METHOD AND CELL LINE FOR PRODUCTION OF POLYKETIDES IN YEAST

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of United States Provisional Patent Application No. 62/460,526, entitled METHOD AND CELL LINE FOR PRODUCTION OF PHYTOCANNABINOIDS IN YEAST, filed February 17, 2017, which is hereby incorporated by reference in its entirety.

FIELD

[0002] The present disclosure relates generally to production of polyketides in yeast.

BACKGROUND

[0003] Polyketides are precursors to many valuable secondary metabolites in plants. For example, phytocannabinoids, which are naturally produced in *Cannabis sativa*, other plants, and some fungi, have significant commercial value. Over 105 phytocannabinoids are known to be biosynthesized in *C. sativa*, or result from thermal or other decomposition from phytocannabinoids biosynthesized in *C. sativa*. While the *C. sativa* plant is also a valuable source of grain, fiber, and other material, growing *C. sativa* for phytocannabinoid production, particularly indoors, is costly in terms of energy and labour. Subsequent extraction, purification, and fractionation of phytocannabinoids from the *C. sativa* plant is also labour and energy intensive.

[0004] Phytocannabinoids are pharmacologically active molecules that contribute to the medical and psychotropic effects of *C. sativa*. Biosynthesis of phytocannabinoids in the *C. sativa* plant scales similarly to other agricultural projects. As with other agricultural projects, large scale production of phytocannabinoids by growing *C. sativa* requires a variety of inputs (e.g. nutrients, light, pest control, CO_2, etc.). The inputs required for cultivating *C. sativa* must be provided. In addition, cultivation of *C. sativa*, where allowed, is currently subject to heavy regulation, taxes, and rigorous quality control where products prepared from the plant are for commercial use, further increasing costs. Phytocannabinoid analogues are pharmacologically active molecules that are structurally similar to phytocannabinoids. Phytocannabinoid analogues are often synthesized chemically, which can be labour intensive and costly. As a result, it may be economical to produce the phytocannabinoids and

phytocannabinoid analogues in a robust and scalable, fermentable organism. *Saccharomyces cerevisiae* is an example of a fermentable organism that has been used to produce industrial scales of similar molecules.

[0005] The time, energy, and labour involved in growing *C. sativa* for production of naturally-occurring phytocannabinoids provides a motivation to produce transgenic cell lines for production of phytocannabinoids by other means. Polyketides, including olivetolic acid and its analogues are valuable precursors to phytocannabinoids.

SUMMARY

[0006] It is an object of the present disclosure to obviate or mitigate at least one disadvantage of previous approaches to producing phytocannabinoids outside of the *C. sativa* plant, and of previous approaches to producing phytocannabinoid analogues. Many of the 105 phytocannabinoids found in *Cannabis sativa* may be biosynthesized from olivetolic acid or olivetol. Phytocannabinoids and their analogues may also be chemically synthesized from olivetol and other reagents. Olivetol and olivetolic acid may also be used in pharmaceutical or nutritional product development as well. As a consequence it may be desirable to improve yeast-based production of olivetol, olivetolic acid or analogues of either olivetol or olivetolic acid. Similarly, an approach that allows for production of phytocannabinoid analogues without the need for labour-intensive synthesis may be desirable.

[0007] The methods and cells lines provided herein may apply and include *Saccharomyces cerevisiae* that has been transformed to include a gene for *Dictyostelium discoideum* polyketide synthase ("**DiPKS**"). DiPKS is a fusion protein consisting of both a type I fatty acid synthase ("**FAS**") and a polyketide synthase ("**PKS**") and is referred to as a hybrid "**FAS-PKS**" protein. DiPKS catalyzes synthesis of methyl-olivetol from malonyl-CoA. The reaction has a 6:1 stoichiometric ratio of malonyl-CoA to methyl-olivetol. Downstream prenyltransferase enzymes catalyzes synthesis of methyl cannabigerol ("**meCBG**") from methyl-olivetol and geranyl pyrophosphate ("**GPP**"), similarly to synthesis of cannabigerolic acid ("**CBGa**") from olivetolic acid and GPP. Hexanoic acid is toxic to *S. cerevisiae*. Hexanoyl-CoA is a precursor for synthesis of olivetol by *Cannabis Sativa* olivetolic acid synthase ("**OAS**"). As a result, when using DiPKS rather than OAS, hexanoic acid need not be added to the growth media, which may result in increased growth of the *S. cerevisiae*

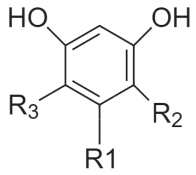
cultures and greater yield of meCBG compared with yields of CBG when using OAS. In addition, in *C. sativa*, the olivetol is carboxylated in the presence of olivetolic acid cyclase ("**OAC**") or another polyketide cyclase into olivetolic acid, which feeds into the CBGa synthesis metabolic pathway, beginning with prenylation of olivetolic acid catalyzed by in *C. sativa* by a membrane-bound prenyltransferase. The option to produce olivetol or methyl-olivetol rather than olivetolic acid may facilitate preparation of decarboxylated species of phytocannabinoids and methylated analogues of phytocannabinoids.

[0008] For some applications, meCBG and methylated downstream phytocannabinoid analogues that can be synthesized from meCBG (similarly to downstream phytocannabinoids being synthesized from CBGa in *C. sativa*) may be valuable. In other cases, phytocannabinoids structurally identical to the decarboxylated forms of naturally-occurring phytocannabinoids may be more desirable. For production of phytocannabinoids that are structurally identical to the decarboxylated forms of naturally-occurring phytocannabinoids, DiPKS may be modified relative to wild type DiPKS to reduce methylation of olivetol, resulting in synthesis of either both olivetol and methyl-olivetol

[0009] Synthesis of olivetol and methyl-olivetol may be facilitated by increased levels of malonyl-CoA in the cytosol. The *S. cerevisiae* may have overexpression of native acetaldehyde dehydrogenase and expression of a mutant acetyl-CoA synthase or other gene, the mutations resulting in lowered mitochondrial acetaldehyde catabolism. Lowering mitochondrial acetaldehyde catabolism by diverting the acetaldehyde into acetyl-CoA production increases malonyl-CoA available for synthesizing olivetol. Acc1 is the native yeast malonyl CoA synthase. The *S. cerevisiae* may have over-expression of Acc1 or modification of Acc1 for increased activity and increase available malonyl-CoA. The *S. cerevisiae* may include modified expression of Maf1 or other regulators of tRNA biosynthesis. Overexpressing native Maf1 has been shown to reduce loss of isopentyl pyrophosphate ("**IPP**") to tRNA biosynthesis and thereby improve monoterpene yields in yeast. IPP is an intermediate in the mevalonate pathway. Upc2 is an activator for sterol biosynthesis in *S. cerevisiae*, and a Glu888Asp mutation of Upc2 may increase monoterpene production in yeast. The *S. cerevisiae* may include a co-factor loading enzyme to increase the activity of DiPKS. Other species of yeast, including *Yarrowia lipolytica*, *Kluyveromyces marxianus*, *Kluyveromyces lactis*, *Rhodosporidium toruloides, Cryptococcus curvatus, Trichosporon pullulan* and *Lipomyces lipoferetc*, may be applied.

[0010] In a first aspect, herein provided is a method and cell line for producing polyketides in yeast. The method applies, and the cell line includes, a yeast cell transformed with a polyketide synthase coding sequence. The polyketide synthase enzyme catalyzes synthesis of olivetol or methyl-olivetol, and may include Dictyostelium discoideum polyketide synthase ("**DiPKS**"). Wild type DiPKS produces methyl-olivetol only. DiPKS may be modified to produce olivetol only or a mixture of both olivetol and methyl-olivetol. The yeast cell may be modified to include a phosphopantetheinyl transferase for increased activity of DiPKS. The yeast cell may be modified to mitigate mitochondrial acetaldehyde catabolism for increasing malonyl-CoA available for synthesizing olivetol or methyl-olivetol.

[0011] In a further aspect, herein provided is a method of producing a polyketide, the method comprising: providing a yeast cell comprising a first polynucleotide coding for a polyketide synthase enzyme and propagating the yeast cell for providing a yeast cell culture. Tpolyketide synthase enzyme is for producing at least one species of polyketide from malonyl-CoA, the polyketide having structure I:



I. On structure I, R1 is a pentyl group. On structure I, R2 is H, carboxyl, or methyl. On structure I, R3 is H, carboxyl, or methyl.

[0012] In some embodiments, the polyketide synthase enzyme comprises a DiPKS polyketide synthase enzyme from *D. discoideum*. In some embodiments, the first polynucleotide comprises a coding sequence for the DiPKS polyketide synthase enzyme with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 535 to 9978 of SEQ ID NO: 13. In some embodiments, the first polynucleotide has between 80% and 100% base sequence identity with bases 535 to 9978 of SEQ ID NO: 13. In some embodiments, the at least one species of polyketide comprises a polyketide with a methyl group at R2. In some embodiments, he DiPKS polyketide synthase enzyme comprises a mutation affecting an active site of a C-Met domain for mitigating methylation of the at least one species of polyketide, resulting in the at least one species of polyketide comprising a first polyketide wherein R2 is methyl and R3 is H, and a second polyketide wherein R2 is H and R3 is H. In some embodiments, the DiPKS polyketide synthase comprises a DiPKS$^{G1516D;\ G1518A}$

polyketide synthase. In some embodiments, the first polynucleotide comprises a coding sequence for the DiPKS$^{G1516D;\ G1518A}$ polyketide synthase enzyme with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 9. In some embodiments, the first polynucleotide has between 80% and 100% base sequence identity with bases 523 to 9966 of SEQ ID NO: 9. In some embodiments, the DiPKS polyketide synthase comprises a DiPKS^{G1516R} polyketide synthase. In some embodiments, the first polynucleotide comprises a coding sequence for the DiPKS^{G1516R} polyketide synthase enzyme with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10. In some embodiments, the first polynucleotide has between 80% and 100% base sequence identity with bases 523 to 9966 of SEQ ID NO: 10. In some embodiments, the DiPKS polyketide synthase enzyme comprises a mutation reducing activity at an active site of a C-Met domain of the DiPKS polyketide synthase enzyme, for preventing methylation of the at least one species of polyketide, resulting in the at least one species of polyketide having a hydrogen R2 group and a hydrogen R3 group. In some embodiments, the yeast cell comprises a second polynucleotide coding for a phosphopantetheinyl transferase enzyme for increasing the activity of DiPKS. In some embodiments, the phosphopantetheinyl transferase comprises NpgA phosphopantetheinyl transferase enzyme from *A. nidulans*. In some embodiments, wherein the second polynucleotide comprises a coding sequence for the NpgA phosphopantetheinyl transferase enzyme from A. nidulans with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 1170 to 2201 of SEQ ID NO: 8. In some embodiments, the second polynucleotide has between 80% and 100% base sequence identity with bases 1170 to 2201 of SEQ ID NO: 8.

[0013] In some embodiments, the polyketide synthase enzyme comprises an active site for synthesizing the at least one species of polyketide from malonyl-CoA without a longer chain ketyl-CoA. In some embodiments, the at least one species of polyketide comprises at least one of olivetol, olivetolic acid, methyl-olivetol, or methyl-olivetolic acid.

[0014] In some embodiments, R2 is H and R3 is H.

[0015] In some embodiments, R2 is carboxyl and R3 is H.

[0016] In some embodiments, R2 is methyl and R3 is H.

[0017] In some embodiments, R2 is carboxyl and R3 is methyl

[0018] In some embodiments, the yeast cell comprises a genetic modification to increase available malonyl-CoA. In some embodiments, the genetic modification comprises increased expression of Maf1. In some embodiments, the yeast cell comprises a second polynucleotide including a coding sequence for Maf1 with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 936 to 2123 of SEQ ID NO: 6. In some embodiments, the second polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 80% and 100% base sequence identity with SEQ ID NO: 6. In some embodiments, the genetic modification comprises cytosolic expression of an aldehyde dehydrogenase and an acetyl-CoA synthase. In some embodiments, the yeast cell comprises a second polynucleotide including a coding sequence for Acs^{L641P} from *S. enterica* with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 3938 to 5893 of SEQ ID NO: 2, and a coding sequence for Ald6 from *S. cerevisiae* with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 1494 to 2999 of SEQ ID NO 2. In some embodiments, the second polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 80% and 100% base sequence identity with bases 51 to 7114 SEQ ID NO: 2. In some embodiments, the genetic modification comprises increased expression of malonyl-CoA synthase. In some embodiments, the yeast cell comprises a second polynucleotide including a coding sequence for a coding sequence for $Acc1^{S659A; S1167A}$ from *S. cerevisiae*. In some embodiments, the second polynucleotide includes a coding sequence for the $Acc1^{S659A; S1167A}$ enzyme, with a portion thereof having a primary structure with between 80% and 100% amino acid residue sequence identity with a protein portion coded for by a reading frame defined by bases 9 to 1716 of SEQ ID NO: 5. In some embodiments, the second polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 80% and 100% base sequence identity with SEQ ID NO: 5. In some embodiments, the genetic modification comprises increased expression of an activator for sterol biosynthesis. In some embodiments, the yeast cell comprises a second polynucleotide including a coding sequence for $Upc2^{E888D}$ from S. cerevisiae with a primary structure having between 80% and

100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 975 to 3701 of SEQ ID NO: 7. In some embodiments, the second polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 80% and 100% base sequence identity with SEQ ID NO: 7

[0019] In some embodiments, the method includes extracting the at least one species of polyketide from the yeast cell culture.

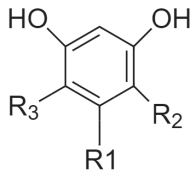
[0020] In a further aspect, herein provided is a yeast cell for producing at least one species of polyketide. The yeast cell includes a first polynucleotide coding for a polyketide synthase enzyme.

[0021] In some embodiments, features of one or more of the yeast cell, the first polynucleotide, or the second polynucleotide described herein are included in the yeast cell.

[0022] In a further aspect, herein provided is a method of transforming a yeast cell for production of at least one species of polyketide, the method comprising introducing a first polynucleotide coding for a polyketide synthase enzyme into the yeast cell line.

[0023] In some embodiments, features of one or more of the yeast cell, the first polynucleotide, or the second polynucleotide described herein are introduced into the yeast cell.

[0024] In a further aspect, herein provided is a method of producing a polyketide, the method comprising: providing a yeast cell comprising a first polynucleotide coding for a polyketide synthase enzyme and propagating the yeast cell for providing a yeast cell culture. The polyketide synthase enzyme is for producing at least one species of polyketide from malonyl-CoA, the polyketide having structure II:



II. On structure II, R1 is an alkyl group having 1, 2, 3, 4 or 5 carbons. On structure II, R2 is H, carboxyl, or methyl. On structure II, R3 is H, carboxyl, or methyl.

[0025] In some embodiments, features of one or more of the yeast cell, the first polynucleotide, or the second polynucleotide described herein are applied to the method.

[0026] In a further aspect, herein provided is a polynucleotide comprising a coding sequence for a DiPKSG1516D; G1518A polyketide synthase. In some embodiments, the

polynucleotide of claim 45 wherein the DiPKSG1516D; G1518A polyketide synthase enzyme has a primary structure with between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 9. In some embodiments, the polynucleotide has between 80% and 100% base sequence identity with bases 523 to 9966 of SEQ ID NO: 9.

[0027] In a further aspect, herein provided is a polynucleotide comprising a coding sequence for a DiPKSG1516R polyketide synthase. In some embodiments, the DiPKS^{G1516R} polyketide synthase enzyme has a primary structure with between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10. In some embodiments, the polynucleotide has between 80% and 100% base sequence identity with bases 523 to 9966 of SEQ ID NO: 10.

[0028] In a further aspect, herein provided is a DiPKS$^{G1516D; G1518A}$ polyketide synthase with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 9.

[0029] In a further aspect, herein provided is a DiPKS^{G1516R} polyketide synthase with a primary structure having between 80% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10.

[0030] Other aspects and features of the present disclosure will become apparent to those ordinarily skilled in the art upon review of the following description of specific embodiments in conjunction with the accompanying figures.

BRIEF DESCRIPTION OF THE DRAWINGS

[0031] Embodiments of the present disclosure will now be described, by way of example only, with reference to the attached Figures.

[0032] Fig. 1 is a schematic of biosynthesis of olivetolic acid and related compounds with different alkyl group chain lengths in *C. sativa*;

[0033] Fig. 2 is a schematic of biosynthesis of CBGa from hexanoic acid, malonyl-CoA, and geranyl pyrophosphate in *C. sativa*;

[0034] Fig. 3 is a schematic of biosynthesis of downstream phytocannabinoids in the acid form from CBGa in *C. sativa*;

[0035] Fig. 4 is a schematic of biosynthesis of olivetolic acid in a transformed yeast cell by DiPKS;

[0036] Fig. 5 is a schematic of biosynthesis of meCBG and downstream methylated phytocannabinoid analogues in a transformed yeast cell from methyl-olivetol;

[0037] Fig. 6 is a schematic of biosynthesis of meCBG and downstream methylated phytocannabinoid analogues in a transformed yeast cell from methyl-olivetol;

[0038] Fig. 7 is a schematic of functional domains in DiPKS, with mutations to a C-methyl transferase that for lowering methylation of olivetol;

[0039] Fig. 8 is a schematic of biosynthesis of methyl-olivetol and olivetol in a transformed yeast cell by DiPKS$^{G1516D;\ G1518A}$;

[0040] Fig. 9 is a schematic of biosynthesis of olivetol in a transformed yeast cell by DiPKS^{G1516R};

[0041] Fig. 10 shows production of methyl-olivetol by DiPKS, and of both methyl-olivetol and olivetol by DiPKS$^{G1516D;\ G1518A}$;

[0042] Fig. 11 shows production of methyl-olivetol by DiPKS in two separate strains of *S. cerevisiae*;

[0043] Fig. 12 shows production of methyl-olivetol by DiPKS in two separate strains of *S. cerevisiae*;

[0044] Fig. 13 shows production of methyl-olivetol by DiPKS, and of both methyl-olivetol and olivetol by DiPKS^{G1516R} in two separate strains of *S. cerevisiae*; and

[0045] Fig. 14 shows production of olivetol by DiPKS^{G1516R}, in three separate strains of *S. cerevisiae*.

DETAILED DESCRIPTION

[0046] Generally, the present disclosure provides methods and yeast cell lines for producing olivetol similar to the olivetolic acid that is naturally biosynthesized in the *Cannabis sativa* plant, and for producing methyl-olivetol. The olivetol and methyl-olivetol may be produced in transgenic yeast. The methods and cell lines provided herein include application of genes for enzymes absent from the *C. sativa* plant. Compared with approaches that use *C. sativa* OAS and OAC, the methods and cell lines provided herein result in olivetol and methyl-olivetol being synthesized rather than olivetolic acid, which may provide one or more benefits including biosynthesis of decarboxylated phytocannabinoids, biosynthesis of

methylated phytocannabinoid analogues, and biosynthesis production of phytocannabinoids without an input of hexanoic acid, which is toxic to *Saccharomyces cerevisiae* and other species of yeast.

[0047] The qualifier "decarboxylated" as used herein references a form of a phytocannabinoid or phytocannabinoid analogue lacking an acid group at, e.g. positions 2 or 4 of Δ9-tetrahydrocannabinol ("**THC**"), or an equivalent location in other phytocannabinoids or analogues corresponding to position 4 of olivetolic acid, which is the precursor to biosynthesis of CBGa in *C. sativa*. Acid forms of phytocannabinoids are biosynthesized from olivetolic acid in *C. sativa*. When the acid forms of phytocannabinoids are heated, the bond between the aromatic ring of the phytocannabinoid and the carboxyl group is broken. Decarboxylation results from heating carboxylated phytocannabinoids produced in *C. sativa*, which occurs rapidly during combustion or heating to temperatures generally above about 110 ºC. For simplicity, as used herein, "decarboxylated" refers to phytocannabinoids lacking the acid groups whether or not the phytocannabinoid included an acid group that was lost during true decarboxylation, or was biosynthesized without the carboxyl group.

[0048] Fig. 1 shows biosynthesis of olivetolic acid from polyketide condensation products of malonyl-CoA and hexanoyl-CoA, as occurs in in *C. sativa*. Olivetolic acid is a metabolic precursor to CBGa. CBGa is a precursor to a large number of downstream phytocannabinoids as described in further detail below. In most varieties of *C. sativa*, the majority of phytocannabinoids are pentyl-cannabinoids, which are biosynthesized from olivetolic acid, which is in turn synthesized from malonyl-CoA and hexanoyl-CoA at a 2:1 stoichiometric ratio. Some propyl-cannabinoids are observed, and are often identified with a "v" suffix in the widely-used three letter abbreviations (e.g. tetrahydrocannabivarin is commonly referred to as "**THCv**", cannabidivarin is commonly referred to as "**CBDv**", etc.). Fig. 1 also shows biosynthesis of divarinolic acid from condensation of malonyl-CoA with *n*-butyl-CoA, which would provide downstream propyl-phytocannabinoids.

[0049] Fig. 1 also shows biosynthesis of orsellinic acid from condensation of malonyl-CoA with acetyl-CoA, which would provide downstream methyl-phytocannabinoids. The term "methyl-phytocannabinoids" in this context means their alkyl side chain is a methyl group, where most phytocannabinoids have a pentyl group on the alkyl side chain and varinnic phytocannabinoids have a propyl group on the alkyl side chain. The context in which meCBG and other methylated phytocannabinoid analogues are called "methylated" is different from

and parallel to use of “methyl” as a prefix in “methyl-phytocannabinoids” and in Fig. 1. Similarly, since olivetol has a side chain of defined length (otherwise it would be one of the other three polyketides shown in Fig. 1 and not “olivetol”), methyl-olivetol is a reference to methylation on the ring and not to a shorter side chain.

[0050] Fig. 1 also shows biosynthesis of 2,4-diol-6-propylbenzenoic acid from condensation of malonyl-CoA with valeryl-CoA, which would provide downstream butyl-phytocannabinoids.

[0051] Fig. 2 shows biosynthesis of CBGa from hexanoic acid, malonyl-CoA, and geranyl pyrophosphate (“**GPP**”) in *C. sativa*, including the olivetolic acid biosynthesis step shown in Fig. 1. Hexanoic acid is activated with coenzyme A by hexanoyl-CoA synthase (“**Hex1**; Reaction 1 in Fig. 2). Polyketide synthase (also called olivetolic acid synthase “**OAS**” despite synthesizing olivetol and not olivetolic acid) and OAC together catalyze production of olivetolic acid from hexanoyl CoA and malonyl-CoA (Reaction 2 in Fig. 2). Prenyltransferase combines olivetolic acid with GPP, providing CBGa Step 3 in Fig. 2).

[0052] Fig. 3 shows biosynthesis of downstream acid forms of phytocannabinoids in *C. sativa* from CBGa. CBGa is oxidatively cyclized into Δ9-tetrahydrocannabinolic acid (“**THCa**”) by THCa synthase. CBGa is oxidatively cyclized into cannabidiolic acid (“**CBDa**”) by CBDa synthase. Other phytocannabinoids are also synthesized in *C. sativa*, such as cannabichromenic acid (“**CBCa**”), cannabielsoinic acid (“**CBEa**”), iso-tetrahydrocannabinolic acid (“**iso-THCa**”), cannabicyclolic acid (“**CBLa**”), or cannabicitrannic acid (“**CBTa**”) by other synthase enzymes, or by changing conditions in the plant cells in a way that affects the enzymatic activity in terms of the resulting phytocannabinoid structure. The acid forms of each of these general phytocannabinoid types are shown in Fig. 3 with a general “R” group to show the alkyl side chain, which would be a 5-carbon chain where olivetolic acid is synthesized from hexanoyl-CoA and malonyl-CoA. In some cases, the carboxyl group is alternatively found on a ring position opposite the R group from the position shown in Fig. 3 (e.g. positions 4 of THC rather than position 2 as shown in Fig. 3, etc.). The decarboxylated forms of the acid forms of the phytocannabinoids shown in Fig. 3 are, respectively, THC, cannabidiol (“**CBD**”), cannabichromene (“**CBC**”), cannabielsoin (“**CBE**”), iso-tetrahydrocannabinol (“**iso-THC**”), cannabicyclol (“**CBL**”), or cannabicitran (“**CBT**”).

[0053] Fig. 4 shows a biosynthetic pathway in transgenic yeast for production of methyl-olivetol from malonyl-CoA. A strain of yeast as provided herein for producing methyl-

olivetol as shown in Fig. 4 may include the DiPKS enzyme, which supports production of polyketides from malonyl-CoA only, with no requirement for hexanoic acid from the media. As above, DiPKS includes functional domains similar to domains found in a fatty acid synthase, a methyltransferase domain, and a Pks III domain (see Fig. 7), and is accordingly referred to as a FAS-PKS enzyme. Examples of yeast strains including a codon optimized synthetic sequence coding for the wildtype DiPKS gene are provided as "**HB80**" and "**HB98**", each of which are described in Table 3.

[0054] Figs. 5 and 6 show prenylation of the methyl-olivetol with GPP as a prenyl group donor, providing meCBG (Reaction 2 in Figs. 5 and 6, following Reaction 1 from Fig. 4). Application of DiPKS rather than OAS facilitates production of phytocannabinoids and phytocannabinoid analogues without hexanoic acid supplementation. Since hexanoic acid is toxic to *S. cerevisiae*, eliminating a requirement for hexanoic acid in the biosynthetic pathway for CBG or meCBG may provide greater yields of CBG or meCBG than the yields of CBG in a yeast cell expressing OAS and Hex1.

[0055] Figs. 5 and 6 show downstream methylated phytocannabinoid analogues corresponding to methyl-tetrahydrocannabinol ("**meTHC**"), methyl-cannabidiol ("**meCBD**"), methyl-cannabichromene ("**meCBC**"), methyl-cannabielsoin ("**meCBE**"), iso-methyl-tetrahydrocannabinol ("**iso-meTHC**"), methyl-cannabicyclol ("**meCBL**"), or methyl-cannabicitran ("**meCBT**"), which are methylated analogues of THC, CBD, CBC, CBE, iso-THC, CBL, and CBT, respectively, that may be prepared when methyl-olivetol is provided as a precursor chemical rather than olivetolic acid or olivetol. The decarboxylated forms of each of these methylated phytocannabinoid analogues are shown in Figs. 5 and 6 with a general "R" group to show the alkyl side chain, which would be a 5-carbon chain where synthesis results from hexanoyl-CoA and malonyl-CoA, or malonyl-CoA only.

[0056] Other than meCBD, a portion of the structure each of the downstream phytocannabinoid anaologues shown in Figs. 5 and 6 includes rotationally constrained groups bonded with the aromatic ring. As a result, each of the downstream phytocannabinoid analogues shown in Figs. 5 and 6 other than meCBD may be synthesized from meCBG in one of two rotational isomers. Depending on the rotational isomer of meCBG during synthesis, the methyl group in the resulting cyclized methylated phytocannabinoid analogues may be at the positions shown for the isomers of meTHC, meCBC, meCBE, iso-meTHC, meCBL, or meCBT in Fig. 5, or at the at the positions shown for the isomers of meTHC,

meCBC, meCBE, iso-meTHC, meCBL, or meCBT in Fig. 6. References to meTHC, meCBC, meCBE, iso-meTHC, meCBL, or meCBT herein include either or both of the isomers shown in Figs. 5 and 6.

[0057] DiPKS includes a C-methyltransferase domain that methylates olivetol at position 4 on the aromatic ring. As a result, any downstream prenylation would be of methyl-olivetol, resulting in meCBG, a phytocannabinoid analogue, rather than CBGa, which is known to be synthesized in *C. sativa*. Any downstream reactions that may produce phytocannabinoids when using CBGa or CBG as an input would correspondingly produce the decarboxylated species of methylated phytocannabinoid analogues shown in Figs. 5 and 6, whereas unmethylated acid form of phytocannabinoids would be produced in *C. sativa* (as in Fig. 3). If OAC or another polyketide cyclase were included, the methyl-olivetol may be converted by the OAC or the other polyketide cyclase into meCBGa, as the methylation and carboxylation carbons may be at differing positions. For example, meTHC synthesized from meCBG may be methylated at carbon 4, and could be carboxylated to methyl-tetrahydrocannabinolic acid ("**meTHCa**") with the carboxyl group of THCa may be at position 2. Alternatively, meTHC synthesized from meCBG may be methylated at carbon 2, in which case the carboxyl group of THCa may be at position 4. THCa is observed in *C. sativa* with the carboxyl group at the 2 position, or at the 4 position.

[0058] Fig. 7 is a schematic of the functional domains of DiPKS showing β-ketoacyl-synthase ("**KS**"), acyl transacetylase ("**AT**"), dehydratase ("**DH**"), C-methyl transferase ("**C-Met**"), enoyl reductase ("**ER**"), ketoreductase ("**KR**"), and acyl carrier protein ("**ACP**"). The "**Type III**" domain is a type 3 polyketide synthase. The KS, AT, DH, ER, KR, and ACP portions provide functions typically associated with a fatty acid synthase. The C-Met domain provides the catalytic activity for methylating olivetol at carbon 4. The C-Met domain is crossed out in Fig. 7, schematically illustrating modifications to DiPKS protein that inactivate the C-Met domain and mitigate or eliminate methylation functionality. The Type III domain catalyzes iterative polyketide extension and cyclization of a hexanoic acid thioester transferred to the Type III domain from the ACP.

[0059] Fig. 8 shows a biosynthetic pathway in transgenic yeast for production of both meCBG and CBG from malonyl-CoA and GPP. A strain of yeast as provided herein for producing both CBG and meCBG as shown in Fig. 8 may include the gene for a prenyltransferase and a gene for a mutant DiPKS with a lowered activity at the C-Met

domain, as shown schematically in Fig. 7. The C-Met domain of the DiPKS protein includes amino acid residues 1510 to 1633 of DiPKS. The C-Met domain includes three motifs. The first motif includes residues 1510 to 1518. The second motif includes residues 1596 to 1603. The third motif includes residues 1623 to 1633. Disruption of one or more of these three motifs may result in lowered activity at the C-Met domain.

[0060] An example of a yeast strain expressing a modified DiPKS with lowered activity in the C-Met domain is provided as "**HB80A**" in Example III below. HB80A includes a modification in a yeast-codon optimized gene coding for the wildtype DiPKS protein. HB80A includes modifications in the DiPKS gene such that the DiPKS protein is modified in the first motif of the C-Met domain. As a result of these modifications to the DiPKS gene, the DiPKS protein has substitutions of Gly1516Asp and Gly1518Ala. HB80A includes DiPKS$^{G1516D; G1518A}$, and as a result catalyzes both step 1A and 1B of Fig. 8, and produces both methyl-olivetol and olivetol.

[0061] Fig. 8 shows production of both methyl-olivetol from malonyl-CoA (Reaction 1A in Fig. 8) and of olivetol from malonyl-CoA (Reaction 1B in Fig. 8). Reactions 1A and 1B are each catalyzed by DiPKS$^{G1516D; G1518A}$. The Gly1516Asp and Gly1518Ala substitutions are in the active site of the C-Met domain and diminish catalysis by DiPKS$^{G1516D; G1518A}$ of methylation on the 4 position of the olivetol ring, allowing a portion of the input malonyl-CoA to be catalyzed according to reaction 1B rather than reaction 1A. A promiscuous αββα prenyltransferase could then catalyze prenylation of both the methyl-olivetol with GPP and the olivetol with GPP, resulting in production of both meCBG (Reaction 2 in Figs. 5 and 6) and CBG through prenylation of olivetol, similar to reaction 3 in Fig. 2 but without the acid group. Any downstream reactions to produce other phytocannabinoids would then correspondingly produce a mixture of methylated phytocannabinoid analogues and species with no functional group at the 4 position on the aromatic ring of CBG (or a corresponding position in downstream phytocannabinoids), whereas acid forms would be produced in *C. sativa*.

[0062] Fig. 9 shows a biosynthetic pathway in transgenic yeast for production of olivetol only, and no methyl-olivetol, from malonyl-CoA. A strain of yeast as provided herein for producing olivetol only as shown in Fig. 9 may include the gene for a mutant DiPKS with a lowered activity at the C-Met domain, as shown schematically in Fig. 7.

[0063] Examples of yeast strains expressing a modified DiPKS with essentially no activity in the C-Met domain are provided as "**HB135**", "**HB137**", and "**HB138**" in Examples VI and VII below. Each of HB135, HB137 and HB138 includes a modification in a yeast-codon optimized gene coding for the wildtype DiPKS protein. HB135, HB137 and HB138 each include a modification of the DiPKS gene such that the DiPKS protein is modified in the first motif of the C-Met domain. As a result of this modification to the DiPKS gene, the DiPKS protein has substitutions of Gly1516Arg.

[0064] $DiPKS^{G1516R}$ catalyzes reaction 1 in Fig. 9. The Gly1516Arg substitution is in the active site of the C-Met domain and diminish catalysis by $DiPKS^{G1516R}$ of methylation on the 4 position of the olivetol ring. The input of malonyl-CoA is catalyzed according to reaction 1 of Fig. 9. Any downstream reactions to produce other phytocannabinoids would then correspondingly produce phytocannabinoid species with no functional group at the 4 position on the aromatic ring of CBG, or a corresponding position in downstream phytocannabinoids, whereas acid forms would be produced in *C. sativa*.

[0065] **Increasing Availability of Biosynthetic Precursors**

[0066] The biosynthetic pathways shown in Figs. 4, 8 and 9 each require malonyl-CoA to produce methyl-olivetol only, both methyl-olivetol and olivetol, and olivetol only, respectively. Yeast cells may be mutated, genes from other species may be introduced, genes may be upregulated or downregulated, or the yeast cells may be otherwise genetically modified to increase the availability of malonyl-CoA or other input metabolites required to support the biosynthetic pathways of any of Figs. 4, 8 or 9.

[0067] The yeast strain may be modified for increasing available malonyl-CoA. Lowered mitochondrial acetaldehyde catabolism results in diversion of the acetaldehyde from ethanol catabolism into acetyl-CoA production, which in turn drives production of malonyl-CoA and downstream polyketides and terpenoids. *S. cerevisiae* may be modified to express an acetyl-CoA synthase from *Salmonella enterica* with a substitution modification of Leucine to Proline at residue 641 ("**Acs^{L641P}**"), and with aldehyde dehydrogenase 6 from *S. cerevisiae* ("**Ald6**"). The Leu641Pro mutation removes downstream regulation of Acs, providing greater activity with the Acs^{L641P} mutant than the wild type Acs. Together, cytosolic expression of these two enzymes increases the concentration of acetyl-CoA in the cytosol. Greater acetyl-CoA concentrations in the cytosol result in lowered mitochondrial catabolism, bypassing mitochondrial pyruvate dehydrogenase ("**PDH**"), providing a PDH bypass. As a result, more

acetyl-CoA is available for malonyl-CoA production. SEQ ID NO: 2 is plasmid based on the pGREG plasmid and including a DNA sequence coding for the genes for Ald6 and *Se*Acs^{L641P}, promoters, terminators, and integration site homology sequences for integration into the *S. cerevisiae* genome at Flagfeldt-site 19 by recombination applying clustered regularly interspaced short palindromic repeats ("**CRISPR**"). As shown in Table 2 below (by the term "PDH bypass"), each of base strains "**HB82**", "**HB100**", "**HB106**", and "**HB110**". have a portion of SEQ ID NO: 2 from bases 1494 to 2999 that code for Ald6 under the TDH_3 promoter, and a portion of SEQ ID NO: 2 from bases 3948 to 5893 that code for *Se*Acs^{L641P} under the $Tef1_P$ promoter. Similarly, each modified yeast strain based on any of HB82, HB100, HB106, or HB110 includes a polynucleotide coding for Ald6 and *Se*Acs^{L641P}.

[0068] Another approach to increasing cytosolic malonyl-CoA is to upregulate Acc1, which is the native yeast malonyl-CoA synthase. The promoter sequence of the Acc1 gene was replaced by a constitutive yeast promoter for the PGK1 gene. The promoter from the PGK1 gene allows multiple copies of Acc1 to be present in the cell. The native Acc1 promoter allows only a single copy of the protein to be present in the cell at a time. The native promoter region was marked is shown in SEQ ID NO: 3. The modified promoter region is shown in SEQ ID NO: 4.

[0069] In addition to upregulating expression of Acc1, *S. cerevisiae* may include one or more modifications of Acc1 to increase Acc1 activity and cytosolic acetyl-CoA concentrations. Two mutations in regulatory sequences were identified in literature that remove repression of Acc1, resulting in greater Acc1 expression and higher malonyl-CoA production. SEQ ID NO: 5 is a polynucleotide that may be used to modify the *S. cerevisiae* genome at the native Acc1 gene by homologous recombination. SEQ ID NO: 5 includes a portion of the coding sequence for the Acc1 gene with Ser659Ala and Ser1167Ala modifications. As a result, the *S. cerevisiae* transformed with this sequence will express Acc1$^{S659A; S1167A}$. A similar result may be achieved, for example, by integrating a sequence with the Tef1 promoter, the Acc1 with Ser659Ala and Ser1167Ala modifications, and the Prm9 terminator at any suitable site. The end result would be that Tef1, Acc1$^{S659A; S1167A}$, and Prm9 are flanked by genomic DNA sequences for promoting integration into the *S. cerevisiae* genome. This was attempted at Flagfeldt site 18 but due to the size of the construct, the approach with SEQ ID NO: 5 described above was followed instead.

[0070] *S. cerevisiae* may include modified expression of Maf1 or other regulators of tRNA biosynthesis. Overexpressing native Maf1 has been shown to reduce loss of IPP to tRNA biosynthesis and thereby improve monoterpene yields in yeast. IPP is an intermediate in the mevalonate pathway. SEQ ID NO: 6 is a polynucleotide that was integrated into the *S. cerevisiae* genome at Maf1-site 5 for genomic integration of Maf1 under the Tef1 promoter. SEQ ID NO: 6 includes the Tef1 promoter, the native Maf1 gene, and the Prm9 terminator. Together, Tef1, Maf1, and Prm9 are flanked by genomic DNA sequences for promoting integration into the *S. cerevisiae* genome. As shown in Table 2 below, base strains HB100, HB106, and HB110 express Maf1 under the Tef1 promoter. Similarly, each modified yeast strain based on any of HB100, HB106, or HB110 includes a polynucleotide including a coding sequence for Maf1 under the Tef1 promoter.

[0071] Upc2 is an activator for sterol biosynthesis in *S. cerevisiae*. A Glu888Asp mutation of Upc2 increases monoterpene production in yeast. SEQ ID NO: 7 is a polynucleotide that may be integrated into the genome to provide expression of $Upc2^{E888D}$ under the Tef1 promoter. SEQ ID NO: 7 includes the Tef1 promoter, the $Upc2^{E888D}$ gene, and the Prm9 terminator. Together, Tef1, $Upc2^{E888D}$, and Prm9 are flanked by genomic DNA sequences for promoting integration into the *S. cerevisiae* genome.

[0072] Any of the above genes, Acs^{L641P}, Ald6, Maf1, $Acc1^{S659A; S1167A}$ or $Upc2^{E888D}$, may be expressed from a plasmid or integrated into the genome of *S. cerevisiae*. Genome integration may be through homologous recombination, including CRISPR recombination, or any suitable approach. The promoter of Acc1 may be similarly modified through recombination. The coding and regulatory sequences in each of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, or SEQ ID NO: 7 may be included in a plasmid for expression (e.g. pYES, etc.) or a linear polynucleotide for integration into the *S. Cerevisiae* genome. Each of base strains HB82, HB100, HB106, or HB110 includes one or more integrated SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, or SEQ ID NO: 8 (see Table 2 below). Integration of SEQ ID NO: 5, or SEQ ID NO: 7 may be applied by similar approaches.

[0073] **Increased DiPKS Function**

[0074] As shown in Fig. 7, DiPKS includes an ACP domain. The ACP domain of DiPKS requires a phosphopantetheine group as a co-factor. **NpgA** is a 4'-phosphopantethienyl transferase from *Aspergillus nidulans*. A codon-optimized copy of NpgA

for *S. cerevisiae* may be introduced into *S. cerevisiae* and transformed into the *S. cerevisiae*, including by homologous recombination. An NpgA gene cassette was integrated into the genome of *Saccharomyces cerevisiae* at Flagfeldt site 14 to create strain HB100. The sequence of the integrated DNA is shown in SEQ ID NO: 8, and includes the Tef1 Promoter, the NpgA coding sequence and the Prm9 terminator. Together the Tef1p, NpgA, and Prm9t are flanked by genomic DNA sequences promoting integration into Flagfeldt site 14 in the *S. cerevisiae* genome. As shown in Table 2 below, base strains HB100, HB106, and HB110 include this integrated cassette. Alternatively, bases 636 to 2782 of SEQ ID NO: 8 may be included on an expression plasmid as in strain HB98.

[0075] Expression of NpgA provides the *A. nidulans* phosphopantetheinyl transferase for greater catalysis of loading the phosphopantetheine group onto the ACP domain of DiPKS. As a result, the reaction catalyzed by DiPKS (reaction 1 in Fig. 4) may occur at greater rate, providing a greater amount of methyl-olivetol.

[0076] **Modification of DiPKS**

[0077] DiPKS may be modified to reduce or eliminate the activity of C-Met.

[0078] SEQ ID NO: 9 is a modified form of a synthetic sequence for DIPKS that is codon optimized for yeast in which DiPKS includes a Gly1516Asp substitution and a Gly1518Ala substitution that together disrupt the activity of the C-met domain. Results of $DiPKS^{G1516D,\ G1518A}$ expression in *S. cerevisiae* cultures are provided below in relation to Example II, which includes strain HB80A. Other modifications may be introduced into DiPKS to disrupt or eliminate the entire active site of C-Met or all of C-Met. Each of these modified DiPKS enzymes may be introduced into *S. cerevisiae* as described for wild type DiPKS.

[0079] SEQ ID NO: 10 is a modified form of a synthetic sequence for DIPKS that is codon optimized for yeast in which DiPKS includes a Gly1516Arg substitution that disrupts the activity of the C-met domain. Results of $DiPKS^{G1516R}$ expression in *S. cerevisiae* cultures are provided below in relation to Example VI, which includes strain HB135 and Example VII, which includes strains HB135, HB137 and HB138.

[0080] In addition to $DiPKS^{G1516D,\ G1518A}$ and $DiPKS^{G1516R}$ specifically, other modifications were introduced into DiPKS to disrupt or eliminate the entire active site of C-Met or all of C-Met: (**a**) substitution of motif 1 with GGGSGGGSG, (**b**) a Gly1516Arg substitution in motif 1 and substitution of motif 2 with GGGSGGGS, (**c**). a Glu1634Ala, which is just outside motif 3 and disrupts tertiary structure at an active site in the C-Met domain,

and (**d**). disruption of an active site in the C-Met domain by a His1608Gln substitution. Codon optimized sequences for each of (**a**) to (**d**) were introduced into yeast on expression plasmids, similarly to expression of DiPKS$^{G1516D, G1518A}$ and DiPKS^{G1516R}, into base strain HB100. In each case, no production of olivetol was observed. Substitution of either motif 1 or motif 2 with GGGSGGGS eliminated production of methyl-olivetol as well. A culture of yeast expressing the DiPKS^{G1634A} mutant provided 2.67 mg methyl-olivetol per l of culture in one example batch. A culture of yeast expressing the DiPKS^{H1608N} mutants provided 3.19 mg methyl-olivetol per l of culture in one example batch.

[0081] **Transforming and Growing Yeast Cells**

[0082] Details of specific examples of methods carried out and yeast cells produced in accordance with this description are provided below as Examples I to VII. Each of these seven specific examples applied similar approaches to plasmid construction, transformation of yeast, quantification of strain growth, and quantification of intracellular metabolites. These common features across the seven examples are described below, followed by results and other details relating to one or more of the seven examples.

[0083] **Plasmid Construction**

[0084] Plasmids assembled to apply and prepare examples of the methods and yeast cells provided herein are shown in Table 1. In Table 1, for the expression plasmids pYES, and pYES2, SEQ ID NOs 11 and 12 respectively provide the plasmids as a whole without an expression cassette. The expression cassettes of SEQ ID NOs: 8 to 10, 13 and 14 can be included in to prepare the plasmids indicated in Table 1. SEQ ID NO: 2 is the pGREG plasmid including a cassette for the PDH bypass genes.

Plasmid	Cassette	Description
pYES	(none)	LEU auxotroph; ampicillin resistance; SEQ ID NO: 11
pYES2	(none)	URA auxotroph; ampicillin resistance; SEQ ID NO: 12

Plasmid	Cassette	Description
pPDH	Bases 1 to 7214 from SEQ ID NO: 2	High copy amplification plasmid with **PDH Bypass** genes for acetaldehyde dehydrogenase (**Ald6**) and acetyl-CoA synthase (**Acs^{L641P}**) assembled in pGREG 505 / G418 flanked by integration site homology sequences as follows: C1-506-BclV-Site 19 UP region-L0 L0-TDH3$_P$-L1-**Ald6**-L2-Adh1$_T$-LTP1 LTP1-Tef1$_P$-L3- **Acs^{L641P}**-L4-Prm9$_T$-LTP2 LTP2-Site 19 down region-C6-506
pNPGa	SEQ ID NO: 8	High copy **NpgA** expression plasmid in pYES2 with: LV3-Tef1$_P$-L1-**NpgA**-L2-Prm9$_T$-LV5
pDiPKSm1	SEQ ID NO: 9	High copy **DiPKS $^{G1516D; G1518A}$** expression plasmid in pYES2 with: LV3-Gal1-L1-**DiPKS$^{G1516D;G1518A}$**-L2-Prm9$_T$-LV5
pDIPKSm2	SEQ ID NO: 10	High copy DIPKS^{G1516R} expression plasmid in pYES2 with: LV3-Gal1-L1-**DiPKS^{G1516R}**-L2-Prm9t$_T$-LV5
pDiPKS	SEQ ID NO: 13	High copy **DiPKS** expression plasmid in pYES2 with: LV3-Gal1-L1-**DiPKS**-L2-Prm9$_T$-LV5
pCRISPR	SEQ ID NO: 14	High copy **Cas9** endonuclease and targeted **gRNA** expression plasmid in pYES2 with: LV3-Tef1$_P$-**Cas9**-Adh1$_T$-LTP1 LTP1-**gRNA**-LV5

Table 1: Plasmids and Cassettes Used to Prepare Yeast Strains

[0085] Plasmids for introduction into *S. cerevisiae* were amplified by polymerase chain reaction ("**PCR**") with primers from Operon Eurofins and Phusion HF polymerase (ThermoFisher F-530S) according to the manufacturer's recommended protocols using an Eppendorf Mastercycler ep Gradient 5341.

[0086] All plasmids were assembled using overlapping DNA parts and transformation assisted recombination in *S. cerevisiae*. The plasmids were transformed into *S. cerevisiae* using the lithium acetate heat shock method as described by Gietz, R. D. and Schiestl, R. H., "High-efficiency yeast transformation using the LiAc/SS carrier DNA/PEG method." *Nat. Protoc.* **2,** 31–34 (2007). The pNPGa, pDiPKSm1, pDiPKSm2, pCRISPR, pDiPKS, and

pPDH plasmids were assembled yeast strain HB25, which is a uracil auxotroph. Transformed *S. cerevisiae* cells were selected by auxotrophic selection on agar petri dishes. Colonies recovered from the petri dishes were grown up in liquid selective media for 16 hrs at 30 ºC while being shaken at 250 RPM.

[0087] After growth in liquid selective media, the transformed *S. cerevisiae* cells were collected and the plasmid DNA was extracted. The extracted plasmid DNA was transformed into *Escherichia coli*. Transformed *E. coli* were selected for by growing on agar petri dishes including ampicillin. The *E. coli* were cultured to amplify the plasmid. The plasmid grown in the *E. coli* was extracted and sequenced with Sanger dideoxy sequencing to verify accurate construction. The sequence-verified plasmid was then used for genome modification or stable transformation of the *S. cerevisiae*.

[0088] **Genome Modification of *S. cerevisiae***

[0089] The *S. cerevisiae* strains described herein may be prepared by stable transformation of plasmids or genome modification. Genome modification may be accomplished through homologous recombination, including by methods leveraging CRISPR.

[0090] Methods applying CRISPR were applied to delete DNA from the *S. cerevisiae* genome and introduce heterologous DNA into the *S. cerevisiae* genome. Guide RNA ("**gRNA**") sequences for targeting the Cas9 endonuclease to the desired locations on the *S. cerevisiae* genome were designed with Benchling online DNA editing software. DNA splicing by overlap extension ("**SOEing**") and PCR were applied to assemble the gRNA sequences and amplify a DNA sequence including a functional gRNA cassette.

[0091] The functional gRNA cassette, a Cas9-expressing gene cassette, and the pYes2 (URA) plasmid were assembled into the pCRISPR plasmid and transformed into *S. cerevisiae* for facilitating targeted DNA double-stranded cleavage. The resulting DNA cleavage was repaired by the addition of a linear fragment of target DNA.

[0092] Genome modification of *S. cerevisiae* was based on strain HB42, which is a Uracil auxotroph based in turn on strain HB25, and which includes an integration of the CDS for an $Erg20^{K197E}$ protein. This integration was for other purposes not directly relevant to production of methyl-olivetol or olivetol, but which may be useful when also synthesizing CBG or meCBG, which requires GPP. The $Erg20^{K197E}$ mutant protein increases GPP levels in the cell.

[0093] Bases 51 to 7114 of SEQ ID NO: 2 were integrated into the HB42 strain by CRISPR to provide the HB82 base strain with the PDH bypass genes in *S. cerevisiae*. The pPDH plasmid was sequence verified after assembly in *S. cerevisiae*. The sequence-verified pPDH plasmid was grown in *E. coli*, purified, and digested with BciV1 restriction enzymes. As in Table 1, digestion by BciV1 provided a polynucleotide including the genes for Ald6 and *Se*Acs^{L641P}, promoters, terminators, and integration site homology sequences for integration into the *S. cerevisiae* genome at PDH-site 19 by Cas9. The resulting linear PDH bypass donor polynucleotide, shown in bases 51 to 7114 of SEQ ID NO: 2, was purified by gel separation.

[0094] With both PDH bypass genes (Ald6 and Acs^{L641P}) on the single PDH bypass polynucleotide, the PDH bypass donor polynucleotide was co-tranformed into *S. cerevisiae* with pCRISPR. Transformation was by the lithium acetate heat shock method as described by Gietz. The pCRISPR plasmid expresses Cas9, which is targeted to a selected location of *S. cerevisiae* the genome by a gRNA molecule. At the location, the Cas9 protein creates a double stranded break in the DNA. The PDH bypass donor polynucleotide was used as a donor polynucleotide in the CRISPR reaction. The PDH bypass donor polynucleotide including Ald6, Acs^{L641P}, promoters, and terminators was integrated into the genome at the site of the break, Site 19, by homologous recombination, resulting in strain HB82.

[0095] The NpgA donor polynucleotide shown in SEQ ID NO: 8 was prepared and amplified. DNA SOEing was used to create a single donor DNA fragment from three polynucleotides for NpgA integration. The first polynucleotide was the 5' region of genomic homology that allows the donor to recombine into the genome at a specific locus. The second polynucleotide coded for the NpgA gene cassette. The NpgA gene cassette includes the Tef1 promoter, the NpgA coding sequence and the Prm9 terminator. The third polynucleotide included the 3' region for genomic homology to facilitate targeted integration into the *S. cerevisiae* genome.

[0096] The NpgA donor polynucleotide was co-transformed with the pCRISPR plasmid into strain HB82. The pCRISPR plasmid was expressed and endonuclease Cas9 was targeted to a location on the *S. cerevisiae* genome by a gRNA molecule. At the location, the Cas9 protein created a double stranded break in the DNA and the NpgA donor polynucleotide was integrated into the genome at the break by homologous recombination to provide the HB100 base strain.

[0097] The Maf1 donor polynucleotide shown in SEQ ID NO: 6 was prepared and amplified. DNA SOEing was used to create a single donor DNA fragment from three polynucleotides for Maf1 integration. The first polynucleotide was the 5' region of genomic homology that allows the donor to recombine into the genome at a specific locus. The second polynucleotide coded for the Maf1 gene cassette. The Maf1 gene cassette includes the Tef1 promoter, the Maf1 coding sequence and the Prm9 terminator. The third polynucleotide included the 3' region for genomic homology to facilitate targeted integration into the *S. cerevisiae* genome.

[0098] The Maf1 donor polynucleotide was co-transformed with the pCRISPR plasmid into the HB100 strain. The pCRISPR plasmid may be expressed and endonuclease Cas9 was targeted to a location on the *S. cerevisiae* genome by a gRNA molecule. At the location, the Cas9 protein may create a double stranded break in the DNA and the Maf1 donor polynucleotide may be integrated into the genome at the break by homologous recombination. Stable transformation of the Maf1 donor polynucleotide into the HB100 strain provides the HB106 base strain.

[0099] The Acc1-PGK1p donor polynucleotide shown in SEQ ID NO: 6 was prepared and amplified. DNA SOEing was used to create a single donor DNA fragment from three polynucleotides for Acc1-PGK1 integration. The first polynucleotide was the 5' region of genomic homology that allows the donor to recombine into the genome at a specific locus. The second polynucleotide coded for the PGK1 promoter region. The third polynucleotide included the 3' region for genomic homology to facilitate targeted integration into the S. cerevisiae genome.

[00100] The Acc1-PGK1 donor polynucleotide was co-transformed with the pCRISPR plasmid. The pCRISPR plasmid was expressed and endonuclease Cas9 was targeted to a location on the S. cerevisiae genome by a gRNA molecule. At the location, the Cas9 protein created a double stranded break in the DNA and the Acc1-PGK1 donor polynucleotide was integrated into the genome at the break by homologous recombination. Stable transformation of donor polynucleotide into the HB100 strain provides the HB110 base strain with Acc1 under regulation of the PGK1 promoter.

[00101] Table 2 provides a summary of the base strains that were prepared by genome modification of *S. cerevisiae*. Each base strain shown in Table 2 is a leucine and uracil auxotroph, and none of them include a plasmid.

Strain	Modification	Integration
HB82	PDH bypass	SEQ ID NO: 2
HB100	PDH bypass, NPGa (site 14)	SEQ ID NOs: 2, 8
HB106	PDH bypass, NPGa (site 14), Maf1 (site 5)	SEQ ID NOs: 2, 8, 6
HB110	PDH bypass, NPGa (site 14), Maf1 (site 5), Acc1 promoter replaced with $PGK1^{p}$	SEQ ID NOs: 2, 8, 6, 4

Table 2: Base Transformed Strains Prepared for Polyketide Production

[00102] **Stable Transformation for Strain Construction**

[00103] Plasmids were transformed into *S. cerevisiae* using the lithium acetate heat shock method as described by Gietz.

[00104] Transgenic *S. cerevisiae* HB80, HB98, HB102, HB135, HB137 and HB138 were prepared from the HB42, HB100, HB106 and HB110 bases strain by transformation of HB42 with expression plasmids, and HB80A was prepared by transformation of HB80, as shown below in Table 3. HB80, HB98 and HB102 each include and express DiPKS. HB80A includes and expresses $DiPKS^{G1516D;\ G1518A}$. HB135, HB137 and HB138 each include and express $DiPKS^{G1516R}$. HB98 includes and expresses DiPKS and NPGa from a plasmid.

Strain	Base Strain	Plasmid
HB80	HB42	pDiPKS
HB80A	HB80	pDIPKSm1
HB98	HB42	pDiPKS pNPGa
HB102	HB100	pDIPKS
HB135	HB100	pDIPKSm2
HB137	HB106	pDIPKSm2
HB138	HB110	pDIPKSm2

Table 3: Strains including plasmids expressing polyketide synthase

[00105] **Yeast Growth and Feeding Conditions**

[00106] Yeast cultures were grown in overnight cultures with selective media to provide starter cultures. The resulting starter cultures were then used to inoculate triplicate 50 ml cultures to an optical density at having an absorption at 600 nm ("$\mathbf{A_{600}}$") of 0.1.

[00107] Yeast was cultured in media including YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO*. "**4DO***" refers to yeast synthetic dropout media supplement lacking leucine and uracil. "**YNB**" is a nutrient broth including the chemicals listed in the first two columns side of Table 4. The chemicals listed in the third and fourth columns of Table 4 are included in the 4DO* supplement.

YNB		**4DO***	
Chemical	**Concentration**	**Chemical**	**Concentration**
Ammonium Sulphate	5 g/L	Adenine	18 mg/L
Biotin	2 µg/L	p-Aminobenzoic acid	8 mg/L
Calcium pantothenate	400 µg/L	Alanine	76 mg/ml
Folic acid	2 µg/L	Arginine	76 mg/ml
Inositol	2 mg/L	Asparagine	76 mg/ml
Nicotinic acid	400 µg/L	Aspartic Acid	76 mg/ml
p-Aminobenzoic acid	200 µg/L	Cysteine	76 mg/ml
Pyridoxine HCl	400 µg/L	Glutamic Acid	76 mg/ml
Riboflavin	200 µg/L	Glutamine	76 mg/ml
Thiamine HCL	400 µg/L	Glycine	76 mg/ml
Citric acid	0.1 g/L	Histidine	76 mg/ml
Boric acid	500 µg/L	myo-Inositol	76 mg/ml
Copper sulfate	40 µg/L	Isoleucine	76 mg/ml
Potassium iodide	100 µg/L	Lysine	76 mg/ml
Ferric chloride	200 µg/L	Methionine	76 mg/ml
Magnesium sulfate	400 µg/L	Phenylalanine	76 mg/ml
Sodium molybdate	200 µg/L	Proline	76 mg/ml

YNB		4DO*	
Chemical	**Concentration**	**Chemical**	**Concentration**
Zinc sulfate	400 µg/L	Serine	76 mg/ml
Potassium phosphate monobasic	1.0 g/L	Threonine	76 mg/ml
Magnesium sulfate	0.5 g/L	Tryptophan	76 mg/ml
Sodium chloride	0.1 g/L	Tyrosine	76 mg/ml
Calcium chloride	0.1 g/L	Valine	76 mg/ml

Table 4: YNB Nutrient Broth and 4DO* Supplement

[00108] **Quantification of Metabolites**

[00109] Intracellular metabolites were extracted from the *S. cerevisiae* cells using methanol extraction. One mL of liquid culture was spun down at 12,000 x g for 3 minutes. 250 µL of the resulting supernatant was used for extracellular metabolite quantification. The resulting cell pellet was suspended in 200 µl of -40 ºC 80% methanol. The mixture was vortexed and chilled on ice for 10 minutes. After chilling on ice for 10 minutes, the mixture was spun down at 15,000 x g at 4 ºC for 14 minutes. The resulting supernatant was collected. An additional 200 µl of -40 ºC 80% methanol was added to the cell debris pellet and the mixture was vortexed and chilled for 10 minutes on ice. After chilling on ice for 10 minutes, the mixture was spun down at 15,000 x g at 4 ºC for 14 minutes. The resulting 200 µl of supernatant was added to the previously collected 200 µl of supernatant, providing a total of 400 µl of 80% methanol with intracellular metabolites.

[00110] Intracellular metabolites were quantified using high performance liquid chromatography ("**HPLC**") and mass spectrometry ("**MS**") methods. An Agilent 1260 autosampler and HPLC system connected to a ThermoFinnigan LTQ mass spectrometer was used. The HPLC system included a Zorbax Eclipse C18 2.1 µm x 5.6 mm x 100 mm column.

[00111] The metabolites were injected in 10 µl samples using the autosampler and separated on the HPLC using at a flow rate of 1 ml/min. The HPLC separation protocol was 20 mins total with (**a**) 0-2 mins of 98% Solvent A and 2% Solvent B; (**b**) 2-15 mins to get to 98% solvent B; (**c**) 15-16.5 minutes at 98% solvent B; (**d**) 16.5-17.5 minutes to get to 98% A;

and (**e**) a final 2.5 minutes of equilibration at 98% Solvent A. Solvent A was acetonitrile + 0.1% formic acid in MS water and solvent B was 0.1% formic acid in MS water.

[00112] After HPLC separation, samples were injected into the mass spectrometer by electrospray ionization and analyzed in positive mode. The capillary temperature was held at 380 ºC. The tube lens voltage was 30 V, the capillary voltage was 0 V, and the spray voltage was 5 kV. Similarly, after HPLC-MS/MS, olivetol was analyzed as a parent ion at 181.2 and a daughter ion at 111, while methyl-olivetol analyzed as a parent ion at 193.2 and a daughter ion at 125.

[00113] Different concentrations of known standards were injected to create a linear standard curve. Standards for olivetol and methyl-olivetol standards were purchased from Sigma Aldrich.

[00114] **Example I**

[00115] The yeast strain HB80 as described above in Table 3 was cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of methyl-olivetol from raffinose and galactose was observed, demonstrating direct production in yeast of methyl-olivetol. The methyl-olivetol was produced at concentrations of 3.259 mg/L.

[00116] **Example II**

[00117] The yeast strain HB80A as described above in Table 3 was cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of both olivetol and methyl-olivetol from raffinose and galactose, catalyzed by $DiPKS^{G1516D;\ G1518A}$, was observed. This data demonstrates direct production in yeast of both olivetol and methyl-olivetol without inclusion of hexanoic acid.

[00118] Fig. 10 shows concentrations of methyl-olivetol produced by HB80 ("**Methyl_Olivetol HB80**") from Example I, and of both olivetol and methyl-olivetol produced by HB80A ("**Methyl_Olivetol HB80A**" and "**Olivetol HB80A**", respectively). Samples of culture were taken at 72 hours. HB80A produces a majority of methyl-olivetol (1.4 mg methyl-olivetol per L of culture compared with 0.010 mg per L of culture olivetol), and produced less methyl-olivetol and olivetol combined than methyl-olivetol that is produced by HB80 (3.26 mg/L).

[00119] **Example III**

[00120] The yeast strain HB98 as described above in Table 3 was cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of methyl-olivetol from

raffinose and galactose, catalyzed by DiPKS, was observed. This data demonstrates increased methyl-olivetol production compared with HB80 as described in Example I, and also without inclusion of hexanoic acid.

[00121] Fig. 11 shows concentrations of methyl-olivetol produced by HB80 ("**Methyl_Olivetol HB80**") from Example I, and of methyl-olivetol produced by HB98 ("**Methyl_Olivetol HB98**") from Example III. Samples of culture were taken at 72 hours. HB98 produced 29.85 mg/L methyl-olivetol while HB80 produced only 3.26 mg methyl-olivetol per L of culture. HB98 produced nearly 10 x as much methyl-olivetol as HB80.

[00122] **Example IV**

[00123] The yeast strain HB102 as described above in Table 3 was cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of methyl-olivetol from raffinose and galactose was observed, demonstrating an increased production in yeast of methyl-olivetol at 42.44 mg/L as compared to strain HB98, which produced only 29.85 mg/L methyl-olivetol. This demonstrated that the genomically integrated version of NpgA is functional.

[00124] Fig. 12 shows concentrations of methyl-olivetol produced by HB102 ("**Methyl_olivetol HB102**") from Example IV as compared to the production of methyl-olivetol from strain HB98 in Example III ("**Methyl_olivetol HB98**").

[00125] **Example V**

[00126] The yeast strain HB135 as described above in Table 3 was cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of olivetol from raffinose and galactose was observed, demonstrating an production in yeast of olivetol without any hexanoic acid and at high titres of 49.24 mg/L and no production of methyl-olivetol. This is comparable to the production of methyl-olivetol by strain HB102 demonstrating that the mutation of DIPKS was effective in production of Olivetol as opposed to methyl-Olivetol.

[00127] Fig. 13 shows concentrations of olivetol and methyl-olivetol produced by HB135 ("**Methyl_olivetol HB135**" and "**Olivetol HB135** respectively) from Example VI as compared to the production of methyl-olivetol from strain HB102 in Example IV ("**Methyl_olivetol HB102**").

[00128] **Example VII**

[00129] The yeast strains HB137 and HB138 as described above in Table 3 were cultured in the YNB + 2% raffinose + 2% galactose + 1.6g/L 4DO* media. Production of olivetol from raffinose and galactose was observed in both strains. Strain HB137 produced 61.26 mg/L of olivetol and strain HB138 produced 74.26 mg/L of olivetol demonstrating the positive effect of Maf1 integration and Acc1-promoter swap on olivetol titres.

[00130] Fig. 14 shows the concentrations of olivetol produced by HB137 ("**Olivetol HB137**") and HB138 ("**Olivetol HB138**") from Example VII as compared to olivetol produced by HB135 ("**Olivetol HB135**") in Example VI.

[00131] **References**

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[00148] **<u>Sequences</u>**

[00149] The following sequences were filed electronically with this application but are also included here.

SEQUENCE LISTING

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<120> METHOD AND CELL LINE FOR PRODUCTION OF POLYKETIDES IN YEAST
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[00150] **Examples Only**

[00151] In the preceding description, for purposes of explanation, numerous details are set forth in order to provide a thorough understanding of the embodiments. However, it will be apparent to one skilled in the art that these specific details are not required.

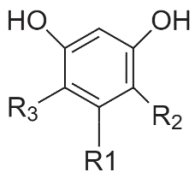
[00152] The above-described embodiments are intended to be examples only. Alterations, modifications and variations can be effected to the particular embodiments by those of skill in the art without departing from the scope, which is defined solely by the claims appended hereto.

WHAT IS CLAIMED IS:

1. A method of producing a polyketide, the method comprising:

providing a yeast cell comprising a first polynucleotide coding for a *D. discoideum* polyketide synthase enzyme (DiPKS) from *D. discoideum*, wherein:

the polyketide synthase enzyme is for producing at least one species of polyketide from malonyl-CoA, the polyketide having structure I:



I

wherein, on structure I, R1 is a pentyl group, R2 is H, carboxyl, or methyl, and R3 is H, carboxyl, or methyl; and

propagating the yeast cell for providing a yeast cell culture;

wherein the DiPKS polyketide synthase enzyme comprises a mutation reducing activity at an active site of a C-Met domain of the DiPKS polyketide synthase enzyme, for preventing methylation of the at least one species of polyketide, resulting in a polyketide wherein R2 is H and R3 is H;

wherein the DiPKS polyketide synthase enzyme comprises a $DiPKS^{G1516R}$ polyketide synthase, and the first polynucleotide comprises a coding sequence for the $DiPKS^{G1516R}$ polyketide synthase enzyme with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10; wherein the said 99 to 100% homology encompasses substitutions only.

2. The method of claim 1, wherein the at least one species of polyketide comprises a polyketide with a methyl group at R2.

3. The method of claim 1 or 2, wherein the yeast cell comprises a phosphopantetheinyl transferase polynucleotide coding for a phosphopantetheinyl transferase enzyme for increasing the activity of the DiPKS polyketide synthase enzyme.

4. The method of claim 3 wherein the phosphopantetheinyl transferase comprises NpgA phosphopantetheinyl transferase enzyme from *A. nidulans*.

5. The method of claim 4 wherein the phosphopantetheinyl transferase polynucleotide comprises a coding sequence for the NpgA phosphopantetheinyl transferase enzyme from *A. nidulans* with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 1170 to 2201 of SEQ ID NO: 8; wherein the said 99 to 100% homology encompasses substitutions only.

6. The method of claim 5 wherein the phosphopantetheinyl transferase polynucleotide has between 80% and 100% base sequence identity with bases 1170 to 2201 of SEQ ID NO: 8; wherein the said 99 to 100% homology encompasses substitutions only.

7. The method of any one of claims 1 to 6 wherein the at least one species of polyketide comprises at least one of olivetol, olivetolic acid, methyl-olivetol, or methyl-olivetolic acid.

8. The method of any one of claims 1 to 7 wherein the at least one species of polyketide comprises a polyketide wherein R2 is carboxyl and R3 is H.

9. The method of any one of claims 1 to 7 wherein the at least one species of polyketide comprises a polyketide wherein R2 is methyl and R3 is H.

10. The method of any one of claims 1 to 7 wherein the at least one species of polyketide comprises a polyketide wherein R2 is carboxyl and R3 is methyl.

11. The method of any one of claims 1 to 10 wherein the yeast cell comprises a genetic modification to increase available malonyl-CoA,

wherein the modification comprises increased expression of Maf1; and

wherein the yeast cell comprises a Maf1 polynucleotide including a coding sequence for Maf1 with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 936 to 2123 of SEQ ID NO: 6; wherein the said 99 to 100% homology encompasses substitutions only.

12. The method of claim 11 wherein the Maf1 polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 99% and 100% base sequence identity with SEQ ID NO: 6; wherein the said 99 to 100% homology encompasses substitutions only.

13. The method of claim 11 wherein the genetic modification comprises cytosolic expression of an aldehyde dehydrogenase and an acetyl-CoA synthase;

wherein the yeast cell comprises an Acs polynucleotide including a coding sequence for Acs^{L641P} from *S. enterica* with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 3938 to 5893 of SEQ ID NO: 2, and a coding sequence for Ald6 from *S. cerevisiae* with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 1494 to 2999 of SEQ ID NO 2; wherein the said 99 to 100% homology encompasses substitutions only.

14. The method of claim 13 wherein the Acs polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 99% and 100% base sequence identity with bases 51 to 7114 SEQ ID NO: 2; wherein the said 99 to 100% homology encompasses substitutions only.

15. The method of claim 11 wherein the genetic modification comprises increased expression of malonyl-CoA synthase;

wherein the yeast cell comprises an Acc1 polynucleotide including a coding sequence for a coding sequence for $Acc1^{S659A; S1157A}$ from *S. cerevisiae*.

16. The method of claim 15 wherein the Acc1 polynucleotide includes a coding sequence for the $Acc1^{S659A; S1157A}$ enzyme, with a portion thereof having a primary structure with

between 99% and 100% amino acid residue sequence identity with a protein portion coded for by a reading frame defined by bases 9 to 1716 of SEQ ID NO: 5; wherein the said 99 to 100% homology encompasses substitutions only.

17. The method of claim 16 wherein the Acc1 polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 99% and 100% base sequence identity with SEQ ID NO: 5; wherein the said 99 to 100% homology encompasses substitutions only.

18. The method of claim 11 wherein the genetic modification comprises increased expression of an activator for sterol biosynthesis;

wherein the yeast cell comprises a Upc2 polynucleotide including a coding sequence for $Upc2^{E888D}$ from *S. cerevisiae* with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 975 to 3701 of SEQ ID NO: 7; wherein the said 99 to 100% homology encompasses substitutions only.

19. The method of claim 18 wherein the Upc2 polynucleotide further comprises a promoter sequence, a terminator sequence and integration sequences, and has between 99% and 100% base sequence identity with SEQ ID NO: 7; wherein the said 99 to 100% homology encompasses substitutions only.

20. The method of any one of claims 1 to 19 further comprising extracting the at least one species of polyketide from the yeast cell culture.

21. A yeast cell for producing at least one species of polyketide, the yeast cell comprising a first polynucleotide coding for a DiPKS polyketide synthase enzyme, DiPKS polyketide synthase enzyme has a primary structure with between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10, with a charged amino acid residue at position amino acid residue 1516 in place of a glycine residue at position 1516 for mitigating methylation of the at least one

species of polyketide, wherein the charged amino acid residue is arginine or aspartate; wherein the said 99 to 100% homology encompasses substitutions only.

22. A method of transforming a yeast cell for production of at least one species of polyketide, the method comprising introducing a first polynucleotide coding for a DiPKS polyketide synthase enzyme into the yeast cell line, wherein the DiPKS polyketide synthase enzyme has a primary structure with between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10, with a charged amino acid residue at position 1516 in place of a glycine residue at position 1516 for mitigating methylation of the at least one species of polyketide, wherein the charged amino acid is arginine or aspartate; wherein the said 99 to 100% homology encompasses substitutions only.

23. A polynucleotide comprising a coding sequence for a DiPKS^{G1516R} polyketide synthase, wherein the DiPKSG1516R polyketide synthase enzyme has a primary structure with between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10,

for use in producing a polyketide according to the method of claim 1 in a yeast cell comprising the polynucleotide; wherein the said 99 to 100% homology encompasses substitutions only.

24. A DiPKS^{G1516R} polyketide synthase enzyme with a primary structure having between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10, for use in producing a polyketide in the yeast cell of claim 32; wherein the said 99 to 100% homology encompasses substitutions only.

25. A *D. discoideum* polyketide synthase (DiPKS) enzyme with a primary structure with between 99% and 100% amino acid residue sequence identity with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO:13, with a charged amino acid residue at amino acid residue position 1516 in place of a glycine residue at position 1516, for use in producing a polyketide in a yeast cell.

26. The DiPKS polyketide synthase of claim 25 wherein amino acid residue 1516 is arginine.

27. The DiPKS polyketide synthase of claim 25 wherein amino acid residue 1516 is aspartate and residue 1518 is alanine.