-3 phosphate acyltransferase.

255. The method of claim 252, wherein the at least one hydrocarbon modification enzyme is selected from a fatty acyl-ACP thioesterase, a fatty acyl-CoA reductase, a fatty aldehyde reductase, a fatty acyl-CoA/aldehyde reductase, a fatty aldehyde decarbonylase, and an acyl carrier protein.

256. A method of culturing a lipid-producing microbe, the method comprising culturing the microbe in the presence of acetic acid and the absence of a fixed nitrogen source.

257. The method of claim 256, wherein the microbe is cultured in the presence of a sufficient amount of acetic acid to increase microbial lipid yield over microbial lipid yield in the absence of acetic acid, wherein culture conditions are otherwise the same between the two cultures.

258. A microbial culture containing:

(a) a population of microorganisms; and

(b) a culture medium comprising glucose, xylose, and a molecule selected from the group consisting of lignin and a species of furfural.

259. The microbial culture of claim 258, wherein the microorganisms are microalgae.

260. The microbial culture of claim 259, wherein the microorganisms are selected from the group consisting of the microalgae listed in Table 1.

261. The microbial culture of claim 260, wherein the microorganisms are a species of the genus *Chlorella*.

262. The microbial culture of claim 261, wherein the microorganisms are selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella*

aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

263. The microbial culture of claim 258, wherein the microorganisms are selected from *Bracteococcus minor, Chlorella ellipsoidea, Chlorella kessleri, Chlorella luteoviridis, Bracteococcus medionucleatus, Chlorella minutissima, Chlorella ovalis, Chlorella protothecoides, Chlorella saccharophila, Chlorella sorokiniana, Chlorella sp., Chlorella vulgaris, Parachlorella kessleri, Prototheca moriformis,* and *Pseudochlorella aquatica.*

264. The microbial culture of claim 258, wherein the microorganisms are oleaginous yeast.

265. The microbial culture of claim 264, wherein the oleaginous yeast are selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

266. The microbial culture of claim 258, wherein the microorganisms are fungi.

267. The microbial culture of claim 266, wherein the fungi are selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus,*

Aspergillus terreus, Pennicillium iilacinum, a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

268. The microbial culture of claim 258, wherein the microorganisms contain at least one exogenous sucrose utilization gene.

269. The microbial culture of claim 268, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

270. The microbial culture of claim 258, wherein the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme.

271. The microbial culture of claim 270, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

272. A method of biodiesel manufacturing, the method comprising:

(a) culturing a lipid-producing microorganism in a first microbial culture;

(b) recovering lipid from the biomass produced by the first microbial culture;

(c) subjecting the lipid to transesterification to produce fatty acid ester(s) and glycerol; and

(d) adding the glycerol to a second microbial culture.

273. The method of claim 272, wherein the first and second microbial cultures are cultures of the same species of microorganism.

274. The method of claim 272, wherein the microorganism is a microalgae.

275. The method of claim 274, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

276. The method of claim 275, wherein the microorganism is a species of the genus *Chlorella*.

277. The method of claim 276, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella pyrenoidosa, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis.*

278. The method of claim 272, wherein the second microbial culture comprises microorganisms selected from the group consisting of *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.,* and *Chlorella sorokiniana.*

279. The method of claim 272, wherein the microorganism is an oleaginous yeast.

280. The method of claim 279, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

281. The method of claim 272, wherein the microorganism is a fungus.

282. The method of claim 281, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus

Chaetomium, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

283. The method of claim 272, wherein the microorganism contains at least one exogenous sucrose utilization gene.

284. The method of claim 283, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

285. The method of claim 272, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

286. The method of claim 285, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

287. A method of fermentation comprising culturing a microorganism in the presence of glycerol and at least one other fixed carbon source.

288. The method of claim 287, wherein the glycerol and the at least one other fixed carbon source are provided to the microorganism simultaneously at a predetermined ratio.

289. The method of claim 288, wherein all of the glycerol and the at least one other fixed carbon source are provided to the microorganism at the beginning of the fermentation.

290. The method of claim 288, wherein all of the glycerol and the at least one other fixed carbon source are fed to the microorganism at a predetermined rate over the course of the fermentation.

291. The method of claim 287, wherein

(a) glycerol is provided to the microorganism in the absence of the at least one other fixed carbon source for a first period of time;

(b) the at least one other fixed carbon source is provided at the end of the first period of time; and

(c) the microorganism is cultured for a second period of time in the presence of the at least one other fixed carbon source.

292. The method of claim 291, wherein the at least one other fixed carbon source is fed to the microorganism at a predetermined rate during the second period of time.

293. The method of claim 291, wherein all of the at least one other fixed carbon source is provided to the microorganism at the end of the first period of time.

294. The method of claim 287, wherein

(a) the at least one other fixed carbon source is provided to the microorganism in the absence of glycerol for a first period of time;

(b) glycerol is provided at the end of the first period of time; and

(c) the microorganism is cultured for a second period of time in the presence of glycerol.

295. The method of claim 287, wherein the microorganism is a microalgae.

296. The method of claim 295, wherein the microalgae is selected from Table 1.

297. The method of claim 295, wherein the microalgae is of the genus *Chlorella*.

298. The method of claim 297, wherein the microalgae is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella*

vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

299. The method of claim 287, wherein the microorganism is an oleaginous yeast.

300. The method of claim 299, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

301. The method of claim 287, wherein the microorganism is a fungus.

302. The method of claim 301, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

303. The method of claim 287, wherein the microorganism contains at least one exogenous sucrose utilization gene.

304. The method of claim 303, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

305. The method of claim 287, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

306. The method of claim 305, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

307. The method of claim 287, wherein the glycerol is a byproduct of a transesterification process.

308. The method of claim 307, wherein the glycerol is acidulated.

309. The method of claim 307, wherein the glycerol is non-acidulated.

310. The method of claim 287, wherein the at least one other fixed carbon source is glucose.

311. The method of claim 287, wherein the at least one other fixed carbon source is depolymerized cellulosic material.

312. The method of claim 287, wherein the at least one other fixed carbon source is sucrose.

313. A fermentor comprising:

(a) a population of microorganisms;

(b) glycerol; and

(c) at least one sugar selected from the group consisting of xylose, glucose, and sucrose.

314. The fermentor of claim 313, wherein the glycerol is a byproduct of a lipid transesterification process.

315. The fermentor of claim 313, wherein the microorganisms are microalgae.

316. The fermentor of claim 315, wherein the microorganisms are selected from the group consisting of the microalgae listed in Table 1.

317. The fermentor of claim 316, wherein the microorganisms are a species of the genus *Chlorella*.

318. The fermentor of claim 317, wherein the microorganisms are selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima,*

Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

319. The fermentor of claim 313, wherein the microorganisms are selected from the group consisting of *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.,* and *Chlorella sorokiniana.*

320. The fermentor of claim 313, wherein the microorganisms are oleaginous yeast.

321. The fermentor of claim 320, wherein the oleaginous yeast are selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

322. The fermentor of claim 313, wherein the microorganisms are fungi.

323. The fermentor of claim 322, wherein the fungi are selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

324. The fermentor of claim 313, wherein the microorganisms contain at least one exogenous sucrose utilization gene.

325. The fermentor of claim 324, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

326. The fermentor of claim 313, wherein the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme.

327. The fermentor of claim 326, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

328. A method of fermenting a microorganism comprising providing byproduct glycerol from a transesterification process as a sole source of fixed carbon energy.

329. The method of claim 328, wherein no light energy is provided to the microorganism.

330. The method of claim 328, wherein light energy is provided to the microorganism.

331. The method of claim 328, wherein the microorganism is a microalgae.

332. The method of claim 331, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

333. The method of claim 332, wherein the microorganism is a species of the genus *Chlorella*.

334. The method of claim 333, wherein the microorganism is selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella*

pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, and *Chlorella zofingiensis.*

335. The method of claim 328, wherein the microorganism is selected from *Parachlorella kessleri, Chlorella protothecoides, Bracteococcus medionucleatus, Prototheca moriformis, Chlorella minutissima, Chlorella sp.,* and *Chlorella sorokiniana.*

336. The method of claim 328, wherein the microorganism is an oleaginous yeast.

337. The method of claim 336, wherein the oleaginous yeast is selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

338. The method of claim 328, wherein the microorganism is a fungus.

339. The method of claim 338, wherein the fungus is selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium.*

340. The method of claim 328, wherein the microorganism contains at least one exogenous sucrose utilization gene.

341. The method of claim 340, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

342. The method of claim 328, wherein the microorganism contains at least one exogenous gene encoding a lipid pathway enzyme.

343. The method of claim 342, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

344. A microorganism containing an exogenous sucrose utilization gene.

345. The microorganism of claim 344, wherein the gene encodes a sucrose transporter.

346. The microorganism of claim 344, wherein the gene encodes a sucrose invertase.

347. The microorganism of claim 344, wherein the gene encodes a fructokinase.

348. The microorganism of claim 344, wherein the microorganism is a microalgae.

349. The microorganism of claim 348, wherein the microorganism is selected from the group consisting of the microalgae listed in Table 1.

350. The microorganism of claim 349, wherein the microorganism is a species of the genus *Chlorella*.

351. The microorganism of claim 350, wherein the microorganism is a species selected from the group consisting of *Chlorella minutissima, Chlorella emersonii, Chlorella sorokiniana, Chlorella ellipsoidea, Chlorella sp.*, or *Chlorella protothecoides*.

352. A cell of the species *Chlorella protothecoides, Chlorella emersonii, or Chlorella minutissima* wherein the cell contains an exogenous gene.

353. The cell of claim 352, wherein the exogenous gene encodes a protein selected from the group consisting of a sucrose transporter, a sucrose invertase, a lipid modification enzyme, a hydrocarbon modification enzyme and a fructokinase.

354. The cell of claim 353, wherein the protein is a sucrose invertase secreted into the extracellular space.

355. The cell of claim 353, wherein the protein is a sucrose invertase targeted to the cytoplasm.

356. A microbial culture containing:

(a) a population of microorganisms; and

(b) a culture medium comprising (i) sucrose, and (ii) a sucrose invertase enzyme.

357. The microbial culture of claim 356, wherein the microorganisms are microalgae.

358. The microbial culture of claim 357, wherein the microorganisms are selected from the group consisting of the microalgae listed in Table 1.

359. The microbial culture of claim 358, wherein the microorganisms are a species of the genus *Chlorella*.

360. The microbial culture of claim 359, wherein the microorganisms are selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis.*

361. The microbial culture of claim 356, wherein the microorganisms are oleaginous yeast.

362. The microbial culture of claim 361, wherein the oleaginous yeast are selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica*.

363. The microbial culture of claim 356, wherein the microorganisms are fungi.

364. The microbial culture of claim 363, wherein the fungi are selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

365. The microbial culture of claim 356, wherein the microorganisms contain at least one exogenous sucrose utilization gene.

366. The microbial culture of claim 365, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

367. The microbial culture of claim 366, wherein the sucrose utilization gene encodes a sucrose transporter.

368. The microbial culture of claim 356, wherein the sucrose invertase enzyme is a secrectable sucrose invertase enzyme encoded by an exogenous sucrose invertase gene expressed by the population of microorganisms.

369. The microbial culture of claim 356, wherein the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme.

370. The microbial culture of claim 369, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

371. A microbial culture containing:

(a) a population of microorganisms; and

(b) a culture medium comprising (i) molasses, and (ii) a sucrose invertase enzyme.

372. The microbial culture of claim 371, wherein the microorganisms are microalgae.

373. The microbial culture of claim 372, wherein the microorganisms are selected from the group consisting of the microalgae listed in Table 1.

374. The microbial culture of claim 373, wherein the microorganisms are a species of the genus *Chlorella*.

375. The microbial culture of claim 374, wherein the microorganisms are selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis*.

376. The microbial culture of claim 371, wherein the microorganisms are oleaginous yeast.

377. The microbial culture of claim 376, wherein the oleaginous yeast are selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus,*

Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis, and *Yarrowia lipolytica*.

378. The microbial culture of claim 371, wherein the microorganisms are fungi.

379. The microbial culture of claim 378, wherein the fungi are selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium iilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

380. The microbial culture of claim 371, wherein the microorganisms contain at least one exogenous sucrose utilization gene.

381. The microbial culture of claim 380, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

382. The microbial culture of claim 381, wherein the sucrose utilization gene encodes a sucrose transporter.

383. The microbial culture of claim 371, wherein the sucrose invertase enzyme is a secrectable sucrose invertase enzyme encoded by an exogenous sucrose invertase gene expressed by the population of microorganisms.

384. The microbial culture of claim 371, wherein the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme.

385. The microbial culture of claim 384, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

386. A microbial culture containing:

(a) a population of microorganisms; and

(b) a culture medium comprising (i) sucrose; (ii) lignin; and (iii) a sucrose invertase enzyme.

387. The microbial culture of claim 386, wherein the microorganisms are microalgae.

388. The microbial culture of claim 387, wherein the microorganisms are selected from the group consisting of the microalgae listed in Table 1.

389. The microbial culture of claim 388, wherein the microorganisms are a species of the genus *Chlorella*.

390. The microbial culture of claim 389, wherein the microorganisms are selected from the group consisting of *Chlorella anitrata, Chlorella antarctica, Chlorella aureoviridis, Chlorella candida , Chlorella capsulata, Chlorella desiccata, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. Actophila, Chlorella infusionum var. Auxenophila, Chlorella kessleri, Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. Lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. airidis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella,* and *Chlorella zofingiensis.*

391. The microbial culture of claim 386, wherein the microorganisms are oleaginous yeast.

392. The microbial culture of claim 391, wherein the oleaginous yeast are selected from the group consisting of *Cryptococcus curvatus, Cryptococcus terricolus, Candida sp., Lipomyces starkeyi, Lipomyces lipofer, Endomycopsis vernalis, Rhodotorula glutinis, Rhodotorula gracilis,* and *Yarrowia lipolytica.*

393. The microbial culture of claim 386, wherein the microorganisms are fungi.

394. The microbial culture of claim 393, wherein the fungi are selected from the group consisting of a species of the genus *Mortierella, Mortierrla vinacea, Mortierella alpine, Pythium debaryanum, Mucor circinelloides, Aspergillus ochraceus, Aspergillus terreus, Pennicillium tilacinum,* a species of the genus *Hensenulo*, a species of the genus *Chaetomium*, a species of the genus *Cladosporium*, a species of the genus *Malbranchea*, a species of the genus *Rhizopus*, and a species of the genus *Pythium*.

395. The microbial culture of claim 386, wherein the microorganisms contain at least one exogenous sucrose utilization gene.

396. The microbial culture of claim 395, wherein the sucrose utilization gene encodes a sucrose transporter, a sucrose invertase, a hexokinase, a glucokinase, or a fructokinase.

397. The microbial culture of claim 396, wherein the sucrose utilization gene encodes a sucrose transporter.

398. The microbial culture of claim 386, wherein the sucrose invertase enzyme is a secrectable sucrose invertase enzyme encoded by an exogenous sucrose invertase gene expressed by the population of microorganisms.

399. The microbial culture of claim 386, wherein the microorganisms contain at least one exogenous gene encoding a lipid pathway enzyme.

400. The microbial culture of claim 399, wherein the lipid pathway enzyme is selected from the group consisting of a stearoyl-ACP desaturase, a glycerolipid desaturase, a pyruvate dehydrogenase, an acetyl-CoA carboxylase, an acyl carrier protein, and a glycerol-3 phosphate acyltransferase.

401. A nucleic acid comprising:

(a) a cDNA encoding a sucrose utilization gene; and

(b) a cDNA encoding a protein conferring resistance to the antibiotic hygromycin or the antibiotic G418.

402. A method of cultivating microalgae, comprising:

(a) providing a microalgae cell capable of performing heterotrophic growth;

(b) placing the microalgae cell in growth media, wherein the growth media comprises depolymerized cellulosic material; and

(c) incubating the microalgae for a period of time sufficient to allow the cell to grow.

CLAIMS

1. A method of producing fuel, comprising:

(a) culturing a population of microalgae in the presence of a fixed carbon source, wherein:

(i) the microalgae express an exogenous sucrose invertase;

(ii) the microalgae accumulate at least 10% of their dry cell weight as lipid; and

(ii) the fixed carbon source is selected from the group consisting of sugar cane juice, sugar cane, sugar beet, molasses, or other sucrose-containing feedstock;

(b) isolating lipid components from the cultured microalgae; and

(c) subjecting the isolated lipid components to one or more chemical reactions to generate fatty acid esters and/or alkanes,

whereby fuel is produced.

2. The method of claim 1, wherein the one or more chemical reactions is selected from the group consisting of transesterification, hydrotreating, hydrocracking, deoxygenation and isomerization.

3. The method of claim 1 or 2, wherein the microalgae are of the genus *Chlorella* or *Prototheca.*

4. The method of claim 3, wherein the microalgae are *Chlorella protothecoides* or *Prototheca moriformis.*

5. A composition of alkanes or fatty acid esters made according to the method of any one of claims 1 to 4.

6. A microalgal cell containing at least 10% of its dry cell weight as lipid, and comprising an exogenous gene encoding a sucrose invertase enzyme.

7. The microalgal cell of claim 6, wherein the sucrose invertase enzyme is a secretable sucrose invertase enzyme.

8. The microalgal cell of claim 6 or 7, wherein the microalga is selected from the group consisting of *Achnanthes orientalis, Agmenellum, Amphiprora hyaline, Amphora coffeiformis, Amphora coffeiformis linea, Amphora coffeiformis punctata, Amphora*

coffeiformis taylori, Amphora coffeiformis tenuis, Amphora delicatissima, Amphora delicatissima capitata, Amphora sp., Anabaena, Ankistrodesmus, Ankistrodesmus falcatus, Boekelovia hooglandii, Borodinella sp., Botryococcus braunii, Botryococcus sudeticus, Bracteococcus minor, Bracteococcus medionucleatus, Carteria, Chaetoceros gracilis, Chaetoceros muelleri, Chaetoceros muelleri subsalsum, Chaetoceros sp., Chlorella anitrata, Chlorella Antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulate, Chlorella desiccate, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. actophila, Chlorella infusionum var. auxenophila, Chlorella kessleri, Chlorella lobophora (strain SAG 37.88), Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella ovalis, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25), Chlorella protothecoides var. acidicola, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. autotrophica, Chlorella vulgaris var. viridis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, Chlorella zofingiensis, Chlorella trebouxioides, Chlorella vulgaris, Chlorococcum infusionum, Chlorococcum sp., Chlorogonium, Chroomonas sp., Chrysosphaera sp., Cricosphaera sp., Crypthecodinium cohnii, Cryptomonas sp., Cyclotella cryptica, Cyclotella meneghiniana, Cyclotella sp., Dunaliella sp., Dunaliella bardawil, Dunaliella bioculata, Dunaliella granulate, Dunaliella maritime, Dunaliella minuta, Dunaliella parva, Dunaliella peircei, Dunaliella primolecta, Dunaliella salina, Dunaliella terricola, Dunaliella tertiolecta, Dunaliella viridis, Dunaliella tertiolecta, Eremosphaera viridis, Eremosphaera sp., Ellipsoidon sp., Euglena, Franceia sp., Fragilaria crotonensis, Fragilaria sp., Gleocapsa sp., Gloeothamnion sp., Hymenomonas sp., Isochrysis aff. galbana, Isochrysis galbana, Lepocinclis, Micractinium, Micractinium (UTEX LB 2614), Monoraphidium minutum, Monoraphidium sp., Nannochloris sp., Nannochloropsis salina, Nannochloropsis sp., Navicula acceptata, Navicula biskanterae, Navicula pseudotenelloides, Navicula pelliculosa, Navicula saprophila, Navicula sp., Nephrochloris sp., Nephroselmis sp., Nitschia communis, Nitzschia alexandrina, Nitzschia communis, Nitzschia dissipata, Nitzschia frustulum,

Nitzschia hantzschiana, Nitzschia inconspicua, Nitzschia intermedia, Nitzschia microcephala, Nitzschia pusilla, Nitzschia pusilla elliptica, Nitzschia pusilla monoensis, Nitzschia quadrangular, Nitzschia sp., Ochromonas sp., Oocystis parva, Oocystis pusilla, Oocystis sp., Oscillatoria limnetica, Oscillatoria sp., Oscillatoria subbrevis, Parachlorella kessleri, Pascheria acidophila, Pavlova sp., Phagus, Phormidium, Platymonas sp., Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis sp., Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pseudochlorella aquatica, Pyramimonas sp., Pyrobotrys, Rhodococcus opacus, Sarcinoid chrysophyte, Scenedesmus armatus, Schizochytrium, Spirogyra, Spirulina platensis, Stichococcus sp., Synechococcus sp., Tetraedron, Tetraselmis sp., Tetraselmis suecica, Thalassiosira weissflogii, and *Viridiella fridericiana.*

9. The microalgal cell of claim 8, wherein the microalga is selected from the group consisting of *Bracteococcus, Chlorella, Parachlorella, Prototheca, Pseudochlorella,* and *Scenedesmus.*

10. The microalgal cell of claim 9, wherein the microalga is *Chlorella protothecoides* or *Prototheca moriformis.*

11. A lipid produced by a microalgal cell of any one of claims 6 to 10.

12. A method of producing a lipid, comprising:

(a) culturing a population of microalgae comprising an exogenous gene encoding a sucrose invertase in a culture medium comprising a fixed carbon source until the microalgae accumulate 10% or more of their dry cell weight as lipid; and

(b) separating the lipid from the microalgae.

13. The method of claim 12, wherein the sucrose invertase gene encodes a secretable sucrose invertase enzyme.

14. The method of claim 12 or 13, wherein the fixed carbon source is selected from the group consisting of depolymerized cellulosic material, sugar cane juice, sugar beet and molasses.

15. The method of any one of claims 12 to 14, wherein the culture medium comprises sucrose provided from a source selected from the group consisting of sugar cane

juice, sugar beet juice and molasses, wherein the sugar cane juice, sugar beet juice or molasses has a sucrose concentration of 50 μM or more.

16. The method of claim 15, wherein the sugar cane juice, sugar beet juice or molasses has a sucrose concentration of 500 μM or more.

17. The method of claim 16, wherein the sugar cane juice, sugar beet juice or molasses has a sucrose concentration of 5 mM or more.

18. The method of claim 17, wherein the sugar cane juice, sugar beet juice or molasses has a sucrose concentration of 50 mM or more.

19. The method of claim 18, wherein the sugar cane juice, sugar beet juice or molasses has a sucrose concentration of 500 mM or more.

20. The method of any one of claims 12 to 19, wherein separating the lipid from the microalgae comprises lysing the microalgae by mechanical means.

21. The method of any one of claim 12 to 20, wherein the culture medium comprises limited nitrogen.

22. The method of any one of claims 12 to 21, wherein the microalgae accumulate at least 60% of their dry cell weight as lipid.

23. The method of any one of claims 12 to 22, further comprising the additional step of forming a food product from the lipid obtained from the microalgae.

24. The method of any one of claims 12 to 23, further comprising (c) subjecting the lipid to one or more chemical reactions selected from the group consisting of ester hydrolysis, transesterification, hydrotreating, hydrocracking, deoxygenation, and/or isomerization.

25. The method of claim 24, wherein the lipid is subjected to transesterification to produce fatty acid esters and glycerol, and the glycerol is added to a second microalgal culture for use as a carbon source.

26. The method of claim 25, wherein the microalgae used to produce the lipid and the microalgae of the second microalgal culture are the same species.

27. The method of any one of claims 12 to 26, wherein the microalgae are selected from the group consisting of *Achnanthes orientalis, Agmenellum, Amphiprora hyaline, Amphora coffeiformis, Amphora coffeiformis linea, Amphora coffeiformis punctata, Amphora coffeiformis taylori, Amphora coffeiformis tenuis, Amphora delicatissima, Amphora delicatissima capitata, Amphora sp., Anabaena, Ankistrodesmus, Ankistrodesmus falcatus, Boekelovia hooglandii, Borodinella sp., Botryococcus braunii, Botryococcus sudeticus, Bracteococcus minor, Bracteococcus medionucleatus, Carteria, Chaetoceros gracilis, Chaetoceros muelleri, Chaetoceros muelleri subsalsum, Chaetoceros sp., Chlorella anitrata, Chlorella Antarctica, Chlorella aureoviridis, Chlorella candida, Chlorella capsulate, Chlorella desiccate, Chlorella ellipsoidea, Chlorella emersonii, Chlorella fusca, Chlorella fusca var. vacuolata, Chlorella glucotropha, Chlorella infusionum, Chlorella infusionum var. actophila, Chlorella infusionum var. auxenophila, Chlorella kessleri, Chlorella lobophora (strain SAG 37.88), Chlorella luteoviridis, Chlorella luteoviridis var. aureoviridis, Chlorella luteoviridis var. lutescens, Chlorella miniata, Chlorella minutissima, Chlorella mutabilis, Chlorella nocturna, Chlorella ovalis, Chlorella parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25), Chlorella protothecoides var. acidicola, Chlorella regularis, Chlorella regularis var. minima, Chlorella regularis var. umbricata, Chlorella reisiglii, Chlorella saccharophila, Chlorella saccharophila var. ellipsoidea, Chlorella salina, Chlorella simplex, Chlorella sorokiniana, Chlorella sp., Chlorella sphaerica, Chlorella stigmatophora, Chlorella vanniellii, Chlorella vulgaris, Chlorella vulgaris f. tertia, Chlorella vulgaris var. autotrophica, Chlorella vulgaris var. viridis, Chlorella vulgaris var. vulgaris, Chlorella vulgaris var. vulgaris f. tertia, Chlorella vulgaris var. vulgaris f. viridis, Chlorella xanthella, Chlorella zofingiensis, Chlorella trebouxioides, Chlorella vulgaris, Chlorococcum infusionum, Chlorococcum sp., Chlorogonium, Chroomonas sp., Chrysosphaera sp., Cricosphaera sp., Crypthecodinium cohnii, Cryptomonas sp., Cyclotella cryptica, Cyclotella meneghiniana, Cyclotella sp., Dunaliella sp., Dunaliella bardawil, Dunaliella bioculata, Dunaliella granulate, Dunaliella maritime, Dunaliella minuta, Dunaliella parva, Dunaliella peircei, Dunaliella primolecta, Dunaliella salina, Dunaliella terricola, Dunaliella tertiolecta, Dunaliella viridis, Dunaliella tertiolecta, Eremosphaera viridis, Eremosphaera sp., Ellipsoidon sp., Euglena, Franceia sp., Fragilaria crotonensis, Fragilaria sp., Gleocapsa sp., Gloeothamnion sp., Hymenomonas sp., Isochrysis aff. galbana, Isochrysis galbana, Lepocinclis, Micractinium, Micractinium (UTEX LB 2614), Monoraphidium minutum, Monoraphidium sp., Nannochloris sp., Nannochloropsis salina, Nannochloropsis sp.,*

Navicula acceptata, Navicula biskanterae, Navicula pseudotenelloides, Navicula pelliculosa, Navicula saprophila, Navicula sp., Nephrochloris sp., Nephroselmis sp., Nitschia communis, Nitzschia alexandrina, Nitzschia communis, Nitzschia dissipata, Nitzschia frustulum, Nitzschia hantzschiana, Nitzschia inconspicua, Nitzschia intermedia, Nitzschia microcephala, Nitzschia pusilla, Nitzschia pusilla elliptica, Nitzschia pusilla monoensis, Nitzschia quadrangular, Nitzschia sp., Ochromonas sp., Oocystis parva, Oocystis pusilla, Oocystis sp., Oscillatoria limnetica, Oscillatoria sp., Oscillatoria subbrevis, Parachlorella kessleri, Pascheria acidophila, Pavlova sp., Phagus, Phormidium, Platymonas sp., Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis sp., Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pseudochlorella aquatica, Pyramimonas sp., Pyrobotrys, Rhodococcus opacus, Sarcinoid chrysophyte, Scenedesmus armatus, Schizochytrium, Spirogyra, Spirulina platensis, Stichococcus sp., Synechococcus sp., Tetraedron, Tetraselmis sp., Tetraselmis suecica, Thalassiosira weissflogii, and *Viridiella fridericiana.*

28. The method of claim 27, wherein the microalgae are selected from the group consisting of *Bracteococcus, Chlorella, Parachlorella, Prototheca, Pseudochlorella,* and *Scenedesmus.*

29. The method of claim 28, wherein the microalgae are *Chlorella protothecoides* or *Prototheca moriformis.*

30. A lipid produced by the method of any one of claims 12 to 23.