improved methods for producing oil in microalgae, particularly for methods that produce oils with shorter chain length and a higher degree of saturation and without pigments, with greater yield and efficiency. The present invention meets this need.

SUMMARY OF THE INVENTION

[0006] The present invention provides oleaginous microbial cells, preferably microalgal cells, having distinct lipid profiles, and includes recombinant cells expressing exogenous genes encoding proteins such as fatty acyl-ACP thioesterases. Also disclosed are~~The present invention also provides~~ methods of making lipids and oil-based products, including fuels such as biodiesel, renewable diesel and jet fuel, from such cells.

[0006a] In a first aspect, the present invention refers to an oil composition produced by cultivating an oleaginous microbe and recovering the oil composition from the microbe, the oil composition comprising triglycerides and sterols produced by the microbe, wherein the fatty acid profile of the triglyceride oil composition comprises at least 60% C18:1, and less than 7% C18:2, wherein the triglyceride oil composition is produced by a recombinant oleaginous microbe comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microbe has been inactivated or mutated to have less enzymatic activity.

[0006b] In a second aspect, the present invention refers to an oil composition produced by cultivating an oleaginous microalgae and recovering the oil composition from the microalgae, the oil composition comprising triglycerides and sterols produced by the microalgae, wherein the fatty acid profile of the triglyceride oil composition comprises at least 60% C18:1, and less than 7% C18:2, wherein the triglyceride oil composition is produced by a recombinant oleaginous microalgae comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microalgae has been inactivated or mutated to have less enzymatic activity.

[0006c] In a third aspect, the present invention refers to an oil composition, produced by cultivating an oleaginous microbe and recovering the oil composition from the microbe, the oil composition comprising triglycerides and sterols produced by the microbe, wherein the fatty acid profile of the triglyceride oil composition comprises at least 50% saturated fatty acids, wherein the triglyceride oil composition is produced by a recombinant oleaginous microbe comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microbe has been inactivated or mutated to have less enzymatic activity.

[0007] In a first ~~aspect~~example, ~~the present invention provides~~disclosed are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 1% or at least 5%, preferably at least 3%, C8:0. In some cases, the lipid profile is at least 10% or at least 15%, preferably at least 12%, C8:0. In some ~~embodiments~~examples, the cell is a recombinant cell. In some cases, the recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain length C8. In some ~~embodiments~~examples, the exogenous gene encodes a *Cuphea palustris* acyl-ACP thioesterase. In some cases, the cell is a *Prototheca* cell. In some cases, the cell is of a microalgal genus or species selected from microalgae identified in Table 1.

[0008] In a second ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 4% C10:0. In some cases, the lipid profile is at least 20%, at least 25% or at least 30%, preferably at least 24%, C10:0. In some cases, the ratio of C10:0 to C12:0 is at least 6:1. In some ~~embodiments~~examples, the cell is a recombinant cell. In some cases, the recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain length C10. In some ~~embodiments~~examples, the exogenous gene encodes an acyl-ACP thioesterase protein from a species selected from the group consisting of *Cuphea hookeriana* and *Ulmus americana*. In some cases, the cell is a *Prototheca* cell. In some ~~embodiments~~examples, the cell is of a microalgal genus or species selected from microalgae identified in Table 1.

[0009] In a third ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 10% or at least 15%, prefereably at least 13%, C12:0. In some cases, the lipid profile is at least 30%, at least 35% or at least 40%, preferably at least 34%, C12:0. In some cases, the ratio of C12 to C14 is at least 5:1. In some cases, the cell is a recombinant cell. In some ~~embodiments~~examples, the

recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain length C12. In some cases, the recombinant cell comprises at least two exogenous genes encoding acyl-ACP thioesterase proteins from *Umbellularia californica* and *Cinnamomum camphora* that have hydrolysis activity towards fatty acyl-ACP substrates of chain length C12. In some ~~embodiments~~examples, the cell is a *Prototheca* cell.

[0010] In a fourth ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 5% or at least 15%, preferably at least 10%, C14:0. In some cases, the lipid profile is at least 40%, at least 45%, or at least 50%, preferably at least 43%, C14:0. In some cases, the ratio of C14:0 to C12:0 is at least 7:1. In some cases, the cell is a recombinant cell. In some ~~embodiments~~examples, the recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain length C14. In some ~~embodiments~~examples, the acyl-ACP thioesterase protein is from a species selected from the group consisting of *Cinnamomum camphora* and *Ulmus americana*. In some cases, the cell is a *Prototheca* cell. In some ~~embodiments~~examples, the cell is of a microalgal genus or species selected from microalgae identified in Table 1.

[0011] In a fifth ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 10% or at least 20%, preferably at least 15%, C16:0. In some cases, the lipid profile is at least 30%, at least 35% or at least 40%, preferably at least 37%, C16:0. In some cases, the cell is a recombinant cell. In some ~~embodiments~~examples, the recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain length C16. In some ~~embodiments~~examples, the recombinant cell comprises at least two exogenous genes encoding acyl-ACP thioesterase proteins from *Umbellularia californica* and *Cinnamomum camphora* that have hydrolysis activity towards fatty acyl-ACP substrates of chain length C16. In some cases, the cell is a *Prototheca* cell.

[0012] In a sixth ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, having a lipid profile that is at least 55% or at least 65%, preferably at least 60%, saturated fatty acids. In some cases the cells,have a lipid profile that is at least 80%, at least 85%, or at least 90%, preferably at least 86%, saturated fatty acids. In some cases, the cell is a recombinant cell. In some ~~embodiments~~examples, the recombinant cell comprises an exogenous gene encoding an acyl-ACP thioesterase protein that has hydrolysis activity towards fatty acyl-ACP substrates of chain lengths C10-C16. In some ~~embodiments~~examples,

the cell comprises an exogenous gene encoding a ketoacyl synthase protein. In some cases, the cell is a *Prototheca* cell.

[0013] In a seventh ~~aspect~~example, ~~the present invention provides~~described are oleaginous microbial cells, preferably microalgal cells, comprising a mutated endogenous desaturase gene, wherein the mutation renders the gene or desaturase inactive. In some cases, the cell has a lipid profile that is at least 40% or at least 50%, preferably at least 45%, saturated fatty acids. In some cases, the cell has a lipid profile that is at least 15%, at least 20% or at least 25%, preferably at least 19%, C18:0. In some ~~embodiments~~examples, the cell comprises a mutated endogenous desaturase gene that results in at least a 2-fold increase in C18:0 fatty acid, as compared to a wild-type cell. In some cases, the microalgal cell has a lipid profile that is no more than 1% or no more than 5%, preferably no more than 2%, C18:2. In some ~~embodiments~~examples, the microalgal cell has a lipid profile that is no more than 5% or no more than 10%, preferably no more than 7%, 18:1.

[0014] In some ~~embodiments~~examples of the recombinant cells discussed herein, the cell comprises a mutated endogenous desaturase gene, wherein the mutation renders the gene or desaturase inactive.

[0015] In a eighth ~~aspect~~example, ~~the present invention provides~~described is a method of making lipid. In one ~~embodiment~~example, the method comprises (a) cultivating a cell as discussed above until the cell is at least 15% or at least 25%, preferably at least 20%, lipid by dry weight, and (b) separating the lipid from water-soluble biomass components.

[0016] In a ninth ~~aspect~~example, ~~the present invention provides~~described is another method of making lipid. In one ~~embodiment~~example, the method comprises (a) cultivating an oleaginous microbial, preferably a microalgae cell, containing exogenous genes encoding two distinct acyl-ACP thioesterases, wherein the lipid profile of the cell is distinct from (i) the profile of the cell without the exogenous genes and (ii) the profile of the cell with only one of the exogenous genes, and (b) separating the lipid from water-soluble biomass components. In some cases, at least one of the exogenous genes encodes a fatty acyl-ACP thioesterase selected from the group consisting of the thioesterases identified in Table 4.

[0017] In a tenth ~~aspect~~example, ~~the present invention provides~~described is a method of making an oil-based product. In one ~~embodiment~~example, the method comprises (a) cultivating a cell as discussed above until the cell is at least 5% or at least 15%, preferably at least 10%, lipid by dry weight, (b) separating the lipid from water-soluble biomass components, and (c) subjecting the lipid to at least one chemical reaction selected from the group consisting of: saponification; metathesis; acid hydrolysis; alkaline hydrolysis; enzymatic hydrolysis; catalytic hydrolysis; hot-

compressed water hydrolysis; a catalytic hydrolysis reaction wherein the lipid is split into glycerol and fatty acids; an amination reaction to produce fatty nitrogen compounds; an ozonolysis reaction to produce mono- and dibasic-acids; a triglyceride splitting reaction selected from the group consisting of enzymatic splitting and pressure splitting; a condensation reaction that follows a hydrolysis reaction; a hydroprocessing reaction; a hydroprocessing reaction and a deoxygenation reaction or a condensation reaction prior to or simultaneous with the hydroprocessing reaction; a gas removal reaction; a deoxygenation reaction selected from the group consisting of a hydrogenolysis reaction, hydrogenation, a consecutive hydrogenation-hydrogenolysis reaction, a consecutive hydrogenolysis-hydrogenation reaction, and a combined hydrogenation-hydrogenolysis reaction; a condensation reaction following a deoxygenation reaction; an esterification reaction; an interestification reaction; a transesterification reaction; a hydroxylation reaction; and a condensation reaction following a hydroxylation reaction, whereby an oil-based product is produced.

[0018] In some cases, the oil-based product is selected from soap or a fuel product. In some ~~embodiments~~examples, the oil-based product is a fuel product selected from the group consisting biodiesel, renewable diesel, and jet fuel. In some cases, the fuel product is biodiesel with one or more of the following attributes: (i) 0.01- 0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.05-0.244 mcg/g, total carotenoids; (ii) less than 0.01 mcg/g, less than 0.005 mcg/g, preferably less than 0.003 mcg/g, lycopene; (iii) less than 0.01 mcg/g, less than 0.005 mcg/g, preferably less than 0.003 mcg/g, beta carotene; (iv) 0.01-0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.045-0.268 mcg/g, chlorophyll A; (v) 1-500 mcg/g, 35-175 mcg/g, preferably 38.3-164 mcg/g, gamma tocopherol; (vi) less than 1%, less than 0.5%, preferably less than 0.25%, brassicasterol, campesterol, stignasterol, or beta-sitosterol; (vii) 100-500 mcg/g, 225-350 mcg/g, preferably 249.6-325.3 mcg/g, total tocotrienols; (viii) 0.001-0.1 mcg/g, 0.0025-0.05 mcg/g, preferably 0.003-0.039 mcg/g, lutein; or (ix) 10-500 mcg/g, 50-300 mcg/g, preferably 60.8-261.7 mcg/g, tocopherols. In some cases, the fuel product is renewable diesel that has a T10-T90 of at least 20°C, 40°C or 60°C. In some cases, the fuel product is jet fuel that meets HRJ-5 and/or ASTM specification D1655.

[0019] In an eleventh ~~aspect~~example, ~~the present invention provides~~described is a triglyceride oil comprising (a) a lipid profile of at least 3% C8:0, at least 4% C10:0, at least 13% C12:0, at least 10% C14:0, and/or at least 60% saturated fatty acids, and (b) one or more of the following attributes: (i) 0.01-0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.05-0.244 mcg/g, total carotenoids; (ii) less than 0.01 mcg/g, less than 0.005 mcg/g, preferably less than 0.003

mcg/g, lycopene; (iii) less than 0.01 mcg/g, less than 0.005 mcg/g, prefereably less than 0.003 mcg/g, beta carotene; (iv) 0.01-0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.045-0.268 mcg/g, chlorophyll A; (v) 1-300 mcg/g, 35-175 mcg/g, preferably 38.3-164 mcg/g, gamma tocopherol; (vi) less than 1%, less than 0.5%, preferably less than 0.25%, brassicasterol, campesterol, stignasterol, or beta-sitosterol; (vii) 100-500 mcg/g, 225-350 mcg/g, preferably 249.6-325.3 mcg/g, total tocotrienols; (viii) 0.001-0.1 mcg/g, 0.0025-0.05 mcg/g, preferably 0.003-0.039 mcg/g, lutein; or (ix) 10-500 mcg/g, 50-300 mcg/g, preferably 60.8-261.7 mcg/g, tocopherols.

[0020] In a twelvth ~~aspect~~example, ~~the present invention provides~~described is an isolated oil from microalgae that has a C8:C10 fatty acid ratio of at least 5:1. In a related ~~aspect~~example, ~~the present invention provides~~described is an isolated oil from microalgae with at least 50% to 75%, preferably at least 60%, saturated fatty acids. In another related ~~aspect~~example, ~~the present invention provides~~described is an isolated oil from microalgae that has a C16:14 fatty acid ratio of about 2:1. In still another related ~~aspect~~example, ~~the present invention provides~~described is an isolated oil from microalgae that has a C12:C14 fatty acid ratio of at least 5:1. In some ~~embodiments~~examples, the microalgae contains at least one exogenous gene. In some cases, the microalgae is of the genus *Prototheca*.

[0021] In a thirteenth ~~aspect~~example, ~~the present invention provides~~described is a triglyceride oil comprising (a) a lipid profile of less than 5% or less than 2%, preferably less than 1%, <C12; between 1%-10%, preferably 2%-7%, C14:0; between 20%-35%, preferably 23%-30%, C16:0; between 5%-20%, preferably 7%-15%, C18:0; between 35-60%, preferably 40-55%, C18:1; and between 1%-20%, preferably 2-15%, C18:2 fatty acids; and (b) one or more of the following attributes: (i) 0.01-0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.05-0.244 mcg/g, total carotenoids; (ii) less than 0.01 mcg/g, less than 0.005 mcg/g, preferably less than 0.003 mcg/g, lycopene; (iii) less than 0.01 mcg/g, less than 0.005 mcg/g, preferably less than 0.003 mcg/g, beta carotene; (iv) 0.01-0.5 mcg/g, 0.025-0.3 mcg/g, preferably 0.045-0.268 mcg/g, chlorophyll A; (v) 1-300 mcg/g, 35-175 mcg/g, preferably 38.3-164 mcg/g, gamma tocopherol; (vi) less than 1%, less than 0.5%, preferably less than 0.25%, brassicasterol, campesterol, stignasterol, or beta-sitosterol; (vii) 100-500 mcg/g, 225-350 mcg/g, preferably 249.6-325.3 mcg/g, total tocotrienols; (viii) 0.001-0.1 mcg/g, 0.0025-0.05 mcg/g, preferably 0.003-0.039 mcg/g, lutein; or (ix) 10-500 mcg/g, 50-300, preferably 60.8-261.7 mcg/g, tocopherols.

[0022] In some cases, the triglyceride oil is isolated from a microbe comprising one or more exogenous gene. In some ~~embodiments~~examples, the one or more exogenous gene encodes a fatty acyl-ACP thioesterase. In some cases, the fatty acyl-ACP thioesterase has hydrolysis

activity towards fatty acyl-ACP substrates of chain length C14. In some ~~embodiments~~examples, the microbe further comprises a mutated endogenous desaturase gene, wherein the mutation renders the gene or desaturase inactive.

[0023] In a fourteenth ~~aspect~~example, ~~the present invention provides~~described is a method of producing a triglyceride oil comprising a lipid profile of less than 5%, or less than 2%, preferably less than 1%, <C12; between 1%-10%, preferably 2%-7%, C14:0; between 20%-35%, preferably 23%-30%, C16:0; between 5%-20%, preferably 7%-15%, C18:0; between 35%-60%, preferably 40-55%, C18:1; and between 1%-20%, preferably 2-15%, C18:2 fatty acids, wherein the triglyceride oil is isolated from a microbe comprising one or more exogenous gene. In some cases, the triglyceride oil comprises a lipid profile of 1%-10%, preferably 3-5%, C14:0; 20%-30%, preferably 25-27%, C16:0; 5%-20%, preferably 10-15%, C18:0; and 35%-50%, preferably 40-45%, C18:1. In some ~~embodiments~~examples, the one or more exogenous gene encodes a fatty acyl-ACP thioesterase. In some cases, the fatty acyl-ACP thioesterase has hydrolysis activity towards fatty acyl-ACP substrates of chain length C14. In some cases, the microbe further comprises a mutated endogenous desaturase gene, wherein the mutation renders the gene or desaturase inactive. In some cases, the one or more exogenous gene is a sucrose invertase. In some ~~embodiments~~examples, the mutated endogenous desaturase gene is a stearoyl-acyl carrier protein desaturase (SAD) (*e.g.*, SEQ ID NOs: 199-200). In some ~~embodiments~~examples, the mutated endogenous desaturase gene is a fatty acid desaturase (FAD).

[0024] In a fifteenth ~~aspect~~example, ~~the present invention provides~~described is a oleaginous microbial cell, preferably a microalgal cell, comprising a triglyceride oil, wherein the fatty acid profile of the triglyceride oil is selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids. In some cases, the oleaginous microbial cell comprises an exogenous gene, and optionally, an endogenous desaturase of the oleaginous microbial cell has been inactivated or mutated to have less enzymatic activity.

[0025] In some cases, the fatty acid profile of the triglyceride oil is similar to the fatty acid profile of a naturally occurring oil. In some cases, the naturally occurring oil is selected from the group consisting of cocoa butter, coconut oil, palm oil, palm kernel oil, shea butter, beef tallow and lard. In some cases, the fatty acid profile of the triglyceride oil comprises a profile selected from the group consisting of, the total combined amounts of C8:0 and C10:0 is at least about 10%, the total combined amount of C10:0, C12:0, and C14:0 is at least about 50%, the total combined amount of C16:0, C18:0 and C18:1 is at least about 60%, the total

combined amount of C18:0, C18:1 and C18:2 is at least about 60%, the total combined amount of C14:0, C16:0, C18:0 and C18:1 is at least about 60%, and the total combined amount of C18:1 and C18:2 is less than about 30%. In some cases, the fatty acid profile of the triglyceride oil comprises a ratio of fatty acids selected from the group consisting of C8:0 to C10:0 ratio of at least about 5 to 1, C10:0 to C12:0 ratio of at least about 6 to 1, C12:0 to C14:0 ratio of at least about 5 to 1, C14:0 to C12:0 ratio of at least about 7:1, and C14:0 to C16:0 ratio of at least about 1 to 2.

[0026] In some cases, the endogenous desaturase is selected from the group consisting of stearoyl ACP desaturase and delta 12 fatty acid desaturase. In some cases, the exogenous gene is selected from the group consisting of a gene encoding an acyl-ACP thioesterase. In some cases, the exogenous gene encodes an acyl-ACP thioesterase selected from the group consisting of those identified in Table 4. In some cases, the oleaginous microbial cell further comprises a gene encoding a sucrose invertase.

[0027] In various ~~embodiments~~examples, the oleaginous microbial cell is a cell of a microalgal genus or species selected from *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, 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 parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25, and CCAP strains 211/17 and 211/8d), 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, Chlorella vulgaris f. tertia, Chlorella*

a combination of a *Cuphea hookeriana* KAS IV gene and a *Cuphea wrightii* FATB2 gene, or a construct designed to disrupt an endogenous KAS II gene.. In some cases, the naturally occurring oil is palm kernel oil and the exogenous gene comprises a combination of a *Cuphea wrightii* FATB2 gene and a construct designed to disrupt an endogenous SAD2B gene.. In some cases, the naturally occurring oil is shea butter. In some cases, the naturally occurring oil is beef tallow. In some cases, the naturally occurring oil is lard and the exogenous gene comprises a combination of *U. californica* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a combination of a *Garcinia mangostana* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a *Brassica napus* thioesterase gene, or a *Cuphea hookeriana* thioesterase gene..

[0031] In a sixteenth ~~aspect~~example, ~~the present invention provides~~described is an oleaginous microbial triglyceride oil composition, wherein the fatty acid profile of the triglyceride oil is selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids. In various ~~embodiments~~examples, the triglyceride oil composition is produced by cultivating a population of oleaginous microbial cells or recombinant oleaginous microbial cells in a culture medium, wherein the oleaginous microbial cells are as described above, in particular those described above in connection with the fifteeth ~~aspect~~example ~~of the invention~~.

[0032] In some cases, the oleaginous microbial triglyceride oil composition further comprises an attribute selected from the group consisting of: (i) less than 0.3 mcg/g total carotenoids; (ii) less than 0.005 mcg/g lycopene; (iii) less than 0.005 mcg/g beta carotene; (iv) less than 0.3 mcg/g chlorophyll A; (v) less than 175 mcg/g gamma tocopherol; (vi) less than 0.25% brassicasterol, campesterol, stignasterol, or beta-sitosterol; (vii) less than 350 mcg/g total tocotrienols; (viii) less than 0.05 mcg/g lutein; or (ix) less than 275 mcg/g tocopherols.

[0033] In a seventeenth ~~aspect~~example, ~~the present invention provides~~described is a method of producing an oleaginous microbial triglyceride oil composition having a fatty acid profile selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids, wherein the method comprises the steps of: (a) cultivating a population of oleaginous microbial cells in a culture medium until at least 10% of the dry cell weight of the oleaginous microbial cells is triglyceride oil; and (b) isolating the triglyceride oil composition from the oleaginous

microbial cells. In various ~~embodiments~~examples, the triglyceride oil composition is produced via cultivation of a population of oleaginous microbial cells or recombinant oleaginous microbial cells as described above, in particular those described above in connection with the fifteenth ~~aspect~~example ~~of the invention~~.

[0034] In an eighteenth ~~aspect~~example, ~~the present invention provides~~described is a method of making an oil-based product, wherein the method comprises the steps of: (a) subjecting the oleaginous microbial triglyceride oil composition, as described above in connection with the sixteenth ~~aspect~~example ~~of the invention~~, to at least one chemical reaction selected from the group consisting of: saponification; metathesis; acid hydrolysis; alkaline hydrolysis; enzymatic hydrolysis; catalytic hydrolysis; hot-compressed water hydrolysis; a catalytic hydrolysis reaction wherein the lipid is split into glycerol and fatty acids; an amination reaction to produce fatty nitrogen compounds; an ozonolysis reaction to produce mono- and dibasic-acids; a triglyceride splitting reaction selected from the group consisting of enzymatic splitting and pressure splitting; a condensation reaction that follows a hydrolysis reaction; a hydroprocessing reaction; a hydroprocessing reaction and a deoxygenation reaction or a condensation reaction prior to or simultaneous with the hydroprocessing reaction; a gas removal reaction; a deoxygenation reaction selected from the group consisting of a hydrogenolysis reaction, hydrogenation, a consecutive hydrogenation-hydrogenolysis reaction, a consecutive hydrogenolysis-hydrogenation reaction, and a combined hydrogenation-hydrogenolysis reaction; a condensation reaction following a deoxygenation reaction; an esterification reaction; an interestification reaction; a transesterification reaction; a hydroxylation reaction; and a condensation reaction following a hydroxylation reaction; and (b) isolating the product of the reaction from the other components.

[0035] In some cases, the oil-based product is selected from the group consisting of a soap, a fuel, a dielectric fluid, a hydraulic fluid, a plasticizer, a lubricant, a heat transfer fluid, and a metal working fluid. In some cases, the oil-based product is a fuel product selected from the group consisting of: (a) biodiesel; (b) renewable diesel; and (c) jet fuel.

[0036] In some cases, the fuel product is biodiesel with one or more of the following attributes: (i) less than 0.3 mcg/g total carotenoids; (ii) less than 0.005 mcg/g lycopene; (iii) less than 0.005 mcg/g beta carotene; (iv) less than 0.3 mcg/g chlorophyll A; (v) less than 175 mcg/g gamma tocopherol; (vi) less than 0.25% brassicasterol, campesterol, stignasterol, or beta-sitosterol; (vii) less than 350 mcg/g total tocotrienols; (viii) less than 0.05 mcg/g lutein; or (ix) less than 275 mcg/g tocopherols.

[0037] In some cases, the fuel product is renewable diesel that has a T10-T90 of at least 20°C, 40°C or 60°C.

[0038] In some cases, the fuel product is jet fuel that meets HRJ-5 and/or ASTM specification D1655.

[0039] These and other aspects, ~~and~~ embodiments ~~of the invention~~ and examples are described in the accompanying drawing, a brief description of which immediately follows, the detailed description of the invention below, and are exemplified in the examples below. Any or all of the features discussed above and throughout the application can be combined in various embodiments of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0040] Figure 1 shows a chromatogram of renewable diesel produced from *Prototheca* triglyceride oil.

DETAILED DESCRIPTION OF THE INVENTION

[0041] The present invention arises from the discovery that *Prototheca* and certain related microorganisms have unexpectedly advantageous properties for the production of oils, fuels, and other hydrocarbon or lipid compositions economically and in large quantities, as well as from the discovery of methods and reagents for genetically altering these microorganisms to improve these properties. The oils produced by these microorganisms can be used in the transportation fuel, oleochemical, and/or food and cosmetic industries, among other applications. Transesterification of lipids yields long-chain fatty acid esters useful as biodiesel. Other enzymatic and chemical processes can be tailored to yield fatty acids, aldehydes, alcohols, alkanes, and alkenes. In some applications, renewable diesel, jet fuel, or other hydrocarbon compounds are produced. The present invention also provides methods of cultivating microalgae for increased productivity and increased lipid yield, and/or for more cost-effective production of the compositions described herein.

[0042] This detailed description of the invention is divided into sections for the convenience of the reader. Section I provides definitions of terms used herein. Section II provides a description of culture conditions useful in the methods of the invention. Section III provides a description of genetic engineering methods and materials. Section IV provides a description of genetic engineering of microorganisms (*e.g.*,*Prototheca*) to enable sucrose utilization. Section V provides a description of genetic engineering of microorganisms (*e.g.*, *Prototheca*) to modify lipid biosynthesis. Section VI describes methods for making fuels and chemicals. Section VII discloses examples and embodiments of the invention. The detailed

WHAT IS CLAIMED IS:

1. An oleaginous microbial cell comprising triglyceride oil, wherein the fatty acid profile of the triglyceride oil is selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids.

2. The oleaginous microbial cell of claim 1, wherein said oleaginous microbial cell comprises an exogenous gene, and wherein optionally, an endogenous desaturase of said oleaginous microbial cell has been inactivated or mutated to have less enzymatic activity.

3. The oleaginous microbial cell of claim 2, wherein the fatty acid profile of the triglyceride oil is similar to the triglyceride oil profile of a naturally occurring oil.

4. The oleaginous microbial cell of claim 3, wherein the naturally occurring oil is selected from the group consisting of cocoa butter, coconut oil, palm oil, palm kernel oil, shea butter, beef tallow and lard.

5. The oleaginous microbial cell of claim 2, wherein the fatty acid profile of the triglyceride oil comprises a profile selected from the group consisting of, the total combined amounts of C8:0 and C10:0 is at least about 10%, the total combined amount of C10:0, C12:0, and C14:0 is at least about 50%, the total combined amount of C16:0, C18:0 and C18:1 is at least about 60%, the total combined amount of C18:0, C18:1 and C18:2 is at least about 60%, the total combined amount of C14:0, C16:0, C18:0 and C18:1 is at least about 60%, and the total combined amount of C18:1 and C18:2 is less than about 30%.

6. The oleaginous microbial cell of claim 1, wherein the fatty acid profile of the triglyceride oil comprises a ratio of fatty acids selected from the group consisting of C8:0 to C10:0 ratio of at least about 5 to 1, C10:0 to C12:0 ratio of at least about 6 to 1, C12:0 to C14:0 ratio of at least about 5 to 1, C14:0 to C12:0 ratio of at least about 7:1, and C14:0 to C16:0 ratio of at least about 1 to 2.

7. The oleaginous microbial cell of claim 2, wherein said endogenous desaturase is selected from the group consisting of stearoyl ACP desaturase and delta 12 fatty acid desaturase.

8. The oleaginous microbial cell of claim 7, wherein said exogenous gene is selected from the group consisting of a gene encoding an acyl-ACP thioesterase.

9. The oleaginous microbial cell of claim 8, wherein said exogenous gene encodes an acyl-ACP thioesterase selected from the group consisting of *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #AAC49001); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #Q39473); *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #Q41635); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71730); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #ABD83939); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAD42220); *Populus tomentosa* fatty acyl-ACP thioesterase (GenBank #ABC47311); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #NP_172327); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #CAA85387); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #CAA85388); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #Q9SQI3); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAA54060); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC72882); *Cuphea calophylla subsp. mesostemon* fatty acyl-ACP thioesterase (GenBank #ABB71581); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAC19933); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAL15645); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #Q39513); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #AAD01982); *Vitis vinifera* fatty acyl-ACP thioesterase (GenBank #CAN81819); *Garcinia mangostana* fatty acyl-ACP thioesterase (GenBank #AAB51525); *Brassica juncea* fatty acyl-ACP thioesterase (GenBank #ABI18986); *Madhuca longifolia* fatty acyl-ACP thioesterase (GenBank #AAX51637); *Brassica napus* fatty acyl-ACP thioesterase (GenBank #ABH11710); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY86877); *Oryza sativa* (japonica cultivar-group) fatty acyl-ACP thioesterase (GenBank #NP_001068400); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY99617); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC49269); *Ulmus Americana* fatty acyl-ACP thioesterase (GenBank #AAB71731); *Cuphea lanceolata* fatty acyl-ACP

thioesterase (GenBank #CAB60830); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49180); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858.1); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49179); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB717291.1); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #U39834); *Umbelluaria californica* fatty acyl-ACP thioesterase (GenBank # M94159); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #U31813); *Cuphea wrightii* fatty acyl-ACOP thioesterase (GenBank #U56103); and *Ricinus communis* fatty acyl-ACP thioesterase (GenBank #ABS30422).

10. The oleaginous microbial cell of claim 2, wherein said oleaginous microbial cell further comprises a gene encoding a sucrose invertase.

11. The oleaginous microbial cell of claim 2, wherein said oleaginous microbial cell is a cell of a microalgal genus or species selected from *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, 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 parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25, and CCAP strains 211/17 and 211/8d), 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, 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., 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, Pascheria acidophila, Pavlova sp., Phagus, Phormidium, Platymonas sp., Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis sp., Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pyramimonas sp., Pyrobotrys, Sarcinoid chrysophyte, Scenedesmus armatus, Spirogyra, Spirulina platensis, Stichococcus sp., Synechococcus sp., Tetraedron, Tetraselmis sp., Tetraselmis suecica, Thalassiosira weissflogii, and *Viridiella fridericiana.*

12. The oleaginous microbial cell of claim 11, wherein said oleaginous microbial cell is a cell of the genus *Prototheca*.

13. The oleaginous microbial cell of claim 12, wherein said oleaginous microbial cell is a cell of the genus *Prototheca moriformis*.

14. The oleaginous microbial cell of claim 2, wherein said oleaginous microbial cell is an oleaginous yeast cell.

15. The oleaginous microbial cell of claim 2, wherein said oleaginous microbial cell is an oleaginous bacterial cell.

16. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is cocoa butter and wherein said exogenous gene comprises a *Carthamus tinctorus* thioesterase gene.

17. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is coconut oil.

18. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is palm oil and wherein said exogenous gene comprises a *Elaeis guiniensis* thioesterase gene, a *Cuphea hookeriana* thioesterase gene, a combination of a *Cuphea hookeriana* KAS IV gene and a *Cuphea wrightii* FATB2 gene, or a construct designed to disrupt an endogenous KAS II gene.

19. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is palm kernel oil and wherein said exogenous gene comprises a combination of a *Cuphea wrightii* FATB2 gene and a construct designed to disrupt an endogenous SAD2B gene.

20. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is shea butter.

21. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is beef tallow.

22. The oleaginous microbial cell of claim 4, wherein said naturally occurring oil is lard and wherein said exogenous gene comprises a combination of *U. californica* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a combination of a *Garcinia mangostana* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a *Brassica napus* thioesterase gene, or a *Cuphea hookeriana* thioesterase gene.

23. An oleaginous microbial triglyceride oil composition, wherein the fatty acid profile of the triglyceride oil is selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids.

24. The oleaginous microbial triglyceride oil composition of claim 23, produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cells comprise an exogenous gene, and wherein optionally, an endogenous desaturase of said oleaginous microbial cells has been inactivated or mutated to have less enzymatic activity.

25. The oleaginous microbial triglyceride oil composition of claim 24, wherein the fatty acid profile of the triglyceride oil is similar to the triglyceride oil profile of a naturally occurring oil.

26. The oleaginous microbial triglyceride oil composition of claim 25, wherein the naturally occurring oil is selected from the group consisting of cocoa butter, coconut oil, palm oil, palm kernel oil, shea butter, beef tallow and lard.

27. The oleaginous microbial triglyceride oil composition of claim 24, wherein the fatty acid profile of the triglyceride oil comprises a profile wherein, the total combined amount of C10:0, C12:0 and C14:0 is at least about 50%, the total combined amount of C16:0, C18:0 and C18:1 is at least about 60%, the total combined amount of C18:0, C18:1 and C18:2 is at least about 60%, the total combined amount of C14:0, C16:0, C18:0 and C18:1 is at least about 60%, the total combined amounts of C8:0 and C10:0 is less than about 50%.

28. The oleaginous microbial triglyceride oil composition of claim 24, wherein the fatty acid profile of the triglyceride oil comprises a ratio of fatty acids selected from the group consisting of C8:0 to C10:0 ratio of at least about 5 to 1, C10:0 to C12:0 ratio of at least about 6 to 1, C12:0 to C14:0 ratio of at least about 5 to 1, C14:0 to C12:0 ratio of at least about 7:1, C14:0 to C16:0 ratio of at least about 1 to 2.

29. The oleaginous microbial triglyceride oil composition of claim 24 produced by cultivating a population of recombinant oleaginous microbial cells in a culture

medium, wherein said endogenous desaturase is selected from the group consisting of stearoyl ACP desaturase and delta 12 fatty acid desaturase.

30. The oleaginous microbial triglyceride oil composition of claim 29 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cells comprise an exogenous gene encoding an acyl-ACP thioesterase.

31. The oleaginous microbial triglyceride oil composition of claim 30 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cells comprise an exogenous gene that encodes an acyl-ACP thioesterase selected from the group consisting of *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #AAC49001); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #Q39473); *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #Q41635); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71730); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #ABD83939); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAD42220); *Populus tomentosa* fatty acyl-ACP thioesterase (GenBank #ABC47311); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #NP_172327); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #CAA85387); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #CAA85388); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #Q9SQI3); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAA54060); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC72882); *Cuphea calophylla subsp. mesostemon* fatty acyl-ACP thioesterase (GenBank #ABB71581); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAC19933); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAL15645); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #Q39513); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #AAD01982); *Vitis vinifera* fatty acyl-ACP thioesterase (GenBank #CAN81819); *Garcinia mangostana* fatty acyl-ACP thioesterase (GenBank #AAB51525); *Brassica juncea* fatty acyl-ACP thioesterase (GenBank #ABI18986); *Madhuca longifolia* fatty acyl-ACP thioesterase (GenBank #AAX51637); *Brassica napus* fatty acyl-ACP thioesterase (GenBank #ABH11710); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY86877); *Oryza sativa* (japonica

cultivar-group) fatty acyl-ACP thioesterase (GenBank #NP_001068400); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY99617); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC49269); *Ulmus Americana* fatty acyl-ACP thioesterase (GenBank #AAB71731); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAB60830); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49180); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858.1); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49179); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB717291.1); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #U39834); *Umbelluaria californica* fatty acyl-ACP thioesterase (GenBank # M94159); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #U31813); *Cuphea wrightii* fatty acyl-ACOP thioesterase (GenBank #U56103); and *Ricinus communis* fatty acyl-ACP thioesterase (GenBank #ABS30422).

32. The oleaginous microbial triglyceride oil composition of claim 31 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cells further comprise a gene encoding a sucrose invertase.

33. The oleaginous microbial triglyceride oil composition of claim 32 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cells is a cell of a microalgal genus or species selected from *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, 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 parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25, and CCAP strains 211/17 and 211/8d), 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, 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., 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, Pascheria acidophila, Pavlova sp., Phagus, Phormidium, Platymonas sp., Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis sp., Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pyramimonas sp., Pyrobotrys, Sarcinoid chrysophyte, Scenedesmus armatus, Spirogyra, Spirulina platensis, Stichococcus sp., Synechococcus sp.,

Tetraedron, Tetraselmis sp., Tetraselmis suecica, Thalassiosira weissflogii, and *Viridiella fridericiana.*

34. The oleaginous microbial triglyceride oil composition of claim 24 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium,wherein said oleaginous microbial cell is a cell of the genus *Prototheca.*

35. The oleaginous microbial triglyceride oil composition of claim 34 produced by cultivating a population of recombinant oleaginous microbial cells in a culture medium, wherein said oleaginous microbial cell is a cell of the genus *Prototheca moriformis.*

36. The oleaginous microbial triglyceride oil of claim 24, wherein said oleaginous microbial cell is an oleaginous yeast cell.

37. The oleaginous microbial triglyceride oil of claim 24, wherein said oleaginous microbial cell is an oleaginous bacterial cell.

38. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is coconut oil.

39. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is palm oil and wherein said exogenous gene comprises a *Elaeis guiniensis* thioesterase gene, a *Cuphea hookeriana* thioesterase gene, a combination of a *Cuphea hookeriana* KAS IV gene and a *Cuphea wrightii* FATB2 gene, or a construct designed to disrupt an endogenous KAS II gene.

40. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is palm kernel oil and wherein said exogenous gene comprises a combination of a *Cuphea wrightii* FATB2 gene and a construct designed to disrupt an endogenous SAD2B gene.

41. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is shea butter.

42. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is beef tallow.

43. The oleaginous microbial triglyceride oil composition of claim 26, wherein said naturally occurring oil is lard and wherein said exogenous gene comprises a combination of *U. californica* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a combination of a *Garcinia mangostana* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a *Brassica napus* thioesterase gene, or a *Cuphea hookeriana* thioesterase gene.

44. The oleaginous microbial triglyceride oil composition of claim 23, wherein the triglyceride oil composition further comprises an attribute selected from the group consisting of:

i. less than 0.3 mcg/g total carotenoids;
ii. less than 0.005 mcg/g lycopene;
iii. less than 0.005 mcg/g beta carotene;
iv. less than 0.3 mcg/g chlorophyll A;
v. less than 175 mcg/g gamma tocopherol;
vi. less than 0.25% brassicasterol, campesterol, stignasterol, or beta-sitosterol;
vii. less than 350 mcg/g total tocotrienols;
viii. less than 0.05 mcg/g lutein; or
ix. less than 275 mcg/g tocopherols.

45. A method of producing an oleaginous microbial triglyceride oil composition, said triglyceride oil composition having a fatty acid profile selected from the group consisting of at least about 1% C8:0, at least about 1% C10:0, at least about 1% C12:0, at least about 2% C14:0, at least about 30% C16:0, at least about 5% C18:0, at least about 60% C18:1, less than about 7% C18:2, and at least about 35% saturated fatty acids, the method comprising the steps of:

a. cultivating a population of oleaginous microbial cells in a culture medium until at least 10% of the dry cell weight of the oleaginous microbial cells is triglyceride oil; and

b. isolating the triglyceride oil composition from the oleaginous microbial cells.

46. The method of claim 45, wherein said oleaginous microbial cell comprises an exogenous gene, and wherein optionally, an endogenous desaturase of said oleaginous microbial cell has been inactivated or mutated to have less enzymatic activity.

47. The method of claim 46, wherein the fatty acid profile of the triglyceride oil is similar to the triglyceride oil profile of a naturally occurring oil.

48. The method of claim 47, wherein the naturally occurring oil is selected from the group consisting of cocoa butter, coconut oil, palm oil, palm kernel oil, shea butter, beef tallow and lard.

49. The method of claim 46, wherein the fatty acid profile of the triglyceride oil comprises a profile wherein, the total combined amount of C10:0, C12:0 and C14:0 is at least about 50%, the total combined amount of C16:0, C18:0 and C18:1 is at least about 60% , the total combined amount of C18:0, C18:1 and C18:2 is at least about 60%, the total combined amount of C14:0, C16:0, C18:0 and C18:1 is at least about 60%, the total combined amounts of C8:0 and C10:0 is less than about 50%.

50. The method of claim 45, wherein the fatty acid profile of the triglyceride oil comprises a ratio of fatty acids selected from the group consisting of C8:0 to C10:0 ratio of at least about 5 to 1, C10:0 to C12:0 ratio of at least about 6 to 1, C12:0 to C14:0 ratio of at least about 5 to 1, C14:0 to C12:0 ratio of at least about 7:1, and C14:0 to C16:0 ratio of at least about 1 to 2.

51. The method of claim 46, said endogenous desaturase is selected from the group consisting of stearoyl ACP desaturase and delta 12 fatty acid desaturase.

52. The method of claim 46, wherein said exogenous gene is selected from the group consisting of a gene encoding an acyl-ACP thioesterase.

53. The method of claim 52, wherein said exogenous gene encodes an acyl-ACP thioesterase selected from the group consisting of *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #AAC49001); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #Q39473); *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank #Q41635); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank #AAB71730); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #ABD83939); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAD42220); *Populus tomentosa* fatty acyl-ACP thioesterase (GenBank #ABC47311); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #NP_172327); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank

#CAA85387); *Arabidopsis thaliana* fatty acyl-ACP thioesterase (GenBank #CAA85388); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #Q9SQI3); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAA54060); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC72882); *Cuphea calophylla subsp. mesostemon* fatty acyl-ACP thioesterase (GenBank #ABB71581); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAC19933); *Elaeis guineensis* fatty acyl-ACP thioesterase (GenBank #AAL15645); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #Q39513); *Gossypium hirsutum* fatty acyl-ACP thioesterase (GenBank #AAD01982); *Vitis vinifera* fatty acyl-ACP thioesterase (GenBank #CAN81819); *Garcinia mangostana* fatty acyl-ACP thioesterase (GenBank #AAB51525); *Brassica juncea* fatty acyl-ACP thioesterase (GenBank #ABI18986); *Madhuca longifolia* fatty acyl-ACP thioesterase (GenBank #AAX51637); *Brassica napus* fatty acyl-ACP thioesterase (GenBank #ABH11710); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY86877); *Oryza sativa* (japonica cultivar-group) fatty acyl-ACP thioesterase (GenBank #NP_001068400); *Oryza sativa* (indica cultivar-group) fatty acyl-ACP thioesterase (GenBank #EAY99617); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #AAC49269); *Ulmus Americana* fatty acyl-ACP thioesterase (GenBank #AAB71731); *Cuphea lanceolata* fatty acyl-ACP thioesterase (GenBank #CAB60830); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49180); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858); *Iris germanica* fatty acyl-ACP thioesterase (GenBank #AAG43858.1); *Cuphea palustris* fatty acyl-ACP thioesterase (GenBank #AAC49179); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB71729); *Myristica fragrans* fatty acyl-ACP thioesterase (GenBank# AAB71729.1); *Cuphea hookeriana* fatty acyl-ACP thioesterase (GenBank #U39834); *Umbellularia californica* fatty acyl-ACP thioesterase (GenBank # M94159); *Cinnamomum camphora* fatty acyl-ACP thioesterase (GenBank #U31813); *Cuphea wrightii* fatty acyl-ACOP thioesterase (GenBank #U56103); and *Ricinus communis* fatty acyl-ACP thioesterase (GenBank #ABS30422).

54. The method of claim 46, wherein said oleaginous microbial cell further comprises a gene encoding a sucrose invertase.

55. The method of claim 46, wherein said oleaginous microbial cell is a cell of a microalgal genus or species selected from *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, 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 parva, Chlorella photophila, Chlorella pringsheimii, Chlorella protothecoides (including any of UTEX strains 1806, 411, 264, 256, 255, 250, 249, 31, 29, 25, and CCAP strains 211/17 and 211/8d), 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, 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., 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, Pascheria acidophila, Pavlova sp., Phagus, Phormidium, Platymonas sp., Pleurochrysis carterae, Pleurochrysis dentate, Pleurochrysis sp., Prototheca wickerhamii, Prototheca stagnora, Prototheca portoricensis, Prototheca moriformis, Prototheca zopfii, Pyramimonas sp., Pyrobotrys, Sarcinoid chrysophyte, Scenedesmus armatus, Spirogyra, Spirulina platensis, Stichococcus sp., Synechococcus sp., Tetraedron, Tetraselmis sp., Tetraselmis suecica, Thalassiosira weissflogii, and *Viridiella fridericiana.*

56. The method of claim 55, wherein said oleaginous microbial cell is a cell of the genus *Prototheca.*

57. The method of claim 56, wherein said oleaginous microbial cell is a cell of the genus *Prototheca moriformis.*

58. The method of claim 48, wherein said naturally occurring oil is coconut oil.

59. The method of claim 48, wherein said naturally occurring oil is palm oil and wherein said exogenous gene comprises a *Elaeis guiniensis* thioesterase gene, a *Cuphea hookeriana* thioesterase gene, a combination of a *Cuphea hookeriana* KAS IV gene and a *Cuphea wrightii* FATB2 gene, or a construct designed to disrupt an endogenous KAS II gene.

60. The method of claim 48, wherein said naturally occurring oil is palm kernel oil and wherein said exogenous gene comprises a combination of a *Cuphea wrightii* FATB2 gene and a construct designed to disrupt an endogenous SAD2B gene.

61. The method of claim 48, wherein said naturally occurring oil is shea butter.

62. The method of claim 48, wherein said naturally occurring oil is beef tallow.

63. The method of claim 48, wherein said naturally occurring oil is lard and wherein said exogenous gene comprises a combination of *U. californica* thioesterase gene

and a construct designed to disrupt an endogenous SAD2B gene, a combination of a *Garcinia mangostana* thioesterase gene and a construct designed to disrupt an endogenous SAD2B gene, a *Brassica napus* thioesterase gene, or a *Cuphea hookeriana* thioesterase gene.

64. A method of making an oil-based product, the method comprising the steps of:

a. subjecting the oleaginous microbial triglyceride oil composition of claim 21 to at least one chemical reaction selected from the group consisting of: saponification; metathesis; acid hydrolysis; alkaline hydrolysis; enzymatic hydrolysis; catalytic hydrolysis; hot-compressed water hydrolysis; a catalytic hydrolysis reaction wherein the lipid is split into glycerol and fatty acids; an amination reaction to produce fatty nitrogen compounds; an ozonolysis reaction to produce mono- and dibasic-acids; a triglyceride splitting reaction selected from the group consisting of enzymatic splitting and pressure splitting; a condensation reaction that follows a hydrolysis reaction; a hydroprocessing reaction; a hydroprocessing reaction and a deoxygenation reaction or a condensation reaction prior to or simultaneous with the hydroprocessing reaction; a gas removal reaction; a deoxygenation reaction selected from the group consisting of a hydrogenolysis reaction, hydrogenation, a consecutive hydrogenation-hydrogenolysis reaction, a consecutive hydrogenolysis-hydrogenation reaction, and a combined hydrogenation-hydrogenolysis reaction; a condensation reaction following a deoxygenation reaction; an esterification reaction; an interestification reaction; a transesterification reaction; a hydroxylation reaction; and a condensation reaction following a hydroxylation reaction; and

b. isolating the product of said reaction from the other components.

65. The method of claim 64, wherein the oil-based product is selected from the group consisting of soap, fuel, dielectric fluid, hydraulic fluid, plasticizer, lubricant, heat transfer fluid, and metal working fluid.

66. The method of claim 65, wherein the oil-based product is a fuel product selected from the group consisting of:

a. biodiesel

b. renewable diesel; and

c. jet fuel.

67. The method of claim 66, wherein the fuel product is biodiesel with one or more of the following attributes:

i. less than 0.3 mcg/g total carotenoids;

ii. less than 0.005 mcg/g lycopene;

iii. less than 0.005 mcg/g beta carotene;

iv. less than 0.3 mcg/g chlorophyll A;

v. less than 175 mcg/g gamma tocopherol;

vi. less than 0.25% brassicasterol, campesterol, stignasterol, or beta-sitosterol;

vii. less than 350 mcg/g total tocotrienols;

viii. less than 0.05 mcg/g lutein; or

ix. less than 275 mcg/g tocopherols.

68. The method of claim 66, wherein the fuel product is renewable diesel that has a T10-T90 of at least 20°C, 40°C or 60°C.

69. The method of claim 66, wherein the fuel product is jet fuel that meets HRJ-5 and/or ASTM specification D1655.

WHAT IS CLAIMED IS:

1. An oil composition produced by cultivating an oleaginous microbe and recovering the oil composition from the microbe, the oil composition comprising triglycerides and sterols produced by the microbe, wherein the fatty acid profile of the triglyceride oil composition comprises at least 60% C18:1, and less than 7% C18:2, wherein the triglyceride oil composition is produced by a recombinant oleaginous microbe comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microbe has been inactivated or mutated to have less enzymatic activity.

2. The oil composition of claim 1, wherein the fatty acid profile of the triglyceride oil composition comprises at least 70% C18:1.

3. The oil composition of claim 2, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1.

4. The oil composition of claim 3, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1.

5. The oil composition of claim 1, wherein the fatty acid profile of the triglyceride oil composition comprises less than 5% C18:2.

6. The oil composition of claim 5, wherein the fatty acid profile of the triglyceride oil composition comprises less than 3% C18:2.

7. The oil composition of claim 6, wherein the fatty acid profile of the triglyceride oil composition comprises less than 2% C18:2.

8. The oil composition of claim 1, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1 and less than 5% C18:2.

9. The oil composition of claim 8, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1 and less than 3% C18:2.

10. The oil composition of claim 9, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1 and less than 3% C18:2.

11. The oil composition of claim 10, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1 and less than 2% C18:2.

12. An oil composition produced by cultivating an oleaginous microalgae and recovering the oil composition from the microalgae, the oil composition comprising triglycerides and sterols produced by the microalgae, wherein the fatty acid profile of the triglyceride oil composition comprises at least 60% C18:1, and less than 7% C18:2, wherein the triglyceride oil composition is produced by a recombinant oleaginous microalgae comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microalgae has been inactivated or mutated to have less enzymatic activity.

13. The oil composition of claim 12, wherein the microalgae is *Prototheca.*

14. The oil composition of claim 13, wherein the microalgae is *Prototheca moriformis.*

15. The oil composition of claim 13, wherein the fatty acid profile of the triglyceride oil composition comprises at least 70% C18:1.

16. The oil composition of claim 15, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1.

17. The oil composition of claim 16, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1.

18. The oil composition of claim 13, wherein the fatty acid profile of the triglyceride oil composition comprises less than 5% C18:2.

19. The oil composition of claim 18, wherein the fatty acid profile of the triglyceride oil composition comprises less than 3% C18:2.

20. The oil composition of claim 19, wherein the fatty acid profile of the triglyceride oil composition comprises less than 2% C18:2.

21. The oil composition of claim 13, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1 and less than 5% C18:2.

22. The oil composition of claim 21, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1 and less than 3% C18:2.

23. The oil composition of claim 22, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1 and less than 3% C18:2.

24. The oil composition of claim 23, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% C18:1 and less than 2% C18:2.

25. The oil composition of claim 13, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% C18:1 and less than 1% C18:2.

26. The oil of claim 12, wherein the microalgae comprises 23S rRNA having at least 85% sequence identity to SEQ ID NO:15.

27. The oil of claim 12, wherein the microalgae comprises 23S rRNA having at least 90% sequence identity to SEQ ID NO:15.

28. The oil of claim 12, wherein the microalgae comprises 23S rRNA having at least 95% sequence identity to SEQ ID NO:15.

29. An oil composition, produced by cultivating an oleaginous microbe and recovering the oil composition from the microbe, the oil composition comprising triglycerides and sterols produced by the microbe, wherein the fatty acid profile of the triglyceride oil composition comprises at least 50% saturated fatty acids, wherein the triglyceride oil composition is produced by a recombinant oleaginous microbe comprising an exogenous gene, and optionally wherein an endogenous desaturase of the oleaginous microbe has been inactivated or mutated to have less enzymatic activity.

30. The oil composition of claim 29, wherein the fatty acid profile of the triglyceride oil composition comprises at least 70% saturated fatty acids.

31. The oil composition of claim 30, wherein the fatty acid profile of the triglyceride oil composition comprises at least 80% saturated fatty acids.

32. The oil composition of claim 31, wherein the fatty acid profile of the triglyceride oil composition comprises at least 90% saturated fatty acids.

33. The oil composition of claim 32, wherein the saturated fatty acids comprise at least 30% C12:0.

34. The oil composition of claim 33, wherein the saturated fatty acids comprise at least 40% C12:0.

35. The oil composition of claim 34, wherein the saturated fatty acids comprise at least 50% C12:0.

36. The oil of claim 29, wherein the microbe is a microalgae.

37. The oil of claim 36, wherein the microalgae comprises 23S rRNA having at least 85% sequence identity to SEQ ID NO:15.

38. The oil of claim 36, wherein the microalgae comprises 23S rRNA having at least 90% sequence identity to SEQ ID NO:15.

39. The oil of claim 36, wherein the microalgae comprises 23S rRNA having at least 95% sequence identity to SEQ ID NO:15.