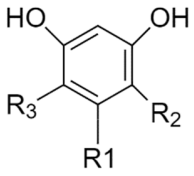
What is claimed is:

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 80% and 100% amino acid residue sequence homology with a protein coded for by a reading frame defined by bases 523 to 9966 of SEQ ID NO: 10; wherein the said 80 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 80% and 100% amino acid residue sequence homology with a protein coded for by a reading frame defined by bases 1170 to 2201 of SEQ ID NO: 8; wherein the said 80 to 100% homology encompasses substitutions only.

6. The method of claim 5 wherein the phosphopantetheinyl transferase polynucleotide has between 80% and 100% base sequence homology with bases 1170 to 2201 of SEQ ID NO: 8; wherein the said 80 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 80% and 100% amino acid residue sequence homology with a protein coded for by a reading frame defined by bases 936 to

2123 of SEQ ID NO: 6; wherein the said 80 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 80% and 100% base sequence homology with SEQ ID NO: 6; wherein the said 80 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 80% and 100% amino acid residue sequence homology 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 homology with a protein coded for by a reading frame defined by bases 1494 to 2999 of SEQ ID NO 2; wherein the said 80 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 80% and 100% base sequence homology with bases 51 to 7114 SEQ ID NO: 2; wherein the said 80 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 80% and 100% amino acid residue sequence homology with a protein portion coded for by a reading frame defined by bases 9 to 1716 of SEQ ID NO: 5; wherein the said 80 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 80% and 100% base sequence homology with SEQ ID NO: 5; wherein the said 80 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 80% and 100% amino acid residue sequence homology with a protein coded for by a reading frame defined by bases 975 to 3701 of SEQ ID NO: 7; wherein the said 80 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 80% and 100% base sequence homology with SEQ ID NO: 7; wherein the said 80 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 80% and 100% amino acid residue sequence homology 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 80 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 80% and 100% amino acid residue sequence homology 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 80 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 80% and 100% amino acid residue sequence homology 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 80 to 100% homology encompasses substitutions only.

24. A DiPKS^{G1516R} polyketide synthase enzyme with a primary structure having between 80% and 100% amino acid residue sequence homology 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 80 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.