Amended claims

1. A yeast cell capable of producing a desaturated fatty acyl-coenzyme A (fatty acyl-CoA) having n' double bonds, wherein at least one of said double bonds is at position 12 and at least one of said double bonds is at position 9, wherein said yeast cell expresses:
    i) a heterologous Δ12 fatty acyl-CoA desaturase, said desaturase being capable of introducing a double bond at position 12 in a saturated or desaturated fatty acyl-CoA, preferably a desaturated fatty acyl-CoA, having a carbon chain length of at least 13 and having n double bond(s),
    ii) a further desaturase, wherein said further desaturase is a homologous desaturase or a heterologous desaturase and is capable of introducing a double bond at position 9 in a saturated or desaturated fatty acyl-CoA,

    wherein n and n' are integers,
    wherein $0 \leq n \leq 3$ and wherein $2 \leq n' \leq 4$,
    wherein said desaturated fatty acyl-CoA having n' double bond(s) has a carbon chain length of at the most 17.

2. The yeast cell according to claim 1, wherein said heterologous Δ12 desaturase is native to an organism of a genus selected from the group consisting of *Cadra, Ephestia, Plodia, Maliarpha, Fumibotys* and *Amorbia*, such as to a species selected from the group consisting of *Cadra cautella, Ephestia elutella, Ephestia kuehniella, Plodia interpunctella, Maliarpha separatella,* and *Amorbia cuneana*, optionally wherein said heterologous Δ12 desaturase is a *Plodia* desaturase, such as a *Plodia interpunctella* desaturase or a *Cadra* desaturase, such as a *Cadra cautella* desaturase, or an *Ephestia* desaturase, such as an *Ephestia elutella* or an *Ephestia kuehniella* desaturase, further optionally wherein said heterologous Δ12 desaturase is a Pid12 desaturase as set forth in SEQ ID NO: 2 or an Eku_d12 desaturase as set forth in SEQ ID NO: 85, or a functional homologue thereof having at least 70% similarity or identity thereto, such as at least 80%, such as at least 90%, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99%, such as 100% similarity or identity thereto.

3. The yeast cell according to any one of the preceding claims, wherein said heterologous Δ12 desaturase is selected from the desaturases set forth in SEQ ID NO: 80, SEQ ID NO: 81 and SEQ ID NO: 82.

4. The yeast cell according to any one of the preceding claims, wherein said saturated or desaturated fatty acyl-CoA having a carbon chain length of at least 13 and having n double bonds:
    i) has a carbon length of at least 14, such as at least 15;
    ii) is tetradecanoyl-CoA or tetradecenoyl-CoA;
    iii) has one double bond (i.e. n = 1); and/or
    iv) is (Z9)-tetradecenoyl-CoA.

5. The yeast cell according to any one of the preceding claims, wherein said desaturated fatty acyl-CoA having n' double bond(s) wherein at least one of said double bond(s) is at position 12 and at least one of said double bond(s) is at position 9:
    i) has a carbon chain length of at the most 16, such as at the most 15, such as at the most 14, such as at least 15, such as at least 16, such as at least 17;
    ii) has two double bonds (i.e. n' = 2);
    iii) is (Z9, E12)-tetradecadienoyl-CoA.

6. The yeast cell according to any one of the preceding claims, wherein said further desaturase is a heterologous desaturase, such as a *Drosophila* or a *Choristoneura* desaturase, such as a *Drosophila melanogaster, Drosophila virilis, Drosophila grimshawi, Drosophila yakuba, Drosophila mojavensis, Drosophila pseudoobscura, Drosophila ananassae* or a *Choristoneura parallela* desaturase, optionally wherein said further heterologous desaturase is selected from the group consisting of Desat59 (SEQ ID NO: 8), Desat61 (SEQ ID NO: 4), Desat56 (SEQ ID NO: 57), Desat60 (SEQ ID NO: 59), Desat74 (SEQ ID NO: 61) and Desat24 (SEQ ID NO: 6) or functional variants thereof having at least 70% similarity or identity thereto, such as at least 80%, such as at least 90%,

such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99%, such as 100% similarity or identity thereto.

7. The yeast cell according to any one of the preceding claims, wherein the yeast cell is capable of producing (Z9, E12)-tetradecadien-1-ol, said yeast cell further expressing at least one alcohol-forming fatty acyl-CoA reductase (FAR) capable of converting at least a part of (Z9, E12)-tetradecadienoyl-CoA into (Z9, E12)-tetradecadien-1-ol; optionally wherein the FAR is native to an organism of a genus selected from the group consisting of *Agrotis, Amyelois, Bicyclus, Bombus, Chilo, Cydia, Helicoverpa, Heliothis, Lobesia, Ostrinia, Plodia, Plutella, Spodoptera, Trichoplusia, Tyta,* and *Yponomeuta*, such as *Agrotis ipsilon, Agrotis segetum, Amyelois transitella, Bicyclus anynana, Bombus lapidarius, Chilo Suppressalis, Cydia pomonella, Helicoverpa armigera, Helicoverpa assulta, Heliothis subflexa, Heliothis virescens, Lobesia botrana, Ostrinia furnacalis, Ostrinia nubilalis, Ostrinia zag, Ostrinia zea, Plodia interpunctella, Plutella xylostella, Spodoptera exigua, Spodoptera frugiperda, Spodoptera littoralis, Spodoptera litura, Trichoplusia ni, Tyta alba,* and *Yponomeuta rorellus,* especially *Spodoptera exigua, Helicoverpa armigera, Spodoptera litura* and *Plodia interpunctella*; further optionally wherein the FAR is selected from the group consisting of FAR1 (SEQ ID NO: 20), FAR16 (SEQ ID NO: 22), FAR17 (SEQ ID NO: 24), FAR19 (SEQ ID NO: 26), FAR28 (SEQ ID NO: 28), FAR32 (SEQ ID NO: 30), FAR44 (SEQ ID NO: 63), FAR48 (SEQ ID NO: 65), FAR49 (SEQ ID NO: 67); FAR38 (SEQ ID NO: 32), FAR4 (SEQ ID NO: 69), FAR6 (SEQ ID NO: 71), FAR8 (SEQ ID NO: 73), FAR12 (SEQ ID NO: 75), FAR11 (SEQ ID NO: 77) or FAR5 (SEQ ID NO: 79), or functional variants thereof having at least 70% similarity or identity thereto, such as at least 80%, such as at least 90%, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99%, such as 100% similarity or identity thereto.

8. The yeast cell according to any one of the preceding claims, wherein the yeast cell belongs to a genus selected from *Saccharomyces*, *Pichia*, *Yarrowia*,

Kluyveromyces, *Candida, Rhodotorula, Rhodosporidium, Cryptococcus, Trichosporon* and *Lipomyces,* optionally wherein the yeast cell belongs to a species selected from *Saccharomyces cerevisiae, Saccharomyces boulardi, Pichia pastoris, Kluyveromyces marxianus, Candida tropicalis, Cryptococcus albidus, Lipomyces lipofera, Lipomyces starkeyi, Rhodosporidium toruloides, Rhodotorula glutinis, Trichosporon pullulan* and *Yarrowia lipolytica,* preferably wherein the yeast cell is a *Yarrowia lipolytica* cell or a *Saccharomyces cerevisiae* cell.

9. The yeast cell according to any one of the preceding claims, wherein the yeast cell is capable of producing:
    i) (Z9, E12)-tetradecadienoic acid with a titer of at least 1 mg/L, such as at least 1.5 mg/L, such as at least 1.7 mg/L or more;
    ii) (Z9, E12)-tetradecadienoic acid with a titer of at least 20 mg/L, such as at least 50 mg/L, such as at least 60 mg/L, such as at least 70 mg/L, such as at least 80 mg/L, such as at least 90 mg/L, such as at least 100 mg/L, such as at least 150 mg/L, such as at least 200 mg/L, such as at least 250 mg/L, such as at least 500 mg/L, such as at least 750 mg/L, such as at least 1 g/L, such as at least 2 g/L, such as at least 3 g/L, such as at least 4 g/L, such as at least 5 g/L, such as at least 6 g/L, such as at least 7 g/L, such as at least 8 g/L, such as at least 9 g/L, such as at least 10 g/L or more; and/or
    iii) (Z9, E12)-tetradecadien-1-ol with a titer of at least 0.005 mg/L, such as at least 0.01 mg/L, such as at least 0.02 mg/L, such as at least 0.03 mg/L, such as at least 0.05 mg/L, such as at least 0.06 mg/L, such as at least 0.075 mg/L, such as at least 0.1 mg/L, such as at least 0.2 mg/L, such as at least 0.3 mg/L, such as at least 0.4 mg/L, such as at least 0.5 mg/L, such as at least 0.6 mg/L, such as at least 0.7 mg/L, such as at least 0.8 mg/L, such as at least 0.9 mg/L, such as at least 1 mg/L, such as at least 2 mg/L, such as at least 3 mg/L, such as at least 4 mg/L, such as at least 5 mg/L, such as at least 6 mg/L, such as at least 7 mg/L, such as at least 8 mg/L, such as at least 9 mg/L, such as at least 10 mg/L or more.

10. A method for producing a desaturated fatty acyl-CoA having n' double bonds, wherein at least one of said double bonds is at position 12 and at least one of said double bonds is at position 9, in a yeast cell, said method comprising the steps of:
    i) providing a yeast cell according to any one of claims 1 and 9,
    ii) incubating said yeast cell in a medium under conditions allowing expression of:
        a. a heterologous Δ12 desaturase, said desaturase being capable of introducing a double bond at position 12 in a saturated or desaturated fatty acyl-CoA, preferably a desaturated fatty-acyl-CoA, having a carbon chain length of at least 13 and having n double bond(s),
        b. a further desaturase, wherein said further desaturase is a homologous desaturase or a heterologous desaturase and is capable of introducing a double bond at position 9 in a saturated or desaturated fatty acyl-CoA,

    wherein n and n' are integers,
    wherein $0 \leq n \leq 3$ and wherein $2 \leq n' \leq 4$,
    thereby producing a desaturated fatty acyl-CoA having n' double bonds,
    wherein at least one of said double bonds is at position 12 and at least one of said double bonds is at position 9,
    wherein said desaturated fatty acyl-CoA having n' double bond(s) has a carbon chain length of at the most 17.

11. The method according to claim 10, wherein:
    i) said heterologous Δ12 desaturase is as defined in claim 0;
    ii) said further desaturase is as defined in claim 0;
    iii) said yeast cell is as defined in any one of claims 1 and 9;
    iv) said desaturated fatty acyl-CoA having n' double bonds is as defined in claim 0; and/or
    v) said saturated or desaturated fatty acyl-CoA having a carbon chain length of at least 13 and having n double bonds is as defined in claim 0.

12. The method according to any one of claims 10 to 11, wherein said yeast cell further expresses at least one alcohol-forming fatty acyl-CoA reductase (FAR)

capable of converting at least part of (Z9, E12)-tetradecadienoyl-CoA into (Z9, E12)-tetradecadien-1-ol, respectively, optionally wherein said FAR is as defined in claim 7.

13. The method according to any one of claims 10 to 12, further comprising the steps of:
    i) recovering the (Z9, E12)-tetradecadien-1-ol;
    ii) converting the (Z9,E12)-tetradecadien-1-ol into (Z9,E12)-tetradecadien-1-ol acetate;
    iii) converting the (Z9, E12)-tetradecadien-1-ol into (Z9, E12)-tetradecadienal, and/or
    iv) formulating (Z9, E12)-tetradecadien-1-ol, (Z9,E12)-tetradecadien-1-ol acetate and/or (Z9, E12)-tetradecadienal in a pheromone composition.

14. A pheromone composition obtainable by a method comprising the following steps:
    i) producing (Z9, E12)-tetradecadien-1-ol by the method according to any one of claims 10 to 13;
    ii) recovering the (Z9, E12)-tetradecadien-1-ol;
    iii) converting the (Z9, E12)-tetradecadien-1-ol into (Z9, E12)-tetradecadien-1-ol acetate;
    iv) converting the (Z9, E12)-tetradecadien-1-ol into (Z9, E12)-tetradecadienal;
    v) formulating said (Z9, E12)-tetradecadien-1-ol, (Z9, E12)-tetradecadien-1-ol acetate and/or (Z9, E12)-tetradecadienal as a pheromone composition.

15. A pheromone composition comprising (Z9, E12)-tetradecadien-1-ol, (Z9, E12)-tetradecadien-1-ol acetate and/or (Z9, E12)-tetradecadienal, wherein said pheromone composition comprises at least 70% biobased carbon, such as at least 75% biobased carbon, such as at least 80% biobased carbon, such as at least 85% biobased carbon, such as at least 90% biobased carbon, such as at least 95% biobased carbon.

16. A pheromone compound selected from the group consisting of (Z9, E12)-tetradecadien-1-ol, (Z9, E12)-tetradecadien-1-ol acetate and (Z9, E12)-tetradecadienal, wherein said pheromone compound comprises at least 70% biobased carbon, such as at least 75% biobased carbon, such as at least 80% biobased carbon, such as at least 85% biobased carbon, such as at least 90% biobased carbon, such as at least 95% biobased carbon.

17. Use of a *Plodia interpunctella* desaturase in a method for introducing a double bond at position 12 in a saturated or desaturated fatty acyl-CoA, optionally wherein the *Plodia interpunctella* desaturase is Pid12 (SEQ ID NO: 2) or functional variants thereof having at least 70% similarity or identity thereto, such as at least 80%, such as at least 90%, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99%, such as 100% similarity or identity thereto.

18. Use of an *Ephestia kuehniella* desaturase in a method for introducing a double bond at position 12 in a saturated or desaturated fatty acyl-CoA, optionally wherein the *Ephestia kuehniella* desaturase is Eku_d12 (SEQ ID NO: 85) or functional variants thereof having at least 70% similarity or identity thereto, such as at least 80%, such as at least 90%, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99%, such as 100% similarity or identity thereto.