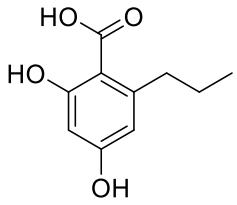
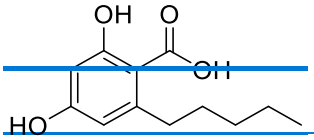
CLAIMS

WHAT IS CLAIMED IS:

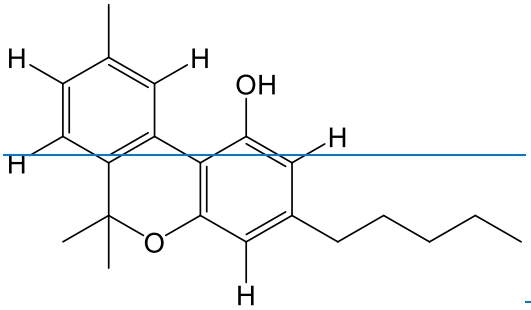
1. A transgenic plant that comprises at least one genetic modification, wherein said genetic modification results in an increased level of the following compounds ~~a compound of:~~



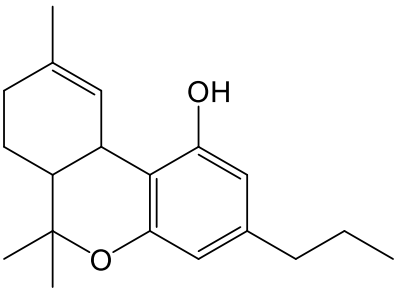
(Divarinic acid (DA), Formula I) or a derivative or analog thereof; and



~~(Olivetolic acid (OA), Formula II);~~



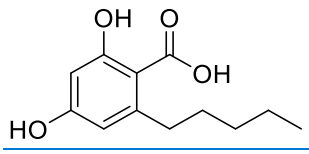
~~(Cannabinol (CBN), Formula V); or~~



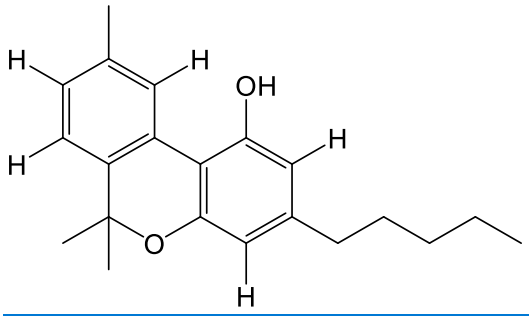
(Tetrahydrocannabivarin (THCV), Formula VI) or a derivative or analog thereof;

compared to a level of said compounds ~~or a derivative or analog thereof, compared to a level of said compound~~ in a comparable plant lacking said genetic modification.

2. The transgenic plant of claim 1, wherein said at least one genetic modification further results in an increased level of a compound of:



(Olivetolic acid (OA), Formula II);



(Cannabinol (CBN), Formula V); or a derivative or analog thereof, compared to a level of said compound in a comparable plant lacking said genetic modification~~is in a promoter or enhancer sequence of a gene encoding a protein~~.

3. The transgenic plant of claim 2, wherein said at least one genetic modification results in an increased level of a compound of Formula V, or a derivative or analog thereof, compared to a level of said compound in a comparable plant lacking said genetic modification~~said gene encodes a polyketide cyclase or a polyketide synthase~~.

~~4. The transgenic plant of claim 3, wherein said polyketide cyclase is olivetolic acid cyclase.~~

~~5. The transgenic plant of claim 3, wherein said polyketide synthase is olivetolic acid synthase.~~

~~6. The transgenic plant of any one of claims 2-5, wherein said at least one genetic modification increases expression of said protein compared to a comparable plant lacking said genetic modification.~~

~~7. The transgenic plant of any one of claims 2-6, wherein said at least one genetic modification increases activity of said promoter or enhancer.~~

~~8.~~4. The transgenic plant of ~~any one of~~ claim 2~~claims 2-6~~, wherein said at least one genetic modification results in an increased level of a compound of Formula II, or a derivative or analog thereof, compared to a level of said compound in a comparable plant lacking said genetic modification.

~~9. The transgenic plant of any one of claims 2-7, wherein said at least one genetic modification results in an increased level of olivetolic acid compared to a comparable plant lacking said genetic modification.~~

~~10. The transgenic plant of any one of claims 2-8, wherein said transgenic plant comprises at least two genetic modifications, wherein each genetic modification is in a promoter or enhancer sequence of a gene encoding a protein.~~

~~11. The transgenic plant of claim 9, wherein said transgenic plant comprises a genetic modification in a promoter or enhancer of a sequence of a gene encoding a polyketide~~

~~cyclase and a genetic modification in a promoter or enhancer of a sequence of a gene encoding a polyketide synthase.~~

~~12. The transgenic plant of claim 10, wherein said polyketide cyclase is olivetolic acid cyclase.~~

~~13. The transgenic plant of claim 10 or 11, wherein said polyketide synthase is olivetolic acid synthase.~~

~~14. The transgenic plant of claim 10 or 11, wherein said at least two genetic modifications increases expression of said olivetolic acid cyclase compared to a comparable plant lacking said at least genetic modification.~~

~~15. The transgenic plant of any one of claims 11-13, wherein said at least two genetic modifications increases expression of said olivetolic acid synthase compared to a comparable plant lacking said at least genetic modification.~~

~~16. The transgenic plant of claim 12, wherein said at least two genetic modifications increases expression of said olivetolic acid synthase and olivetolic acid synthase compared to a comparable plant lacking said at least genetic modification.~~

~~17. The transgenic plant of claim 2, wherein said gene encodes Geranyl-pyrophosphate—olivetolic acid geranyltransferase (GOT).~~

~~18. The transgenic plant of claim 17, wherein said at least one genetic modification increases expression of Geranyl-pyrophosphate—olivetolic acid geranyltransferase (GOT) protein.~~

~~19. The transgenic plant of claim 17 or 18, wherein said at least one genetic modification results in an increased level of a compound of Formula IV, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~20. The transgenic plant of any one of claims 17-19, wherein said at least one genetic modification results in an increased level of cannabigerolic acid (CBGA), compared to a comparable plant lacking said genetic modification.~~

~~21. The transgenic plant of any one of claims 17-20, wherein said at least one genetic modification increases activity of said promoter or enhancer.~~

~~22.~~5. The transgenic plant of claim 1, wherein said at least one genetic modification is in a gene sequence that encodes a protein.

~~23.~~6. The transgenic plant of claim 5~~22~~, wherein said at least one genetic modification disrupts expression of said protein.

~~24.~~7. The transgenic plant of claim 5~~22 or 23~~, wherein said at least one genetic modification decreases expression of said protein compared to a comparable plant lacking said genetic modification.

~~25.~~8. The transgenic plant of claim 7~~24~~, wherein said at least one genetic modification decreases expression of said protein by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%, compared to a comparable plant lacking said genetic modification.

~~26.~~9. The transgenic plant of claim 5~~any one of claims 22-25~~, wherein said at least one genetic modification is in a gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase.

~~27.~~10. The transgenic plant of claim 5~~any one of claims 22-26~~, wherein said transgenic plant comprises at least two genetic modifications each in a gene sequence that encodes a protein.

~~28.~~11. The transgenic plant of claim 5~~any one of claims 22-26~~, wherein said transgenic plant comprises at least two genetic modifications each in a different gene sequence that encode different proteins.

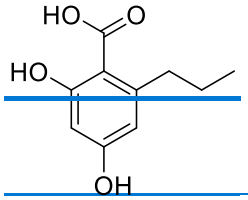
~~29.~~12. The transgenic plant of claim 5~~claim 27 or 28~~, wherein said at least two genetic modifications disrupts expression of said proteins.

~~30. The transgenic plant of claim 27 or 28, wherein said at least two genetic modifications decrease expression of said proteins compared to a comparable plant lacking said at least two genetic modifications.~~

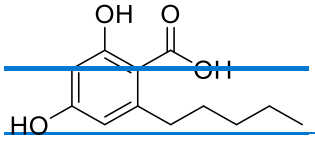
~~31. The transgenic plant of claim 30, wherein said at least two genetic modifications decrease expression of said proteins by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said at least two genetic modifications.~~

~~32. The transgenic plant of any one of claims 28-31, wherein said at least two genetic modifications are in a gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase.~~

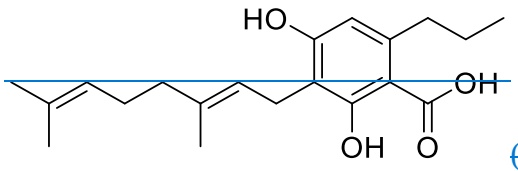
~~33. A transgenic plant that comprises at least one genetic modification, wherein said genetic modification results in an increased level of a compound of:~~



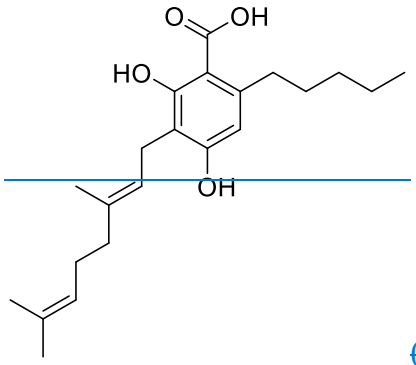
~~(Divarinic acid (DA), Formula I);~~



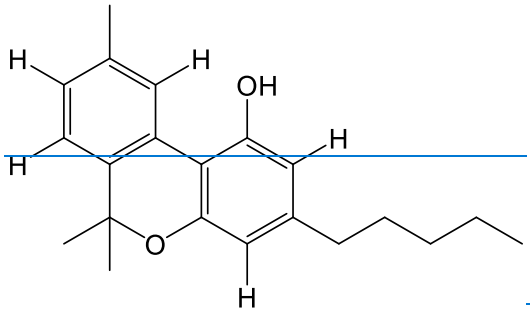
~~(Olivetolic acid (OA), Formula II);~~



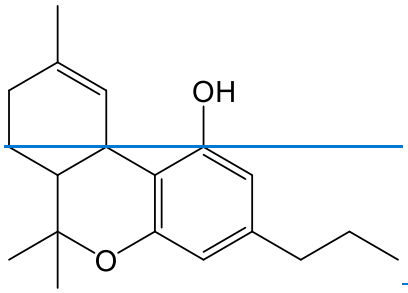
(Cannabigerovarinic Acid (CBGVA), Formula III);



(Cannabigerolic acid (CBGA), Formula IV);



(Cannabinol (CBN), Formula V); or



(Tetrahydrocannabivarin (THCV), Formula IV); or a derivative or analog thereof, compared to a level of said compound in a comparable plant lacking said genetic modification.

34. A transgenic plant that comprises:

a genetic modification in a promoter or enhancer sequence of a gene encoding a polyketide cyclase or a polyketide synthase, wherein said genetic modification in said promoter or enhancer increases expression of said polyketide cyclase or polyketide synthase, compared to a comparable plant lacking said genetic modificationin said promoter or enhancer sequence; and

a genetic disruption in a gene sequence that encodes a Tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase, wherein said genetic disruption decreases expression of said tetrahydrocannabinolic acid synthase, cannabidiolic acid synthase, or cannabichromenic acid synthase; compared to a comparable plant

lacking said genetic disruption in said gene sequence that encodes a Tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase.

35. The transgenic plant of claim 34, wherein said genetic modification in said promoter or enhancer increases expression of said polyketide cyclase or polyketide synthase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.
36. The transgenic plant of claim 34, wherein said genetic modification in said promoter or enhancer increases expression of said polyketide cyclase or polyketide synthase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.
37. The transgenic plant of any one of claims 34-36, wherein said genetic disruption in said gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase decreases expression of said tetrahydrocannabinolic acid synthase, cannabidiolic acid synthase, or cannabichromenic acid synthase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase.
38. The transgenic plant of any one of claims 34-36, wherein said genetic disruption in said gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase decreases expression of said tetrahydrocannabinolic acid synthase, cannabidiolic acid synthase, or cannabichromenic acid synthase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a tetrahydrocannabinolic acid synthase, a cannabidiolic acid synthase, or a cannabichromenic acid synthase.
39. The transgenic plant of any one of claims 2-38, wherein said wherein said at least one genetic modification results in an increased level of a compound of Formula IV, compared to a level of said compound in a comparable plant lacking said genetic modification.
40. The transgenic plant of claim 2, wherein said gene encodes tetrahydrocannabinolic acid synthase.
41. The transgenic plant of any one of claims 40, wherein said at least one genetic modification increases expression of said tetrahydrocannabinolic acid synthase compared to a comparable plant lacking said at least one genetic modification.

42. The transgenic plant of claim 40 or 41, wherein said at least one genetic modification increases activity of said promoter or enhancer.

43. The transgenic plant of any one of claims 40-42, wherein said at least one genetic modification results in an increased level of a compound of Formula V, compared to a level of said compound in a comparable plant lacking said genetic modification.

44. The transgenic plant of any one of claims 40-43, wherein said at least one genetic modification results in an increased level of cannabinol compared to a comparable plant lacking said genetic modification.

45. The transgenic plant of claim 43, wherein said at least one genetic modification is in a gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

46. The transgenic plant of claim 45, wherein said at least one genetic modification disrupts expression of said protein.

47. A transgenic plant that comprises:

a genetic modification in a promoter or enhancer sequence of a gene encoding a THCA synthase, wherein said genetic modification in said promoter or enhancer increases expression of said THCA synthase, compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence; and

a genetic disruption in a gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase, wherein said genetic disruption decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase; compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

48. The transgenic plant of claim 47, wherein said genetic modification in said promoter or enhancer increases expression of said THCA synthase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.

49. The transgenic plant of claim 47, wherein said genetic modification in said promoter or enhancer increases expression of said THCA synthase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.

50. The transgenic plant of any one of claims 47-49, wherein said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase decreases expression of said cannabidiolic acid synthase or said

cannabichromenic acid synthase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

51. The transgenic plant of any one of claims 47-49, wherein said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

52. The transgenic plant of any one of claims 47-49, wherein said wherein said at least one genetic modification results in an increased level of a compound of Formula V, compared to a level of said compound in a comparable plant lacking said genetic modification.

53. The transgenic plant of any one of claims 37-51, wherein said wherein said at least one genetic modification results in an increased level of a cannabinoil (CBN), compared to a level of said compound in a comparable plant lacking said genetic modification.

54. The transgenic plant of claim 2, wherein said gene encodes THCA synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase.

55. The transgenic plant of claim 54, wherein said gene encodes THCA synthase.

56. The transgenic plant of claim 54, wherein said gene encodes olivetolate geranyltransferase (GOT).

57. The transgenic plant of claim 54, wherein said gene encodes geranyl pyrophosphate synthase (GPPS).

58. The transgenic plant of claim 54, wherein said gene encodes polyketide synthase.

59. The transgenic plant of claim 54, wherein said gene encodes divarinic acid cyclase.

60. The transgenic plant of any one of claims 54-59, wherein said at least one genetic modification increases expression of said protein compared to a comparable plant lacking said genetic modification.

61. The transgenic plant of any one of claims 54-60, wherein said at least one genetic modification increases activity of said promoter or enhancer.

~~62. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula I, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~63. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula II, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~64. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula III, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~65. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~66. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula I, Formula II, Formula III, and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~67. The transgenic plant of any one of claims 54-61, wherein said at least one genetic modification results in an increased level of a compound of Formula III and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~68. The transgenic plant of any one of claims 54-67, wherein said at least one genetic modification results in an increased level of tetrahydrocannabivarinic Acid (THCVA) compared to a comparable plant lacking said genetic modification.~~

~~69. The transgenic plant of any one of claims 54-68, wherein said at least one genetic modification results in an increased level of cannabigerovarinic acid (CBGVA) compared to a comparable plant lacking said genetic modification.~~

~~70. The transgenic plant of claim 54, wherein said transgenic plant comprises a genetic modification in a promoter or enhancer sequence of at least one, two, three, four, or five different genes, wherein said genes encode for olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase.~~

~~71. The transgenic plant of claim 54, wherein said transgenic plant comprises a genetic modification in a promoter or enhancer of a gene that encodes for olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, and divarinic acid cyclase.~~

~~72. The transgenic plant of claim 70 or 71, wherein said genetic modifications increase expression of olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, and divarinic acid cyclase.~~

13~~73~~. The transgenic plant of claim 6~~25~~, wherein said at least one genetic modification is in a gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

14~~74~~. The transgenic plant of claim 13~~73~~, wherein said at least one genetic modification disrupts expression of said protein.

15~~75~~. The transgenic plant of claim ~~73 or 74~~14, wherein said at least one genetic modification decreases expression of said protein compared to a comparable plant lacking said genetic modification.

~~76. The transgenic plant of any one of claims 73-75, wherein said at least one genetic modification decreases expression of said protein by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic modification.~~

~~77. The transgenic plant of any one of claims 73-76, wherein said at least one genetic modification decreases expression of said protein by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold, compared to a comparable plant lacking said genetic modification.~~

~~78. The transgenic plant of any one of claims 73-77, wherein said at least one genetic modification results in an increased level of a compound of Formula I, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~79. The transgenic plant of any one of claims 73-77, wherein said at least one genetic modification results in an increased level of a compound of Formula II, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~80. The transgenic plant of any one of claims 73-77, wherein said at least one genetic modification results in an increased level of a compound of Formula III, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~81. The transgenic plant of any one of claims 67-77, wherein said at least one genetic modification results in an increased level of a compound of Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

~~82. The transgenic plant of any one of claims 73-77, wherein said at least one genetic modification results in an increased level of a compound of Formula I, Formula II, Formula III, and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.~~

83. The transgenic plant of any one of claims 73-77, wherein said at least one genetic modification results in an increased level of a compound of Formula III and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.

84. The transgenic plant of any one of claims 73-83, wherein said at least one genetic modification results in an increased level of tetrahydrocannabivarinic Acid (THCVA) compared to a comparable plant lacking said genetic modification.

85. The transgenic plant of any one of claims 73-84, wherein said at least one genetic modification results in an increased level of cannabigerovarinic acid (CBGVA) compared to a comparable plant lacking said genetic modification.

86. A transgenic plant that comprises:

a genetic modification in a promoter or enhancer sequence of a gene encoding THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase, wherein said genetic modification in said promoter or enhancer increases expression of said THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase, compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence;

a genetic disruption in a gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase, wherein said genetic disruption decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase; compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

87. A transgenic plant that comprises:

a genetic modification in a promoter or enhancer sequence of at least one, two, three, four, or five different genes, wherein said genes encode for THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase, wherein said genetic modification in said promoter or enhancer increases expression of said THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase, compared to a comparable plant lacking said genetic modificationin said promoter or enhancer sequence; and

a genetic disruption in at least one or two gene sequences that encode a cannabidiolic acid synthase or a cannabichromenic acid synthase, wherein said genetic disruption decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase; compared

to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

88. The transgenic plant of claim 86 or 87, wherein said genetic modification in said promoter or enhancer increases expression of said THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.

89. The transgenic plant of claim 86 or 87, wherein said genetic modification in said promoter or enhancer increases expression of said THC synthase, olivetolate geranyltransferase (GOT), geranyl pyrophosphate synthase (GPPS), polyketide synthase, or divarinic acid cyclase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold compared to a comparable plant lacking said genetic modification in said promoter or enhancer sequence.

90. The transgenic plant of any one of claims 86-89, wherein said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

91. The transgenic plant of any one of claims 86-90, wherein said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase decreases expression of said cannabidiolic acid synthase or said cannabichromenic acid synthase by at least 2 fold, 5 fold, 10 fold, 100 fold, 500 fold, 1000 fold, or 10000 fold, compared to a comparable plant lacking said genetic disruption in said gene sequence that encodes a cannabidiolic acid synthase or a cannabichromenic acid synthase.

92. The transgenic plant of any one of claims 86-91, wherein said wherein said at least one genetic modification results in an increased level of a compound of Formula II, compared to a level of said compound in a comparable plant lacking said genetic modification.

93. The transgenic plant of any one of claims 86-92, wherein said wherein said at least one genetic modification results in an increased level of a compound of Formula IV, compared to a level of said compound in a comparable plant lacking said genetic modification.

94. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula I, compared to a level of said compound in a comparable plant lacking said genetic modification.

95. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula II, compared to a level of said compound in a comparable plant lacking said genetic modification.

96. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula III, compared to a level of said compound in a comparable plant lacking said genetic modification.

97. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.

98. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula I, Formula II, Formula III, and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.

99. The transgenic plant of any one of claims 86-93, wherein said at least one genetic modification results in an increased level of a compound of Formula III and Formula VI, compared to a level of said compound in a comparable plant lacking said genetic modification.

100. The transgenic plant of any one of claims 86-99, wherein said at least one genetic modification results in an increased level of tetrahydrocannabivarinic Acid (THCVA) compared to a comparable plant lacking said genetic modification.

101. The transgenic plant of any one of claims 86-100, wherein said at least one genetic modification results in an increased level of cannabigerovarinic acid (CBGVA) compared to a comparable plant lacking said genetic modification.

16. 102. The transgenic plant of claim 1, wherein said transgenic plant further comprises an increased amount of cannabigerol (CBG), derivative or analog thereof, compared to an amount of the same compound in a comparable control plant without said genetic modification.

103. The transgenic plant of claim 1 or 16102, wherein said genetic modification comprises a genetic disruption that results in an increased expression of Formula II, or a derivative or analog thereof.

17104. The transgenic plant of claim 16 103, wherein said at least said at least one genetic modification comprises modification of a first group of genes that comprise comprisesolivetolic acid cyclase (OAC) and olivetolic acid synthase (OLS).

105. The transgenic plant of any of claims 1-104, wherein said genetic modification comprises a disruption of gene encoding prenyl-transferase, wherein said disruption results in an increased

~~amount of prenyl-transferase compared to an amount of the same compound comparable control plant without said disruption.~~

~~106. The transgenic plant of claim 105, wherein said prenyl-transferase is olivetolic acid geranyltransferase (GOT).~~

~~107. The transgenic plant of any of claims 103-106, wherein said disruption is in a promoter region of said genes.~~

18~~108~~. The transgenic plant of claim 1~~any of claims 1-103~~, wherein said genetic modification comprises a disruption of a ~~second of~~ group of genes encoding CBCA synthase, CBDA synthase, and THCA synthase.

~~109. The transgenic plant of claim 108, wherein said disruption results in a decreased amount of CBCA synthase, CBDA synthase, THCA synthase, derivatives or analogs thereof compared to an amount of the same compound of a comparable control plant without said disruption.~~

~~110. The transgenic plant of either claim 108 or 109, wherein said disruption is in a coding region of said genes.~~

~~111. The transgenic plant of any of the preceding claims comprising 10%, 25%, 35%, or 50% more Formula IV measured by dry weight as compared to a comparable control plant without said modification.~~

~~112. The transgenic plant of any of the preceding claims comprising 10% less cannabichromenic acid (CBCA) measured by dry weight as compared to a comparable control plant without said modification.~~

~~113. The transgenic plant of any of the preceding claims comprising 10% less cannabidiolic acid (CBDA) measured by dry weight as compared to a comparable control plant without said modification.~~

~~114. The transgenic plant of any of the preceding claims comprising 10% less tetrahydrocannabinolic acid (THCA) measured by dry weight as compared to a comparable control plant without said modification.~~

~~115. The transgenic plant of any of claim 1, wherein said transgenic plant comprises an increased amount of cannabinol (CBN), derivative or analog thereof compared to an amount of the same compound in a comparable control plant without said genetic modification.~~

~~116. The transgenic plant of either of claims 1 or 115, wherein said genetic modification comprises a disruption of gene encoding THCA synthase.~~

~~117. The transgenic plant of claim 116, wherein said disruption results in an increased amount of THCA synthase compared to an amount of the same compound in a comparable control plant without said disruption.~~

~~118. The transgenic plant of any of claims 1-117, wherein said genetic modification comprises a disruption of genes encoding CBDA synthase and CBCA synthase respectively.~~

~~119. The transgenic plant of any of claims of 118, wherein said disruption results in decreased amount of CBDA synthase and CBCA synthase compared to a comparable control plant without said disruption.~~

~~120. The transgenic plant of any of claims 115-119, wherein said genetic modification comprises a disruption of a third group of genes, wherein said disruption results in increased UV absorption of said transgenic plant compared to a comparable control without said disruption.~~

~~121. The transgenic plant of any of claims 115-120 comprising 10%, 25%, 35%, or 50% more THC measured by dry weight as compared to a comparable control plant without said genetic modification.~~

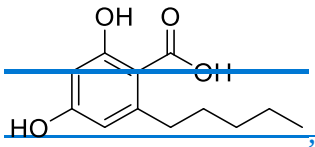
~~122. The transgenic plant of any of claims 110-121 comprising 10% less CBCA measured by dry weight as compared to a comparable control plant without said genetic modification.~~

~~123. The transgenic plant of any of claims 110-122 comprising 10% less CBDA measured by dry weight as compared to a comparable control plant without said genetic modification.~~

~~124. The transgenic plant of claim 1, wherein the transgenic plant comprises an increased amount of tetrahydrocannabivarin (THCV), derivative or analog thereof compared to an amount of the same compound in a comparable control plant without said genetic modification.~~

~~125. The transgenic plant of claim 124, wherein said genetic modification comprises a disruption of a first of group of genes, wherein said disruption results in an increased amount of Formula I, derivative or analog thereof.~~

~~126. The transgenic plant of any of claim 125, wherein said genetic modification comprises a disruption of a second group of genes, wherein said disruption results in a decreased amount of~~



~~, derivative or analog thereof.~~

~~127. The transgenic plant of claim 126, wherein said second group of genes comprises OAC and OLS.~~

~~128. The transgenic plant of either of claims 126 or 127, wherein said disruption is in a coding region of said genes.~~

~~129. The transgenic plant of any of claims 126-128, wherein said genetic modification comprises a disruption of a THCA synthase.~~

~~130. The transgenic plant of claim 129, wherein said disruption results in an increased amount of THCA synthase, derivative or analog thereof, compared to an amount of the same compound in a comparable control plant without said disruption.~~

~~131. The transgenic plant of either claims 129 or 130, wherein said disruption is in a promoter region of said genes.~~

~~132. The transgenic plant of any of claims 123-131, wherein said genetic modification comprises a disruption of a third group of genes encoding CBCA synthase and CBDA synthase respectively.~~

~~133. The transgenic plant of claim 132, wherein said disruption results in a decreased amount of CBCA synthase and CBDA synthase, derivatives or analogs thereof.~~

~~134. The transgenic plant of either claims 131 or 132, wherein said disruption is in a coding region of said genes.~~

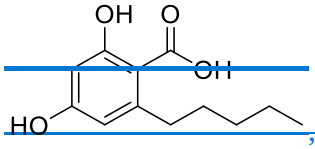
~~135. The transgenic plant of claims 124-134 comprising 10%, 25%, 35%, or 50% more tetrahydrocannabivarin (THCV) measure by dry weight as compared to a comparable control plant without said modification.~~

~~136. The transgenic plant of claims 121-127 comprising 10% less cannabichromevarin (CBCV) measure by dry weight as compared to a comparable control plant without said modification.~~

~~137. The transgenic plant of claims 121-127 comprising 10% less cannabidivarin (CBDV) measure by dry weight as compared to a comparable control plant without said modification.~~

~~138. A transgenic plant comprising a genetic modification, wherein said genetic modification results in an increased amount of cannabigerol (CBG), derivative or analog thereof, compared to an amount of the same compound in a comparable control plant without said genetic modification.~~

~~139. The transgenic plant of claim 138, wherein said genetic modification comprises a disruption of a first group of genes, wherein said disruption results in an increased amount of~~



~~, derivative or analog thereof.~~

~~140. The transgenic plant of claim 139, wherein said first group of genes comprises olivetolic acid cyclase (OAC) and olivetolic acid synthase (OLS).~~

~~141. The transgenic plant of any of claims 138-139, wherein said genetic modification comprises a disruption of gene encoding prenyl-transferase, wherein said disruption results in an increased amount of prenyl-transferase compared to a comparable control plant without said disruption.~~

~~142. The transgenic plant of claim 139, wherein said prenyl-transferase is olivetolic acid geranyltransferase (GOT).~~

~~143. The transgenic plant of any of claims 139-142, wherein said disruption is in a promoter region of said genes.~~

~~144. The transgenic plant of any of claims 138-143, wherein said genetic modification comprises a disruption of a second of group of genes encoding CBCA synthase, CBDA synthase, and THCA synthase.~~

~~145. The transgenic plant of claim 144, wherein said disruption results in a decreased amount of CBCA synthase, CBDA synthase, THCA synthase, derivatives or analogs thereof, compared to an amount of the same compound in a comparable control plant without said disruption.~~

~~146. The transgenic plant of either claim 144 or 145, wherein said disruption is in a coding region of said genes.~~

~~147. The transgenic plant of any of claims 138-146 comprising 10%, 25%, 35%, or 50% more Formula IV measured by dry weight as compared to a comparable control plant without said modification.~~

~~148. The transgenic plant of any of claims 135-144 comprising 10% less cannabichromenic acid (CBCA) measured by dry weight as compared to a comparable control plant without said modification.~~

~~149. The transgenic plant of any of claims 135-144 comprising 10% less cannabidiolic acid (CBDA) measured by dry weight as compared to a comparable control plant without said modification.~~

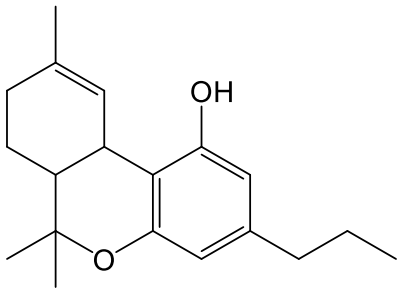
~~150. The transgenic plant of any of claims 135-144 comprising 10% less tetrahydrocannabinolic acid (THCA) measured by dry weight as compared to a comparable control plant without said modification.~~

19. ~~151.~~ A pharmaceutical composition comprising an extract of said transgenic plant of claim 2~~any of claims 1-150~~.

20. ~~152.~~ The pharmaceutical composition of claim 19~~151~~, further comprising a pharmaceutically acceptable excipient, diluent, or carrier.

21. ~~153.~~ The pharmaceutical composition of claim ~~15~~20, comprising said pharmaceutically acceptable excipient, wherein said pharmaceutically acceptable excipient is a lipid.

22. ~~154. A nutraceutical composition comprising an extract of said transgenic plant of any of claims 1-150~~transgenic plant that comprises at least one genetic modification, wherein said genetic modification results in at least about 50% more of a compound that is



(Tetrahydrocannabivarin (THCV), Formula VI) or a derivative or analog thereof compared to a level of said compound in a comparable plant lacking said genetic modification.

23. ~~155. A food supplement composition comprising an extract of said transgenic plant of any of claims 1-150~~ method of ~~-~~suppressing appetite in a subject, the method comprising administering an effective amount of the transgenic plant of claim 22 to the subject, thereby suppressing appetite in the subject.

24~~156~~. The pharmaceutical composition of claim 20 ~~any one of claims 151-153, the nutraceutical composition of claim 154, or the food supplement of claim 155~~ in an oral form, a transdermal form, an oil formulation, an edible food, a food substrate, an aqueous dispersion, an emulsion, a solution, a suspension, an elixir, a gel, a syrup, an aerosol, a mist, a powder, a tablet, a lozenge, a gel, a lotion, a paste, a formulated stick, a balm, a cream, or an ointment.

25~~157~~. ~~A method of treating a disease or condition comprising administering~~ The pharmaceutical composition of claim 20 for use in therapy~~any one of claims 151-153, the nutraceutical composition of claim 154, or the food supplement of claim 155 to a subject~~.

26~~158~~. Use of the pharmaceutical composition of claim 20 in the manufacture of a medicament for treating a disease or condition in a subject, wherein the medicament is to be administered to the subject, thereby treating the disease or condition, ~~The method of claim 157,~~ wherein said disease or condition is selected from the group consisting of anorexia, emesis, pain, inflammation, multiple sclerosis, Parkinson's disease, Huntington's disease, Tourette's syndrome, Alzheimer's disease, epilepsy, glaucoma, osteoporosis, schizophrenia, cardiovascular disorders, cancer, and obesity.

~~159. A method for generating a transgenic *Cannabis sativa*, said method comprising:~~

~~(a) contacting a cell comprising a gene with an endonuclease or a polynucleotide encoding said endonuclease, wherein said endonuclease introduces a genetic modification in the gene; and~~

~~(b) culturing said cell with said genomic modification in the gene to generate a transgenic *Cannabis sativa*.~~

~~160. The method of claim 159, wherein said cell is derived from a callus, a cotyledon, a hypocotyl, a protoplast, a root, a leaf, or a fraction thereof.~~

~~161. A method for generating a transgenic plant of any one of claims 1-150.~~

~~162. A method for generating a transgenic plant, said method comprising:~~

~~(a) contacting an immature female flower with a solution comprising a vector that contains a nucleotide sequence encoding an endonuclease to introduce a genetic modification in the female flower;~~

~~(b) contacting the female flower with a sufficient amount of pollen to produce one or more seeds that comprise the genetic modification; and~~

~~(c) culturing said seed to generate a transgenic plant.~~

~~163. The method of claim 162, wherein the plant is a cannabis plant.~~