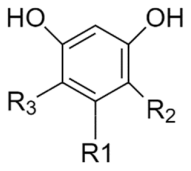
WHAT IS CLAIMED IS:

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~~ identity 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.~~ 2. 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. 3. The method of claim ~~3~~ 2 wherein the phosphopantetheinyl transferase comprises NpgA phosphopantetheinyl transferase enzyme from *A. nidulans*.

~~5.~~ 4. The method of claim 4 3 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~~ identity 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.~~ 5. The method of any one of claims 1 to ~~10~~ 4 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~~ identity encompasses substitutions only.

~~12.~~ 6. The method of claim ~~11~~ 5 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~~ identity encompasses substitutions only.

~~13.~~ 7. The method of claim ~~11~~ 5 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~~ identity encompasses substitutions only.

~~14.~~ 8. The method of claim ~~13~~ 7 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~~ identity 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.~~ 9. The method of claim ~~11~~ 5 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~~ identity encompasses substitutions only.

~~19.~~ 10. The method of claim ~~18~~ 9 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~~ identity encompasses substitutions only.

~~20.~~ 11. The method of any one of claims 1 to ~~19~~ 10 further comprising extracting the at least one species of polyketide from the yeast cell culture.

~~21.~~ 12. 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~~ with an arginine or aspartate at amino acid residue 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 residue is arginine or aspartate~~; wherein the said 99 to 100% ~~homology~~ identity encompasses substitutions only.

~~22.~~ 13. 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~~ with an arginine or aspartate at amino acid residue 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~~ identity encompasses substitutions only.

~~23.~~ 14. A polynucleotide comprising a coding sequence for a DiPKS^{G1516R} polyketide synthase, wherein the ~~DiPKSG1516R~~ DiPKS^{G1516R} 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~~ identity encompasses substitutions only.

~~24.~~ 15. 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 12 ~~32~~; wherein the said 99 to 100% ~~homology~~ identity encompasses substitutions only.

~~25.~~16. 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~~ with an arginine or aspartate 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.~~17. The DiPKS polyketide synthase of claim ~~25~~ 16 wherein amino acid residue 1516 is arginine.

~~27.~~18. The DiPKS polyketide synthase of claim ~~25~~ 16 wherein amino acid residue 1516 is aspartate and residue 1518 is alanine.