NOVEL ACETYL CoA CARBOXYLASES

ABSTRACT OF THE DISCLOSURE

[00581] Provided herein are novel ACCases and nucleotides encoding the same, that when introduced into a cell or organism results in an increase and/or accumulation of fatty acids, glycerol lipids, and/or oils in the cell or organism, and/or a change in the types of fatty acids, glycerol lipids, and/or oils that are normally present in the cell or organism. Also provided herein are organisms transformed with the novel ACCases.

Refer to figure 1

CLAIMS

What is claimed is:

1. An isolated polynucleotide capable of transforming a photosynthetic organism comprising a nucleic acid sequence encoding an acetyl CoA carboxylase, wherein the acetyl CoA carboxylase comprises:

1) an amino acid sequence of SEQ ID NO: 157; or

2) an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

2. An acetyl CoA carboxylase present in a photosynthetic organism comprising:

1) an amino acid sequence of SEQ ID NO: 157; or

2) an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

3. A nucleotide sequence encoding an acetyl CoA carboxylase wherein the nucleotide sequence comprises:

1) a nucleic acid sequence of SEQ ID NO: 114 or SEQ ID NO: 155; or

2) a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 114 or SEQ ID NO: 115, wherein the nucleotide sequence is capable of transforming a photosynthetic organism.

4. A vector comprising a nucleotide sequence encoding an acetyl CoA carboxylase, wherein t he acetyl CoA carboxylase comprises:

1) an amino acid sequence of SEQ ID NO: 157; or

2) an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157, wherein the vector is used to transform a photosynthetic organism.

5. The vector of claim 4, wherein the vector is an expression vector.

6. The vector of claim 4 or 5, wherein the vector further comprises a 5' regulatory region.

7. The vector of claim 6, wherein the 5' regulatory region further comprises a promoter.

8. The vector of claim 7, wherein the promoter is a constitutive promoter.

9. The vector of claim 7, wherein the promoter is an inducible promoter.

10. The vector of claim 9, wherein the inducible promoter is a light inducible promoter, a nitrate inducible promoter, or a heat responsive promoter.

11. The vector of any one of claims 4 to 10, further comprising a 3' regulatory region.

12. A method for increasing production of malonyl CoA in a photosynthetic organism, comprising transforming the photosynthetic organism with a polynucleotide encoding an ACCase comprising an amino acid sequence of SEQ ID NO: 157, or with a polynucleotide encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

13. The method of claim 12, wherein the photosynthetic organism is a prokaryote.

14. The method of claim 13, wherein the prokaryote is a cyanobacterium.

15. The method of claim 12, wherein the photosynthetic organism is a eukaryote.

16. The method of claim 15, wherein the eukaryote is a vascular plant.

17. The method of claim 15, wherein the eukaryote is a non-vascular photosynthetic organism.

18. The method of claim 17, wherein the non-vascular photosynthetic organism is an alga.

19. The method of claim of any one of claims 12 to 18, further comprising transforming a plastid with the polynucleotide.

20. The method of claim 19, wherein the plastid is a chloroplast.

21. A method for increasing fatty acid synthesis in a photosynthetic organism comprising transforming the photosynthetic organism with a polynucleotide encoding an ACCase comprising an amino acid sequence of SEQ ID NO: 157, or with a polynucleotide encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

22. The method of claim 21, wherein the photosynthetic organism is a prokaryote.

23. The method of claim 22, wherein the prokaryote is a cyanobacterium.

24. The method of claim 21, wherein the organism is a eukaryote.

25. The method of claim 24, wherein the eukaryote is a vascular plant.

26. The method of claim 24, wherein the eukaryote is a non-vascular photosynthetic organism.

27. The method of claim 21, wherein the photosynthetic organism is an alga.

28. The method of claim of any one of claims 21 to 27, further comprising transforming a plastid with the polynucleotide.

29. The method of claim 28, wherein the plastid is a chloroplast.

30. A transgenic host cell comprising a nucleotide sequence encoding an ACCase comprising an amino acid sequence of SEQ ID NO: 157, or comprising a nucleotide sequence encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

31. The transgenic host cell of claim 30, wherein the host cell is a prokaryote.

32. The transgenic host cell of claim 31, wherein the prokaryote is a cyanobacterium.

33. The transgenic host cell of claim 30, wherein the host cell is a plant cell.

34. The transgenic host cell of claim 33, wherein the plant cell is from a vascular plant.

35. The transgenic host cell of claim 33, wherein the plant cell is from an alga.

36. The transgenic host cell of claim 35, wherein the alga is a green alga.

37. The transgenic host cell of claim 36, wherein the green alga is a *Chlorophycean*.

38. A transgenic plastid comprising a polynucleotide encoding an acetyl CoA carboxylase comprising an amino acid sequence of SEQ ID NO: 157, or encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

39. The transgenic plastid of claim 38, wherein the plastid is a chloroplast.

40. A host cell comprising the transgenic plastid of claim 38 or claim 39.

41. The host cell of claim 40, wherein the host cell is a prokaryote.

42. The host cell of claim 41, wherein the host cell is a cyanobacterium.

43. The host cell of claim 40, wherein the host cell is a plant cell.

44. The host cell of claim 43, wherein the plant cell is from a vascular plant.

45. The host cell of claim 40, wherein the plant cell is an alga.

46. The transgenic host cell of 45, wherein the alga is a green alga

47. The transgenic host cell of claim 46, wherein the green alga is a *Chlorophycean.*

48. An acetyl CoA carboxylase present in a photosynthetic organism comprising:
an amino acid sequence of a mammalian acetyl CoA carboxylase.

49. The acetyl CoA carboxylase of claim 48, wherein the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 157, or an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 157.

50. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15, SEQ ID

NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

51. An acetyl CoA carboxylase comprising an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

52. A nucleotide sequence encoding a beta subunit of an acetyl CoA carboxylase wherein the nucleotide sequence comprises:

1) a nucleic acid sequence of SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO:160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 168, or SEQ ID NO: 169; or

2) a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO:160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 168, or SEQ ID NO: 169.

53. A vector comprising a nucleotide sequence encoding a beta subunit of an acetyl CoA carboxylase wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

54. The vector of claim 53, wherein the vector is an expression vector.

55. The vector of claim 53 or claim 54, wherein the vector further comprises a 5' regulatory region.

56. The vector of claim 55, wherein the 5' regulatory region further comprises a promoter.

57. The vector of claim 56, wherein the promoter is a constitutive promoter.

58. The vector of claim 56, wherein the promoter is an inducible promoter.

59. The vector of claim 58, wherein the inducible promoter is a light inducible promoter, a nitrate inducible promoter, or a heat responsive promoter.

60. The vector of any one of claims 53 to 59, further comprising a 3' regulatory region.

61. A method for increasing production of malonyl CoA in a photosynthetic organism comprising transforming the photosynthetic organism with a polynucleotide encoding a beta subunit of an ACCase, wherein the beta subunit of the ACCase comprises an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

62. The method of claim 61, wherein the photosynthetic organism is a prokaryote.

63. The method of claim 62, wherein the prokaryote is a cyanobacterium.

64. The method of claim 61, wherein the organism is a eukaryote.

65. The method of claim 64, wherein the eukaryote is a vascular plant.

66. The method of claim 64, wherein the eukaryote is a non-vascular photosynthetic organism.

67. The method of claim 66, wherein the non-vascular photosynthetic organism is an alga.

68. The method of claim of any one of claims 61 to 67, further comprising transforming a plastid with the polynucleotide.

69. The method of claim 68, wherein the plastid is a chloroplast.

70. A method for increasing fatty acid synthesis in a photosynthetic organism comprising transforming the photosynthetic organism with a polynucleotide encoding an ACCase comprising an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

71. The method of claim 70, wherein the photosynthetic organism is a prokaryote.

72. The method of claim 71, wherein the prokaryote is a cyanobacterium.

73. The method of claim 70, wherein the organism is a eukaryote.

74. The method of claim 73, wherein the eukaryote is a vascular plant.

75. The method of claim 70, wherein the eukaryote is a non-vascular photosynthetic organism.

76. The method of claim 75, wherein the non-vascular photosynthetic organism is an alga.

77. The method of claim of any one of claims 70 to 76, further comprising transforming a plastid with the polynucleotide.

78. The method of claim 77, wherein the plastid is a chloroplast.

79. A transgenic host cell comprising a nucleotide sequence encoding an ACCase comprising an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) encoding an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acids sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

80. The transgenic host cell of claim 79, wherein the host cell is a prokaryote.

81. The transgenic host cell of claim 80, wherein the prokaryote is a cyanobacterium.

82. The transgenic host cell of any one of claims 79 to 81, wherein the host cell is a plant cell.

83. The transgenic host cell of claim 82, wherein the plant cell is from a vascular plant.

84. The transgenic host cell of claim 82, wherein the plant cell is from an alga.

85. The transgenic host cell of claim 84, wherein the alga is a green alga.

86. The transgenic host cell of claim 85, wherein the green alga is a *Chlorophycean.*

87. A transgenic plastid comprising a polynucleotide encoding a beta subunit of an acetyl CoA carboxylase comprising an amino acid sequence of:

a) SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167; or

b) comprising an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acids sequence of SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 163, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

88. The transgenic plastid of claim 87, wherein the plastid is a chloroplast.

89. A host cell comprising the transgenic plastid of claim 87 or claim 88.

90. The host cell of claim 89, wherein the host cell is a prokaryote.

91. The host cell of claim 90, wherein the prokaryote is a cyanobacterium.

92. The host cell of 89, wherein the host cell is a plant cell.

93. The host cell of claim 92, wherein the plant cell is from a vascular plant.

94. The host cell of claim 92, wherein the plant cell is an alga.

95. The host cell of 94, wherein the alga is a green alga

96. The host cell of claim 95, wherein the green alga is a *Chlorophycean.*

97. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 15; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 15.

98. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 16; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 16.

99. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 17; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 17.

100. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 18; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 18.

101. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 19; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 19.

102. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO:

20; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 20.

103. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 21; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 21.

104. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 22; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 22.

105. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 23; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 23.

106. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 24; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 24.

107. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 163; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 163.

108. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 164; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 164.

109. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 165; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 165.

110. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 166; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 166.

111. An isolated polynucleotide comprising a nucleic acid sequence encoding a beta subunit of an acetyl CoA carboxylase, wherein the beta subunit of the acetyl CoA carboxylase comprises an amino acid sequence of SEQ ID NO: 167; or comprises an amino acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the amino acid sequence of SEQ ID NO: 167.

112. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 158; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 158.

113. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 159; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 159.

114. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 160; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 160.

115. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 161; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 161.

116. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 162; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 162.

117. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 168; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 168.

118. An isolated polynucleotide comprising a nucleic acid sequence of SEQ ID NO: 169; or comprising a nucleic acid sequence that has at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least at least 99% sequence identity to the nucleic acid sequence of SEQ ID NO: 169.

119. An isolated polynucleotide comprising a sequence encoding an acetyl CoA carboxylase comprising an amino acid sequence of:
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNY
HLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVA
LGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6AN
LLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLK
GALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)
wherein
X_1 is T or D or E or N or H or Q or K;
X_2 is T or D or E or N or H or Q or K;
X_3 is S or D or E or N or H or Q or K;
X_4 is S or D or E or N or H or Q or K;
X_5 is S or D or E or N or H or Q or K;
X_6 is C or D or E or N or H or Q or K;
X_7 is Y or D or E or N or H or Q or K;
provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

120. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

121. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

122. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

123. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

124. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

125. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is D and X_7 is Y.

126. The isolated polynucleotide of claim 119, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

127. An acetyl CoA carboxylase comprising an amino acid sequence of:
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNYHLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVALGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6ANLLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLKGALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)
wherein
X_1 is T or D or E or N or H or Q or K;
X_2 is T or D or E or N or H or Q or K;
X_3 is S or D or E or N or H or Q or K;
X_4 is S or D or E or N or H or Q or K;
X_5 is S or D or E or N or H or Q or K;
X_6 is C or D or E or N or H or Q or K;
X_7 is Y or D or E or N or H or Q or K;
provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

128. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

129. The acetyl CoA carboxylase of claim 127 wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

130. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

131. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

132. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

133. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is D and X_7 is Y.

134. The acetyl CoA carboxylase of claim 127, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

135. A vector comprising a nucleotide sequence encoding an acetyl CoA carboxylase comprising an amino acid sequence of:

AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNYHLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVALGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6ANLLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLKGALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)

wherein

X_1 is T or D or E or N or H or Q or K;

X_2 is T or D or E or N or H or Q or K;

X_3 is S or D or E or N or H or Q or K;

X_4 is S or D or E or N or H or Q or K;

X_5 is S or D or E or N or H or Q or K;

X_6 is C or D or E or N or H or Q or K;

X_7 is Y or D or E or N or H or Q or K;

provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

136. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

137. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

138. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

139. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

140. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

141. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is D and X_7 is Y.

142. The vector of claim 135, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

143. The vector of any one of claims 135 to 142, wherein the vector is an expression vector.

144. The vector of any one of claims 135 to 143, wherein the vector further comprises a 5' regulatory region.

145. The vector of claim 144, wherein the 5' regulatory region further comprises a promoter.

146. The vector of claim 145, wherein the promoter is a constitutive promoter.

147. The vector of claim 145, wherein the promoter is an inducible promoter.

148. The vector of claim 147, wherein the inducible promoter is a light inducible promoter, nitrate inducible promoter or a heat responsive promoter.

149. The vector of any one of claims 135 to 148, further comprising a 3' regulatory region.

150. A method for increasing production of malonyl CoA in a photosynthetic organism comprising transforming the photosynthetic organism with a polynucleotide encoding
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNY
HLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVA
LGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6AN
LLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLK
GALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)
wherein
X_1 is T or D or E or N or H or Q or K;
X_2 is T or D or E or N or H or Q or K;
X_3 is S or D or E or N or H or Q or K;
X_4 is S or D or E or N or H or Q or K;
X_5 is S or D or E or N or H or Q or K;
X_6 is C or D or E or N or H or Q or K;
X_7 is Y or D or E or N or H or Q or K;
provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

151. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

152. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

153. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

154. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

155. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

156. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is D and X_7 is Y.

157. The method of claim 150, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

158. The method of any one of claims 150 to 157, wherein the photosynthetic organism is a prokaryote.

159. The method of claim 158, wherein the prokaryote is a cyanobacterium.

160. The method of claim 150, wherein the organism is a eukaryote.

161. The method of claim 160, wherein the eukaryote is a vascular plant.

162. The method of claim 160, wherein the eukaryote is a non-vascular photosynthetic organism.

163. The method of claim 162, wherein the non-vascular photosynthetic organism is an alga.

164. The method of any one of claims 150 to 163, further comprising transforming a plastid with the polynucleotide.

165. The method of claim 164, wherein the plastid is a chloroplast.

166. A method for increasing fatty acid synthesis in a photosynthetic organism comprising transforming the photosynthetic organism with a polynucleotide encoding
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNYHLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVALGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6ANLLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLKGALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)
wherein
X_1 is T or D or E or N or H or Q or K;
X_2 is T or D or E or N or H or Q or K;
X_3 is S or D or E or N or H or Q or K;
X_4 is S or D or E or N or H or Q or K;
X_5 is S or D or E or N or H or Q or K;
X_6 is C or D or E or N or H or Q or K;
X_7 is Y or D or E or N or H or Q or K;
provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

167. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

168. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

169. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

170. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

171. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

172. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is D and X_7 is Y.

173. The method of claim 166, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

174. The method of any one of claims 166 to 173, wherein the photosynthetic organism is a prokaryote.

175. The method of claim 174, wherein the prokaryote is a cyanobacterium.

176. The method of claim 166, wherein the organism is a eukaryote.

177. The method of claim 176, wherein the eukaryote is a vascular plant.

178. The method of claim 176, wherein the eukaryote is a non-vascular photosynthetic organism.

179. The method of claim 178, wherein the non-vascular photosynthetic organism is an alga.

180. The method of any one of claims 166 to 179, further comprising transforming a plastid with the polynucleotide.

181. The method of claim 180, wherein the plastid is a chloroplast.

182. A transgenic host cell comprising a nucleotide sequence encoding
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNY
HLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVA
LGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6AN
LLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLK
GALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)
wherein
X_1 is T or D or E or N or H or Q or K;
X_2 is T or D or E or N or H or Q or K;
X_3 is S or D or E or N or H or Q or K;

X_4 is S or D or E or N or H or Q or K;
X_5 is S or D or E or N or H or Q or K;
X_6 is C or D or E or N or H or Q or K;
X_7 is Y or D or E or N or H or Q or K;
provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

183. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

184. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

185. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

186. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

187. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

188. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is D and X_7 is Y.

189. The transgenic host cell of claim 182, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

190. The transgenic host cell of any one of claims 182 to 189, wherein the host cell is a prokaryote.

191. The transgenic host cell of claim 190, wherein the host cell is a cyanobacterium.

192. The transgenic host cell of claim 182, wherein the host cell is a plant cell.

193. The transgenic host cell of claim 192, wherein the plant cell is from a vascular plant.

194. The transgenic host cell of claim 182, wherein the plant cell is from an alga.

195. The transgenic host cell of claim 194, wherein the alga is a green alga.

196. The transgenic host cell of claim 195, wherein the green alga is a *Chlorophycean.*

197. A transgenic plastid comprising a polynucleotide encoding an acetyl CoA carboxylase comprising an amino acid sequence of:
AGEANGSPIVTGPISVNPSMSPALDPVAAAEAGKSAKAVDRSKGLWTRCDKCGTILYIKHLKEHHHICFGCNY
HLKMSSMERINHLIDAGX_1WRPLDEX_2LX_3PVDPLEFX_4DLKX_5YTDRIKEAQEKTGLQDGVRTGTGLLHGIPVA

LGVMDFTYMGGSMGSVVGEKLTRLIEYATQEGMPVIIVCTSGGARMQEGIFSLMQMAKISAALHVHQNX_6ANLLYIAILTSPTTGGVTASFGMLGDVIIAEPQAIIGFAGRRVIEQTLQEQLPDDFQTAEYLLEHGLLDLVVPRSFLKGALX_7EIIDFYRAAPYKKRGMIPFGVQHGTFLTTEEKV (SEQ ID NO: 11)

wherein

X_1 is T or D or E or N or H or Q or K;

X_2 is T or D or E or N or H or Q or K;

X_3 is S or D or E or N or H or Q or K;

X_4 is S or D or E or N or H or Q or K;

X_5 is S or D or E or N or H or Q or K;

X_6 is C or D or E or N or H or Q or K;

X_7 is Y or D or E or N or H or Q or K;

provided, however, that the combination of X_1, X_2, X_3, X_4, X_5, X_6 and X_7 is not T, T, S, S, S, C, Y, respectively.

198. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is S, X_6 is C and X_7 is Y.

199. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is D, X_6 is C and X_7 is Y.

200. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is D and X_7 is Y.

201. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is S, X_5 is S, X_6 is C and X_7 is D.

202. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is Y.

203. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is D and X_7 is Y.

204. The transgenic plastid of claim 197, wherein X_1 is T, X_2 is T, X_3 is S, X_4 is D, X_5 is D, X_6 is C and X_7 is D.

205. The transgenic plastid of any one of claims 197 to 204, wherein the plastid is a chloroplast.

206. A host cell comprising the transgenic plastid of any one of claims 197 to 205.

207. The host cell of claim 206, wherein the host cell is a prokaryote.

208. The host cell of claim 207, wherein the prokaryote is a cyanobacterium.

209. The host cell of claim 206, wherein the host cell is a plant cell.

210. The host cell of claim 209, wherein the plant cell is from a vascular plant.

211. The host cell of claim 209, wherein the plant cell is an alga.

212. The transgenic host cell of 211, wherein the alga is a green alga

213. The transgenic host cell of claim 212, wherein the green alga is a *Chlorophycean.*

214. The ACCase of claim 48, wherein the mammalian ACCase comprises the amino acid sequence of mouse (Mus Musculus: NM_133360.2 Identity: 99%); cattle (Bos Taurus: NM_174224.2. Identity: 97%); dog (Canis Lupus: XM_862501.1. Identity: 96%); chicken (Gallus gallus: NM_205505.1. Identity: 92%); or goat (Capra hircus: DQ370054.1. Identity: 98%).

215. The isolated polypeptide of claim 1, wherein the photosynthetic organism is *Chlamydomonas reinhardtii.*

Dated this 24th day of February 2012

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AGENTS FOR THE APPLICANTS

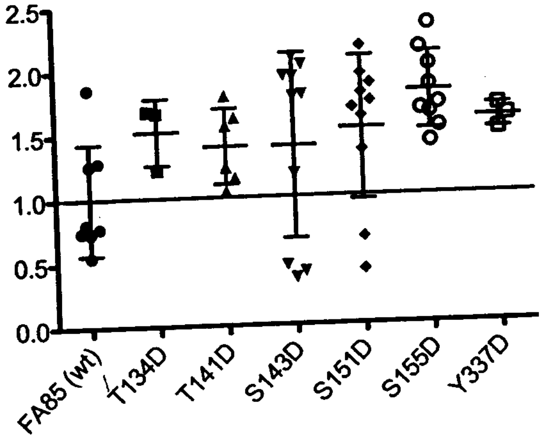

FIG. 1

ORIGINAL

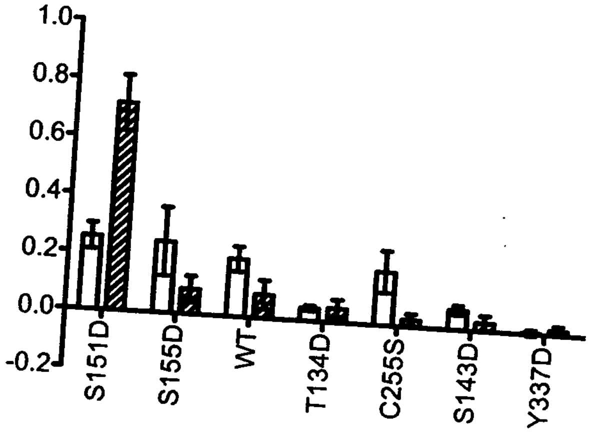

FIG. 2

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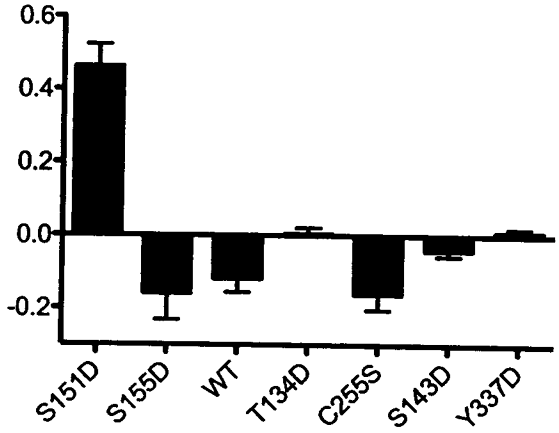

FIG. 3

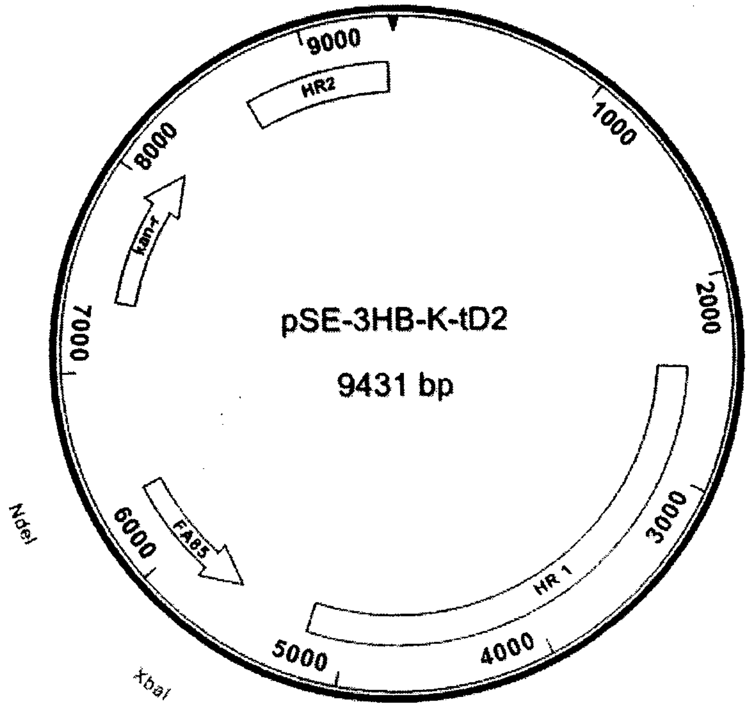

FIG. 4

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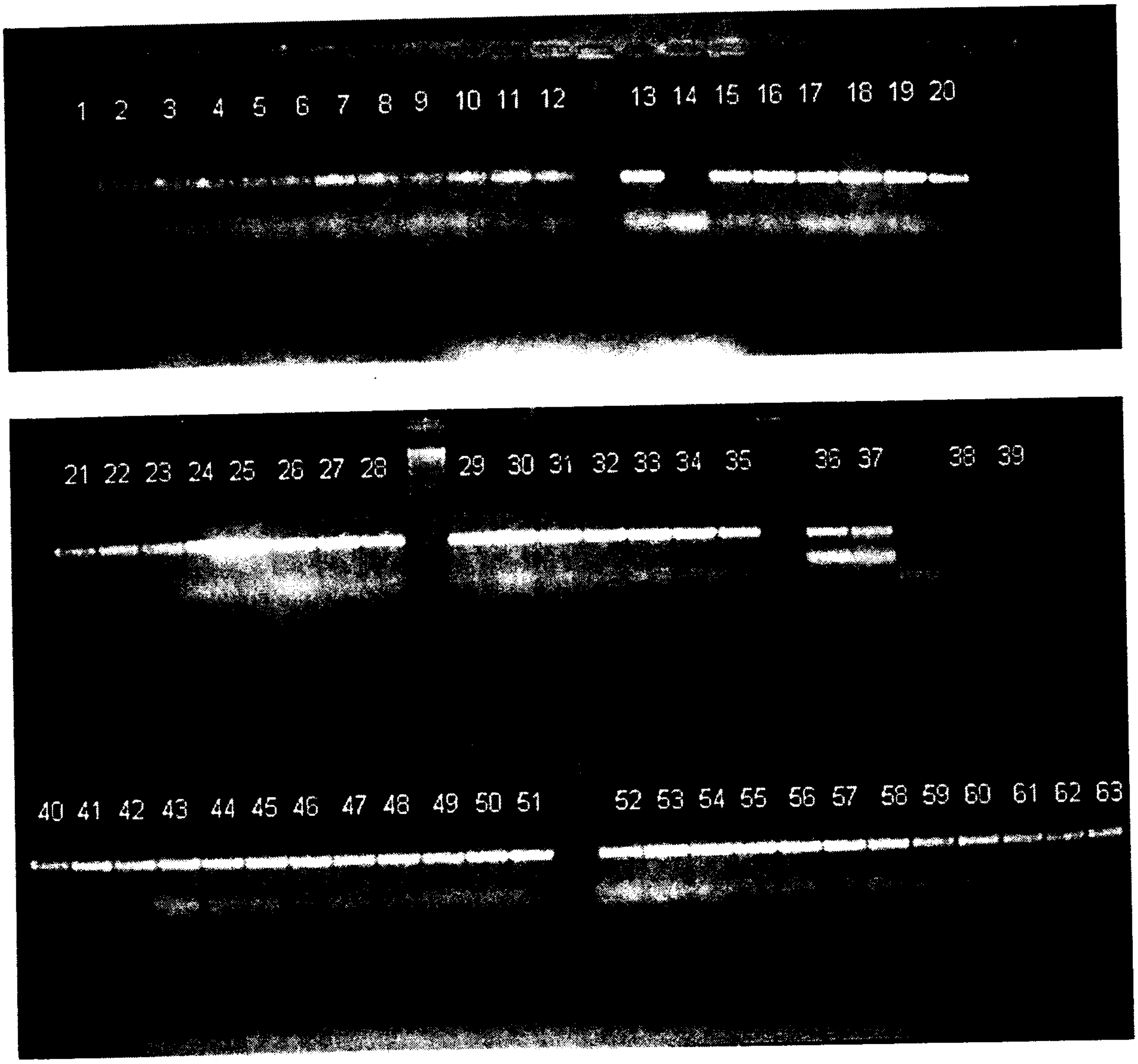

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63

FIG. 5

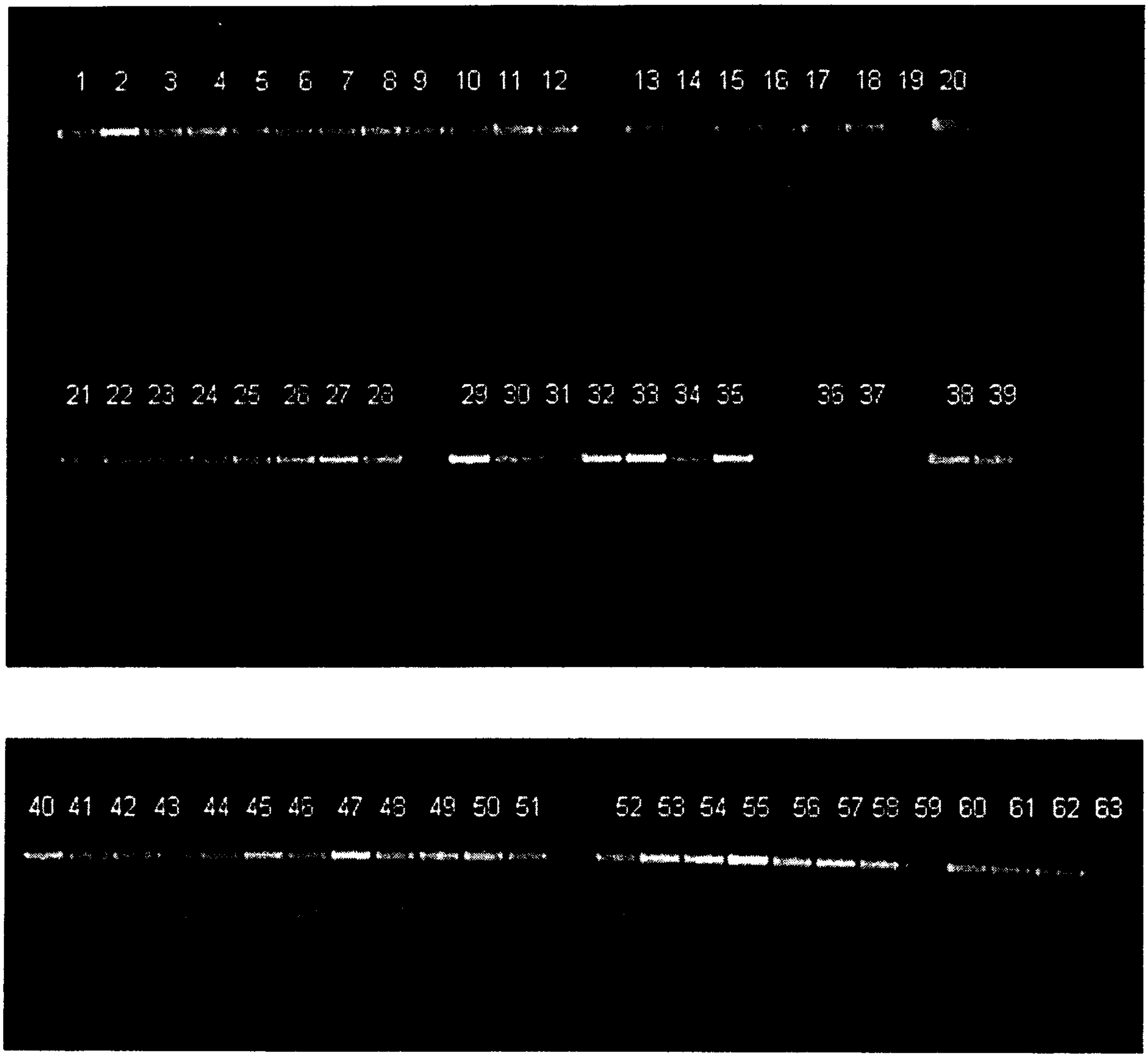
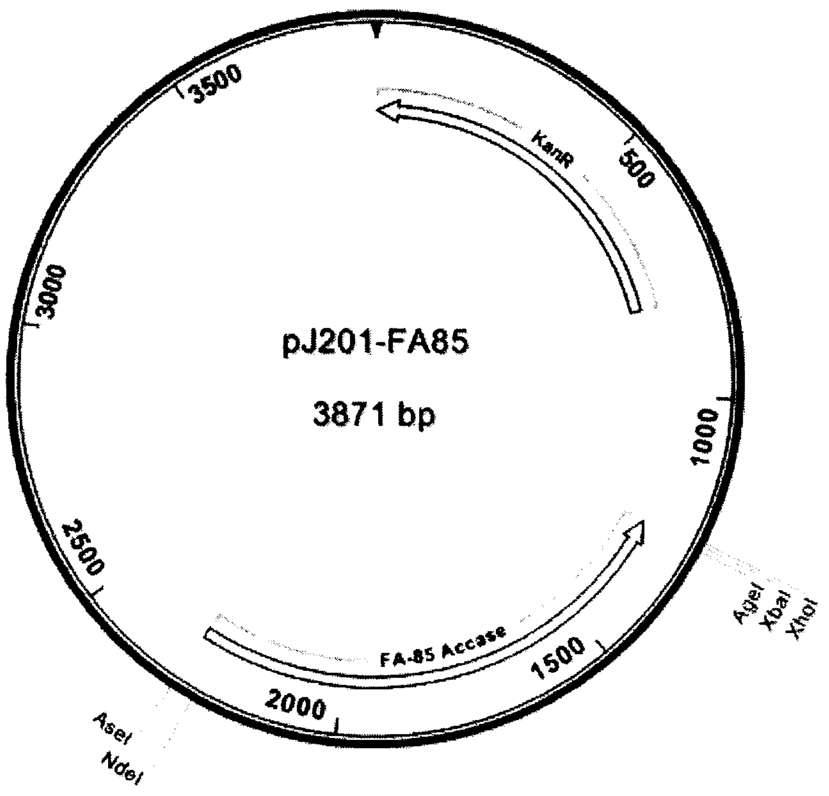

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39
40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63

FIG. 6


pJ201-FA85
3871 bp
KanR
FA-85 Accase
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3500
AgeI
XbaI
XhoI
AseI
NdeI

FIG. 7

FIG. 8A

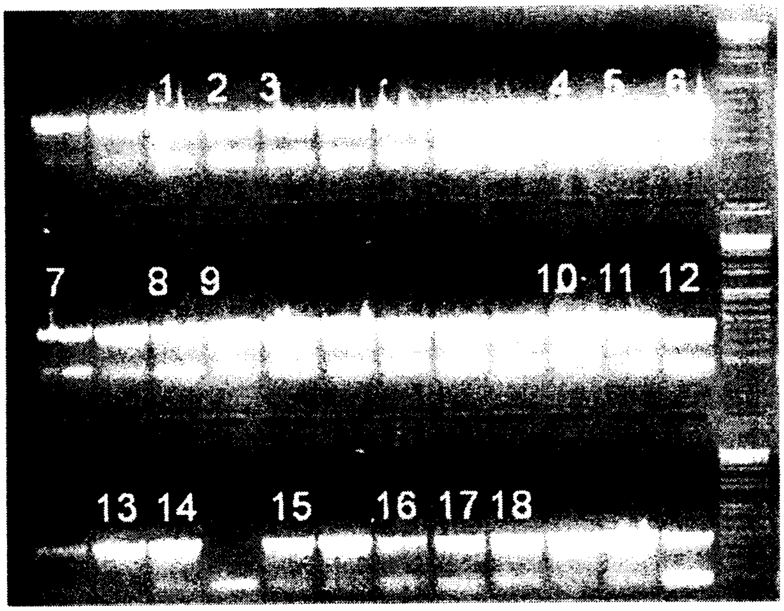
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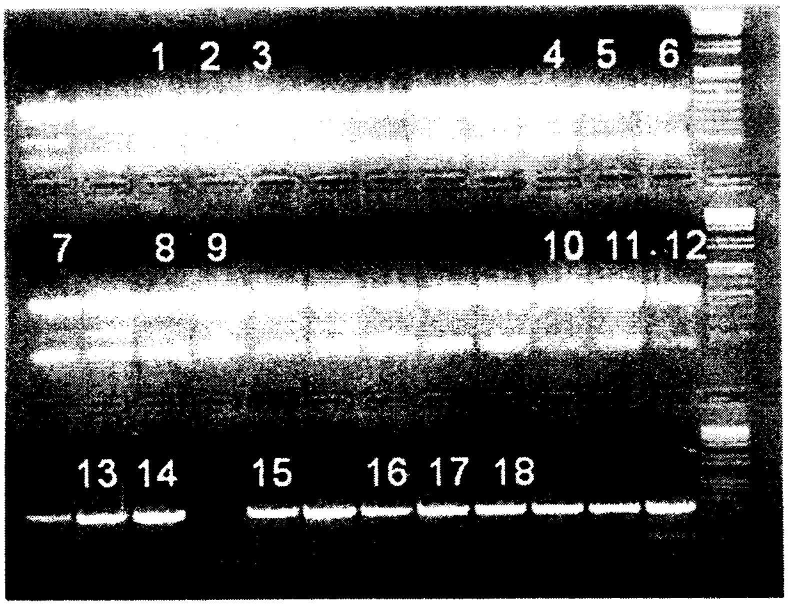
FIG. 8B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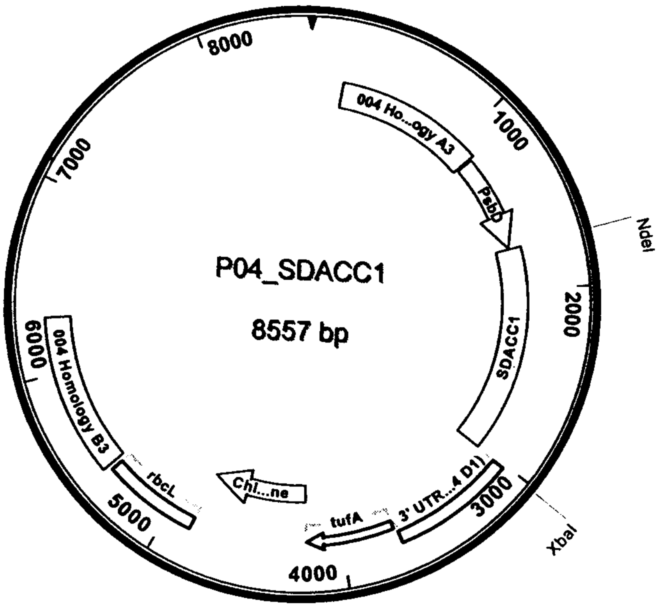

FIG. 9

Shanker

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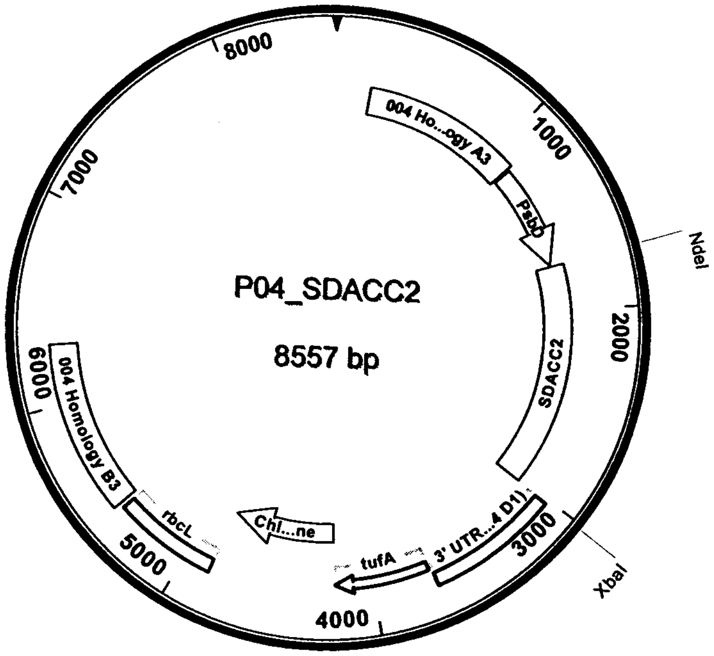

FIG. 10

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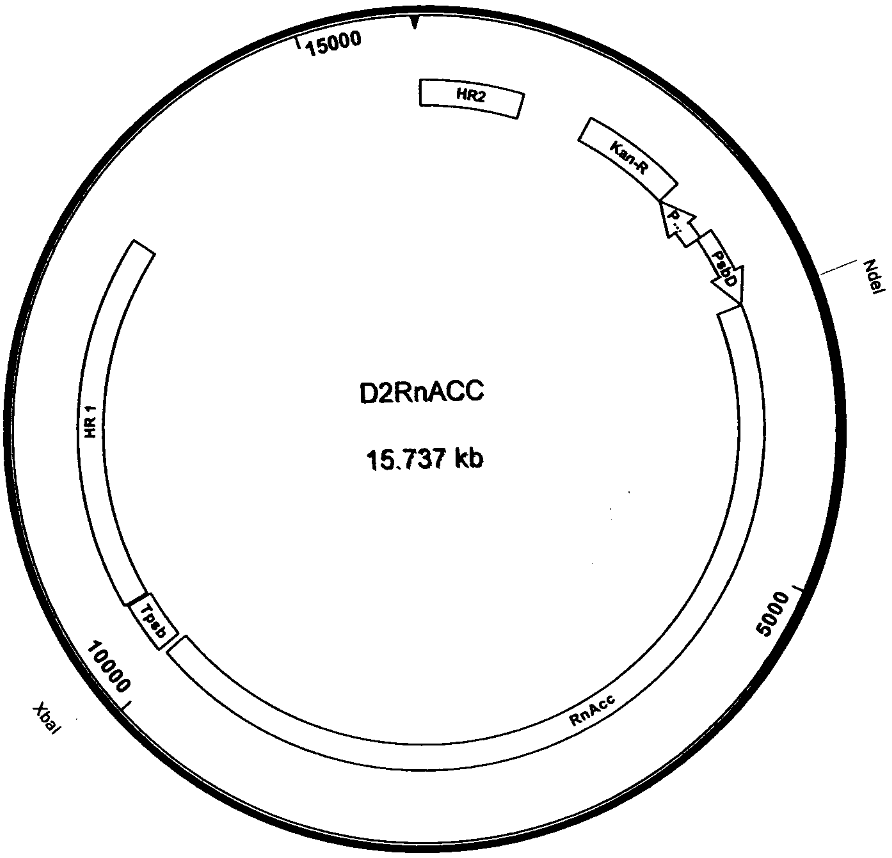

FIG. 11

Shanker

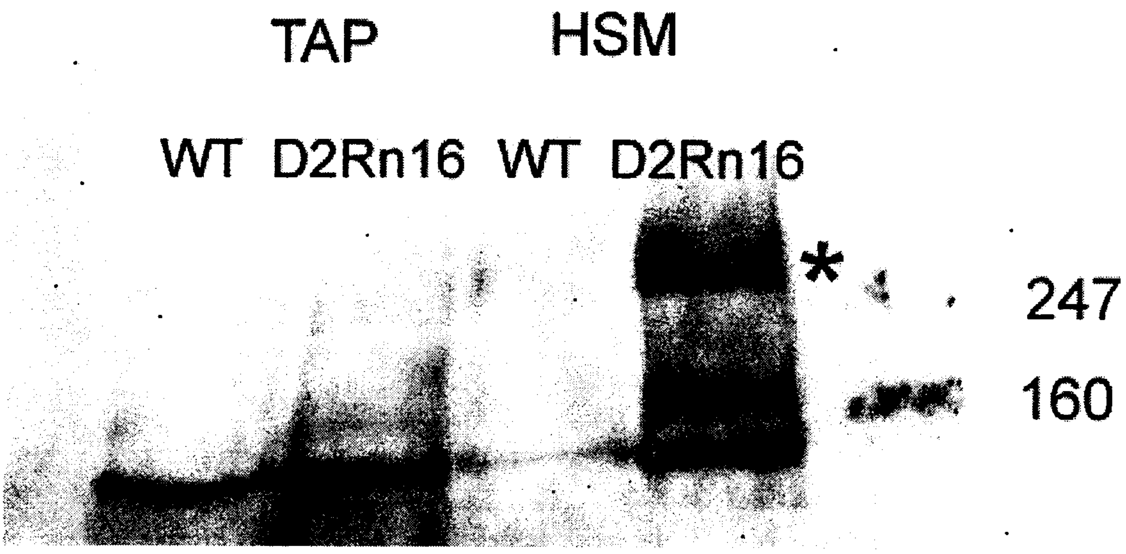

FIG. 12

Shanker

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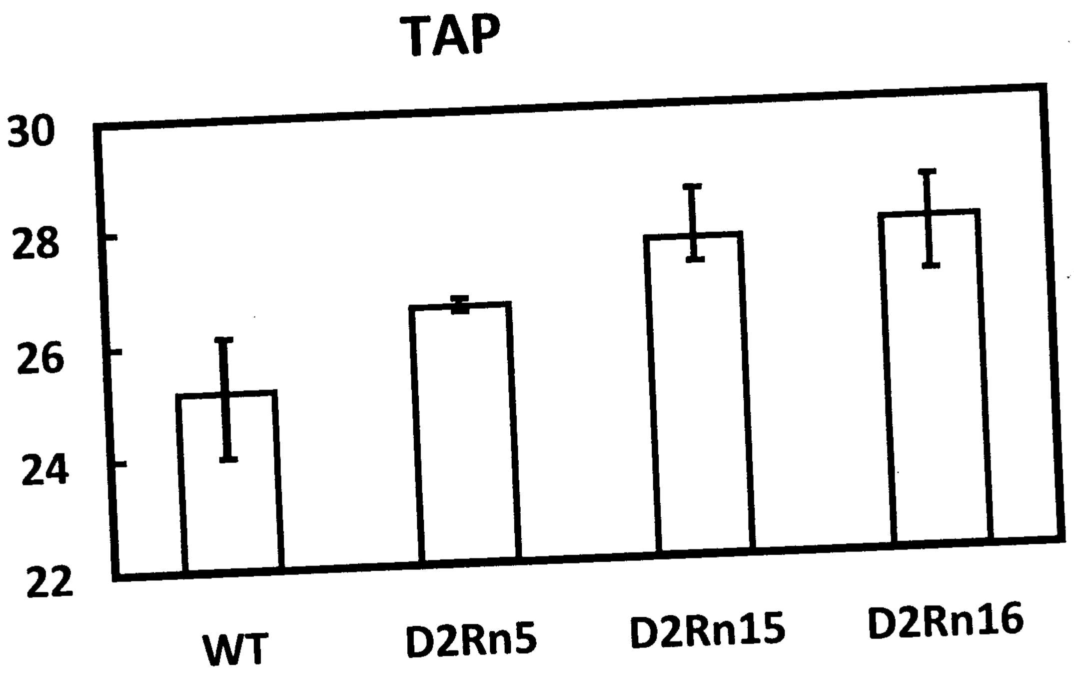

FIG. 13

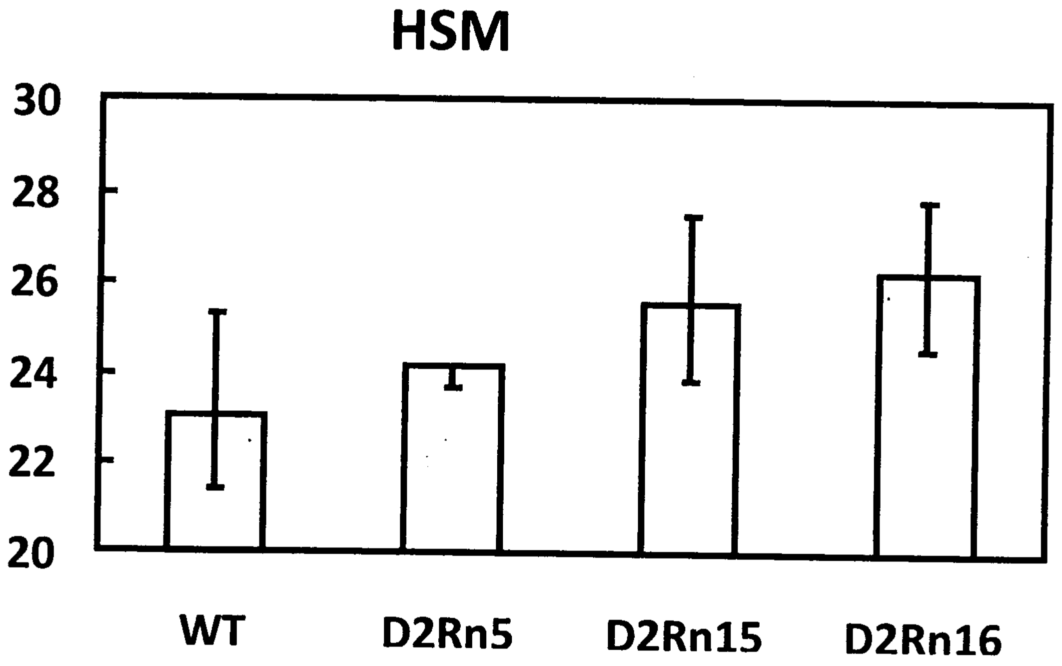

FIG. 14

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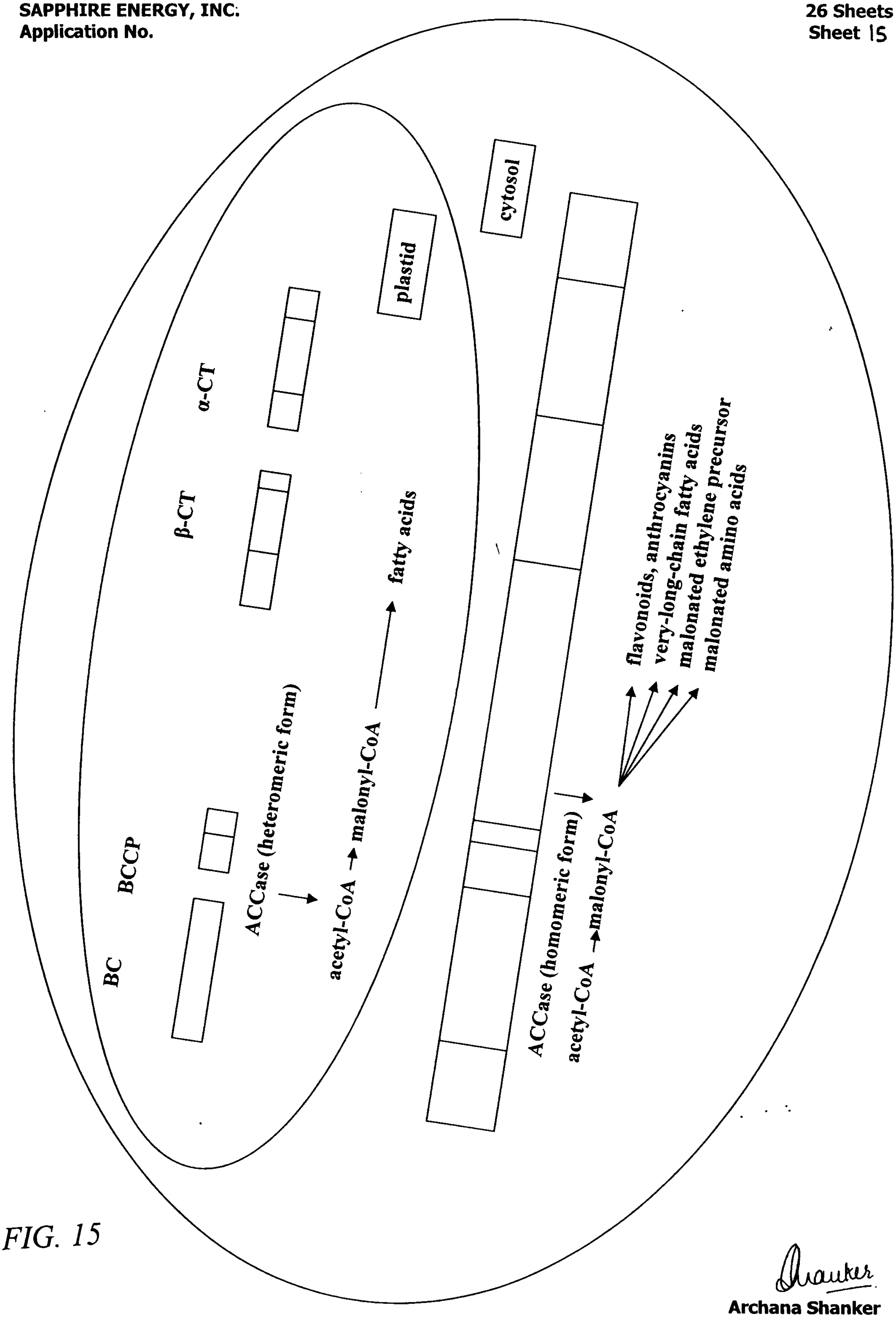

FIG. 15

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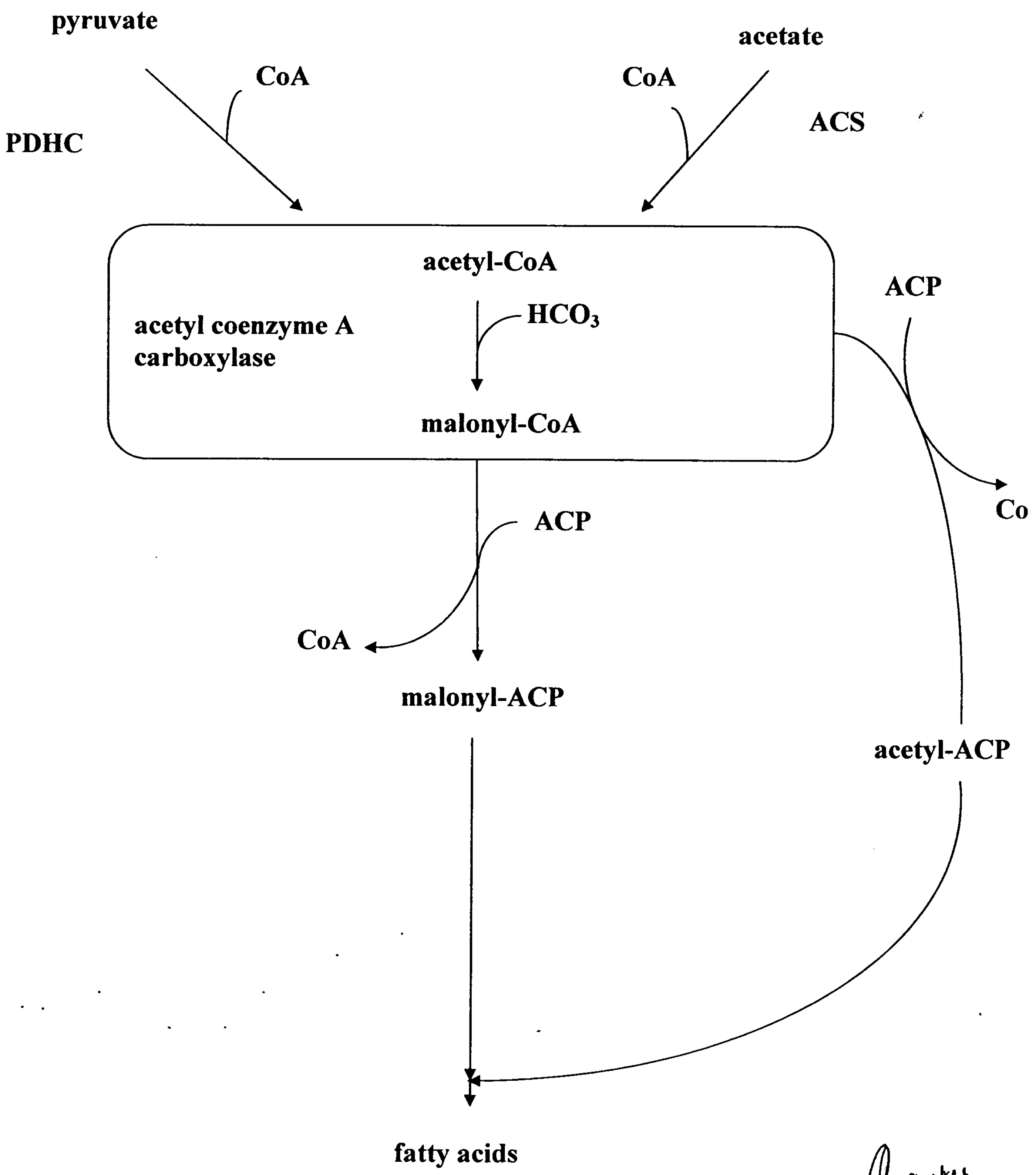
FIG. 16



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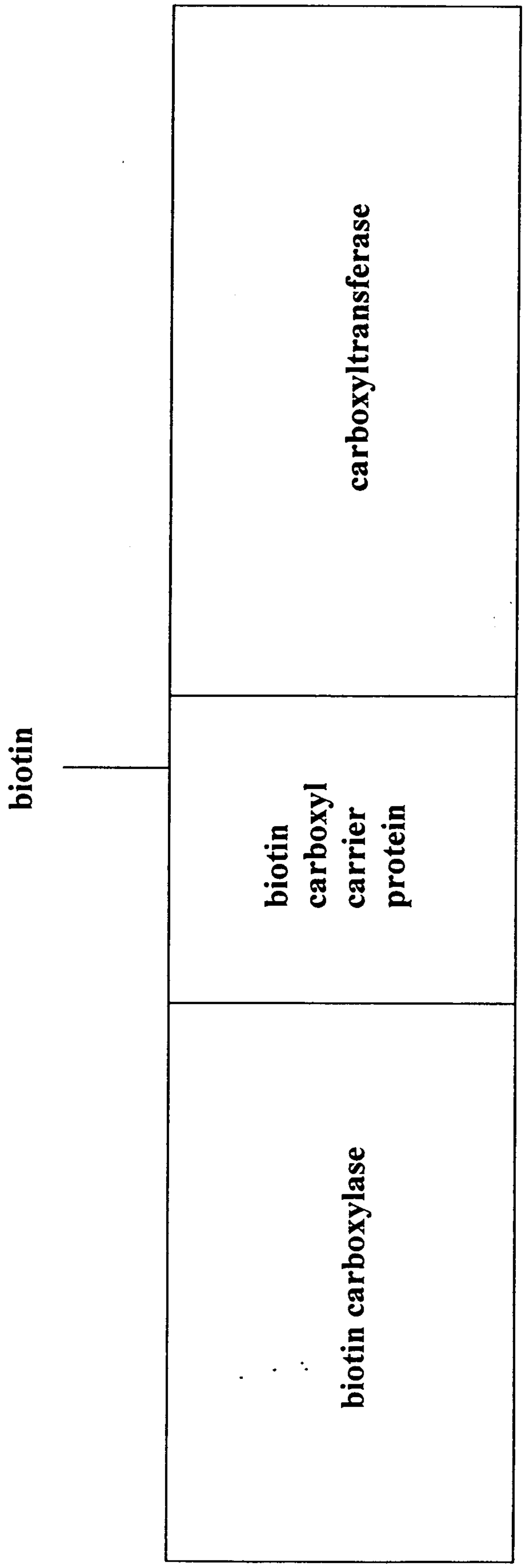
biotin
carboxyltransferase
biotin carboxyl carrier protein
biotin carboxylase

FIG. 17

ATGTCTCTTAAGTCCAGCGTGGGCCCCAGCCTGGCCGGCAAGGCGTGC
CACGGAGCAAATGCGCAGGTGCTGCCGCGCATGGCAGTGCCAGCGCCG
CTTGCAGGAACAGCAGTGCGCCCCAGCCTCGCAGTCAATGCAGTCAAC
CCTGAGAAAAACGGCGCTTATGAGGGCTCCCCCATTGTCAGCGGCCCC
ATTTCTGTGGGTGCTATGGACAAGGACTCCAAGGGCTCTTCCAAGCCTG
TTGACCGCAGCAAGGGCCTCTGGACGCGCTGCGACAAGTGCGGCGTGA
TTCTCTACATCAAGCACCTGAAGGAGCACCACCACATCTGCTTCGGCTG
CAACTACCACCTCAAGATGAGCAGCCAGGAGAGGATCGACCACATGAT
CGACCCAGGCTCATGGCGCCCCTTTGACGAGACGCTGTCTCCCTGCGAC
CCGCTGGACTTTGTGGACATGAAGCCATACCCAGACAGGGTGCGCGAC
AGCCAGGACAAGACAGGCATGAACGATGCCATCCGCACAGGCACGGG
CCTGCTGCACGGCATCCCAGTGGCGCTGGCAGTGATGGAGTTTGGCTTC
ATGGGCGGCAGCATGGGCAGCGTGGTGGGGGAGAAGCTGACGCGCCT
GATTGAGTACGCCACGCAGGAGGGGCTCACGCTGCTGGTGGTGTGCAC
CAGCGGAGGCGCGCGCATGCAGGAGGGCATCATGAGCCTGATGCAGAT
GGCCAAGATCAGCGGCGCGCTGCACGTGCACCAGAATGAGGCCAACCT
GCTGTACATCTCCATCCTGACCAGCCCCACCACAGGTGGCGTGACCGCA
AGCTTTGGCATGCTGGGGGATGTCATCATTGCTGAGCCGCAGGCCATCA
TCGGCTTTGCAGGACGGCGTGTGATCGAGCAGACGCTGCGTGAGGAGC
TGCCAGATGACTTCCAGACCGCGGAGTACCTGCTTGACAAGGGCCTGC
TCGACCTGGTGGTGCCGCGCAGCTTCCTGAAGGGCGCGCTGTTTGAGAT
CATCGACTTCTACAAGAACGCACCCTACAAGCGCCGCGGCAAGATTCC
ATTTGGCGTGCAGCGCGGTACGTACGGCCTGACCGCTGAGGAGAAGAT
GCGGCGCAGGTGGAGGGAGTGGAGCTCAGCTGGCAGCAACGGCTCGG
GCACGCCCGCGCTGGCAGCAGCAGCAGCATCAGCAGCAGTTGGGTCAG
CAGCCACTTGCGGCAGCTGCCAGCAGCAGCAGCTGGCGCTGTGGGCGG
TGCTGGCAGGCTGTGGCAGCTGTGGGCAGTGGCTGTGGTTTGCTCAGG
GGGTAGGTGCGCTTGAGCGCACAGCGGCAACAGCAGCAGTACTGAGAG
AGGGCAGCGTGCTGCTAGCAGGCGTCTGTTGTTAA

FIG. 18

Shanker

ATGTCTCTTAAGTCCAGCGTGGGCCCCAGCCTGGCCGGCAAGGCGTGC
CACGGAGCAAATGCGCAGGTGCTGCCGCGCATGGCAGTGCCAGCGCCG
CTTGCAGGAACAGCAGTGCGCCCCAGCCTCGCAGTCAATGCAGTCAAC
CCTGAGAAAAACGGCGCTTATGAGGGCTCCCCCATTGTCAGCGGCCCC
ATTTCTGTGGGTGCTATGGACAAGGACTCCAAGGGCTCTTCCAAGCCTG
TTGACCGCAGCAAGGGCCTCTGGACGCGCTGCGACAAGTGCGGCGTGA
TTCTCTACATCAAGCACCTGAAGGAGCACCACCACATCTGCTTCGGCTG
CAACTACCACCTCAAGATGAGCAGCCAGGAGAGGATCGACCACATGAT
CGACCCAGGCTCATGGCGCCCCTTTGACGAGACGCTGTCTCCCTGCGAC
CCGCTGGACTTTGTGGACATGAAGCCATACCCAGACAGGGTGCGCGAC
AGCCAGGACAAGACAGGCATGAACGATGCCATCCGCACAGGCACGGG
CCTGCTGCACGGCATCCCAGTGGCGCTGGCAGTGATGGAGTTTGGCTTC
ATGGGCGGCAGCATGGGCAGCGTGGTGGGGGAGAAGCTGACGCGCCT
GATTGAGTACGCCACGCAGGAGGGGCTCACGCTGCTGGTGGTGTGCAC
CAGCGGAGGCGCGCGCATGCAGGAGGGCATCATGAGCCTGATGCAGAT
GGCCAAGATCAGCGGCGCGCTGCACGTGCACCAGAATGAGGCCAACCT
GCTGTACATCTCCATCCTGACCAGCCCCACCACAGGTGGCGTGACCGCA
AGCTTTGGCATGCTGGGGGATGTCATCATTGCTGAGCCGCAGGCCATCA
TCGGCTTTGCAGGACGGCGTGTGATCGAGCAGACGCTGCGTGAGGAGC
TGCCAGATGACTTCCAGACCGCGGAGTACCTGCTTGACAAGGGCCTGC
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ATTTGGCGTGCAGCGCGGTACGTACGGCCTGACCGCTGAGGAGAAGAT
GCGGCGCAGGTGGAGGGAGTGGAGCTCAGTTGGCAGCATGTTGCATAG
TGTTCACTATGCAGGCCACTGGCCCTCTGGGTGTGCTGGGATGTTGCTG
GGCCAGCGCCCACTTCATATGCATTGGCATGTCAATGAAGGGTCAGGTT
GTAGCAAGACCACGTGCCAGAGCTTTAAGTATTGGTCAGCATGTGCTG
CTTGGCATGCAGTGTGCCATCGGCGAGGAACACTTCTTGAACATGAACT
TACCAAGCTGATTTCCTGGCAGTTTGATTCATGCTGTTGGCGTGCTGCC
AAAGGTATTCTGCTTAGATCTTGCAATGCTGTGTATGTATATGTGTAA

FIG. 19

ATGTCTCTTAAGTCCAGCGTGGGCCCCAGCCTGGCCGGCAAGGCGTGC
CACGGAGCAAATGCGCAGGTGCTGCCGCGCATGGCAGTGCCAGCGCCG
CTTGCAGGAACAGCAGTGCGCCCCAGCCTCGCAGTCAATGCAGTCAAC
CCTGAGAAAAACGGCGCTTATGAGGGCTCCCCCATTGTCAGCGGCCCC
ATTTCTGTGGGTGCTATGGACAAGGACTCCAAGGGCTCTTCCAAGCCTG
TTGACCGCAGCAAGGGCCTCTGGACGCGCTGCGACAAGTGCGGCGTGA
TTCTCTACATCAAGCACCTGAAGGAGCACCACCACATCTGCTTCGGCTG
CAACTACCACCTCAAGATGAGCAGCCAGGAGAGGATCGACCACATGAT
CGACCCAGGCTCATGGCGCCCCTTTGACGAGACGCTGTCTCCCTGCGAC
CCGCTGGACTTTGTGGACATGAAGCCATACCCAGACAGGGTGCGCGAC
AGCCAGGACAAGACAGGCATGAACGATGCCATCCGCACAGGCACGGG
CCTGCTGCACGGCATCCCAGTGGCGCTGGCAGTGATGGAGTTTGGCTTC
ATGGGCGGCAGCATGGGCAGCGTGGTGGGGAGAAGCTGACGCGCCT
GATTGAGTACGCCACGCAGGAGGGGCTCACGCTGCTGGTGGTGTGCAC
CAGCGGAGGCGCGCGCATGCAGGAGGGCATCATGAGCCTGATGCAGAT
GGCCAAGATCAGCGGCGCGCTGCACGTGCACCAGAATGAGGCCAACCT
GCTGTACATCTCCATCCTGACCAGCCCCACCACAGGTGGCGTGACCGCA
AGCTTTGGCATGCTGGGGGATGTCATCATTGCTGAGCCGCAGGCCATCA
TCGGCTTTGCAGGACGGCGTGTGATCGAGCAGACGCTGCGTGAGGAGC
TGCCAGATGACTTCCAGACCGCGGAGTACCTGCTTGACAAGGGCCTGC
TCGACCTGGTGGTGCCGCGCAGCTTCCTGAAGGGCGCGCTGTTTGAGAT
CATCGACTTTTACAAGAACGCACCCTACAAGCGCCGCGGCAAGATTCC
ATTTGGCGTGCAGCGCGGTACGTACGGCCTGACCGCTGAGGAGAAGAT
GCGGCGCAGGTGGAGGGAGTGGAGCTCAGCTGGCAGCAACGGCTCGG
GCACGCCCGCGCTGGCAGCAGCAGCAGCAGTGGTGGCGCCGTGCAGCA
GTGGAGGAGTTGCATGCGCACTGAGACGAGCTTGTTCAAGAGTTAGTC
GGATGGGCGGGGTGGGGAGCTTGCTACGCTGCTAG

FIG. 20

ATGTCTCTTAAGTCCAGCGTGGGCCCCAGCCTGGCCGGCAAGGCGTGC
CACGGAGCAAATGCGCAGGTGCTGCCGCGCATGGCAGTGCCAGCGCCG
CTTGCAGGAACAGCAGTGCGCCCCAGCCTCGCAGTCAATGCAGTCAAC
CCTGAGAAAAACGGCGCTTATGAGGGCTCCCCCATTGTCAGCGGCCCC
ATTTCTGTGGGTGCTATGGACAAGGACTCCAAGGGCTCTTCCAAGCCTG
TTGACCGCAGCAAGGGCCTCTGGACGCGCTGCGACAAGTGCGGCGTGA
TTCTCTACATCAAGCACCTGAAGGAGCACCACCACATCTGCTTCGGCTG
CAACTACCACCTCAAGATGAGCAGCCAGGAGAGGATCGACCACATGAT
CGACCCAGGCTCATGGCGCCCCTTTGACGAGACGCTGTCTCCCTGCGAC
CCGCTGGACTTTGTGGACATGAAGCCATACCCAGACAGGGTGCGCGAC
AGCCAGGACAAGACAGGCATGAACGATGCCATCCGCACAGGCACGGG
CCTGCTGCACGGCATCCCAGTGGCGCTGGCAGTGATGGAGTTTGGCTTC
ATGGGCGGCAGCATGGGCAGCGTGGTGGGGGAGAAGCTGACGCGCCT
GATTGAGTACGCCACGCAGGAGGGGCTCACGCTGCTGGTGGTGTGCAC
CAGCGGAGGCGCGCGCATGCAGGAGGGCATCATGAGCCTGATGCAGAT
GGCCAAGATCAGCGGCGCGCTGCACGTGCACCAGAATGAGGCCAACCT
GCTGTACATCTCCATCCTGACCAGCCCCACCACAGGTGGCGTGACCGCA
AGCTTTGGCATGCTGGGGGATGTCATCATTGCTGAGCCGCAGGCCATCA
TCGGCTTTGCAGGACGGCGTGTGATCGAGCAGACGCTGCGTGAGGAGC
TGCCAGATGACTTCCAGACCGCGGAGTACCTGCTTGACAAGGGCCTGC
TCGACCTGGTGGTGCCGCGCAGCTTCCTGAAGGGCGCGCTGTTTGAGAT
CATCGACTTGTACAAGAAAGCACCCCCCAAGCGGCGGGGCAAGATTCC
ATTTGGCGTGCATAGCGGTACGTACGGCCAACCGCCGAGGAGAAGATC
CGGCGCAGGTGGAGGGAGGGGAGTTCAGCTGGCAGCAACGGGTGGGG
CACGCCCGCGCTGGCAGCAGCAGCAGCAGGGGGGCGGTGCGGGTTTTG
GCGCCAAGCCATTCCAGGGGGTTGGTATATGTGACAGCAGCCTGTTTG
GTCACAGTCTGGATGGTGCGGCATAA

FIG. 21

ATGTCTCTTAAGTCCAGCGTGGGCCCCAGCCTGGCCGGCAAGGCGTGC
CACGGAGCAAATGCGCAGGTGCTGCCGCGCATGGCAGTGCCAGCGCCG
CTTGCAGGAACAGCAGTGCGCCCCAGCCTCGCAGTCAATGCAGTCAAC
CCTGAGAAAAACGGCGCTTATGAGGGCTCCCCCATTGTCAGCGGCCCC
ATTTCTGTGGGTGCTATGGACAAGGACTCCAAGGGCTCTTCCAAGCCTG
TTGACCGCAGCAAGGGCCTCTGGACGCGCTGCGACAAGTGCGGCGTGA
TTCTCTACATCAAGCACCTGAAGGAGCACCACCACATCTGCTTCGGCTG
CAACTACCACCTCAAGATGAGCAGCCAGGAGAGGATCGACCACATGAT
CGACCCAGGCTCATGGCGCCCCTTTGACGAGACGCTGTCTCCCTGCGAC
CCGCTGGACTTTGTGGACATGAAGCCATACCCAGACAGGGTGCGCGAC
AGCCAGGACAAGACAGGCATGAACGATGCCATCCGCACAGGCACGGG
CCTGCTGCACGGCATCCCAGTGGCGCTGGCAGTGATGGAGTTTGGCTTC
ATGGGCGGCAGCATGGGCAGCGTGGTGGGGGAGAAGCTGACGCGCCT
GATTGAGTACGCCACGCAGGAGGGGCTCACGCTGCTGGTGGTGTGCAC
CAGCGGAGGCGCGCGCATGCAGGAGGGCATCATGAGCCTGATGCAGAT
GGCCAAGATCAGCGGCGCGCTGCACGTGCACCAGAATGAGGCCAACCT
GCTGTACATCTCCATCCTGACCAGCCCCACCACAGGTGGCGTGACCGCA
AGCTTTGGCATGCTGGGGGATGTCATCATTGCTGAGCCGCAGGCCATCA
TCGGCTTTGCAGGACGGCGTGTGATCGAGCAGACGCTGCGTGAGGAGC
TGCCAGATGACTTCCAGACCGCGGAGTACCTGCTTGACAAGGGCCTGC
TCGACCTGGTGGTGCCGCGCAGCTTCCTGAAGGGCGCGCTGTTTGAGAT
CATCGACTTTTACAAGAACGCACCCTGCAAGCGCCGCGGCAAGATTCC
ATTTGGCGTGCAGCGCGGTACGTACGGCCTGACCGCTGAGGAGAAGAT
GCGGCGCAGGTGGAGGGAGTGGAGCTCAGCTGGCAGCAACGGCTCGG
GCACGCCCGCGCTGGCAGCAGCAGCAGCAGAGCTGAGAGAGGGCAGC
GTGCTGCTAGCAGGCGTCTGTTGTTAA

FIG. 22

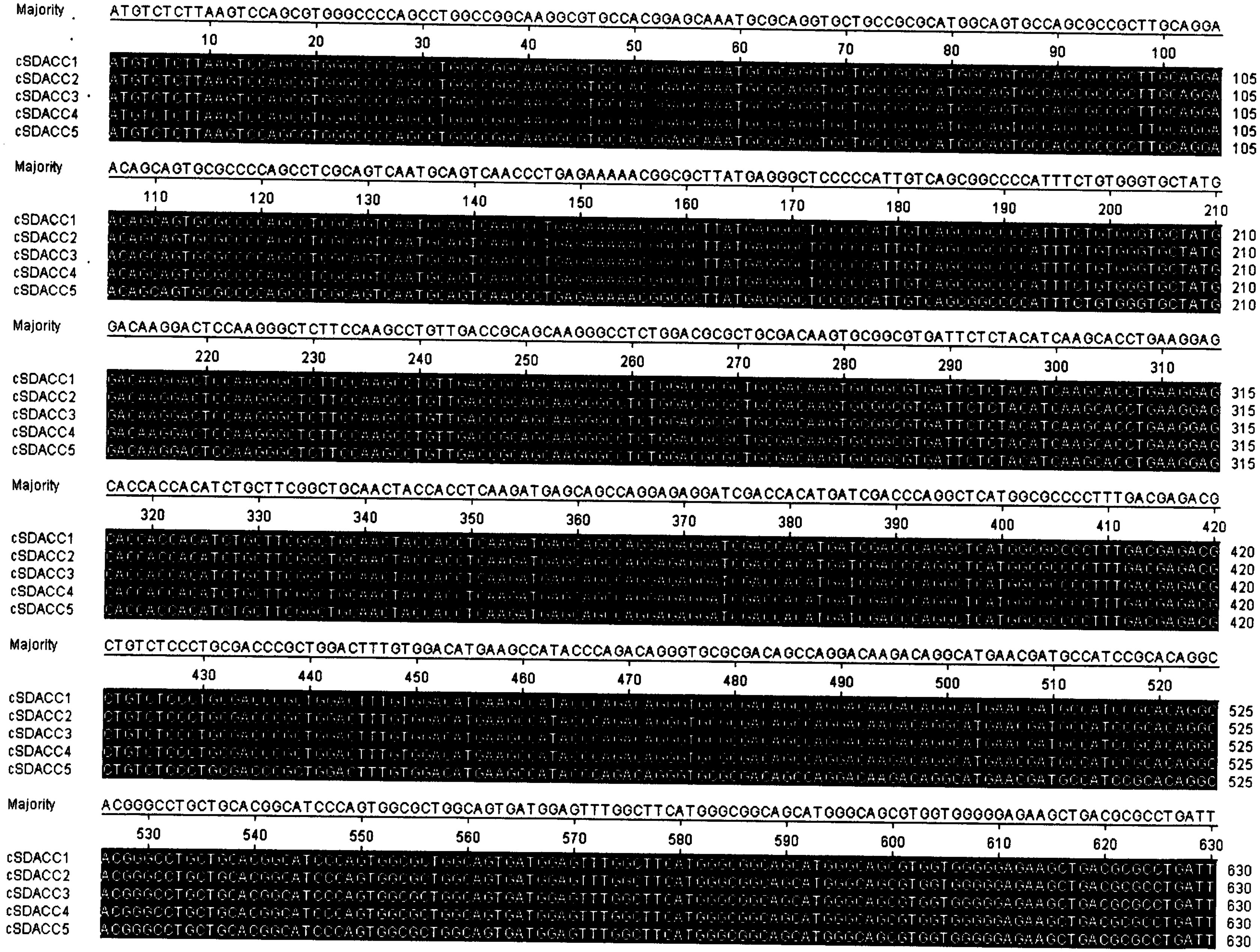

FIG. 23

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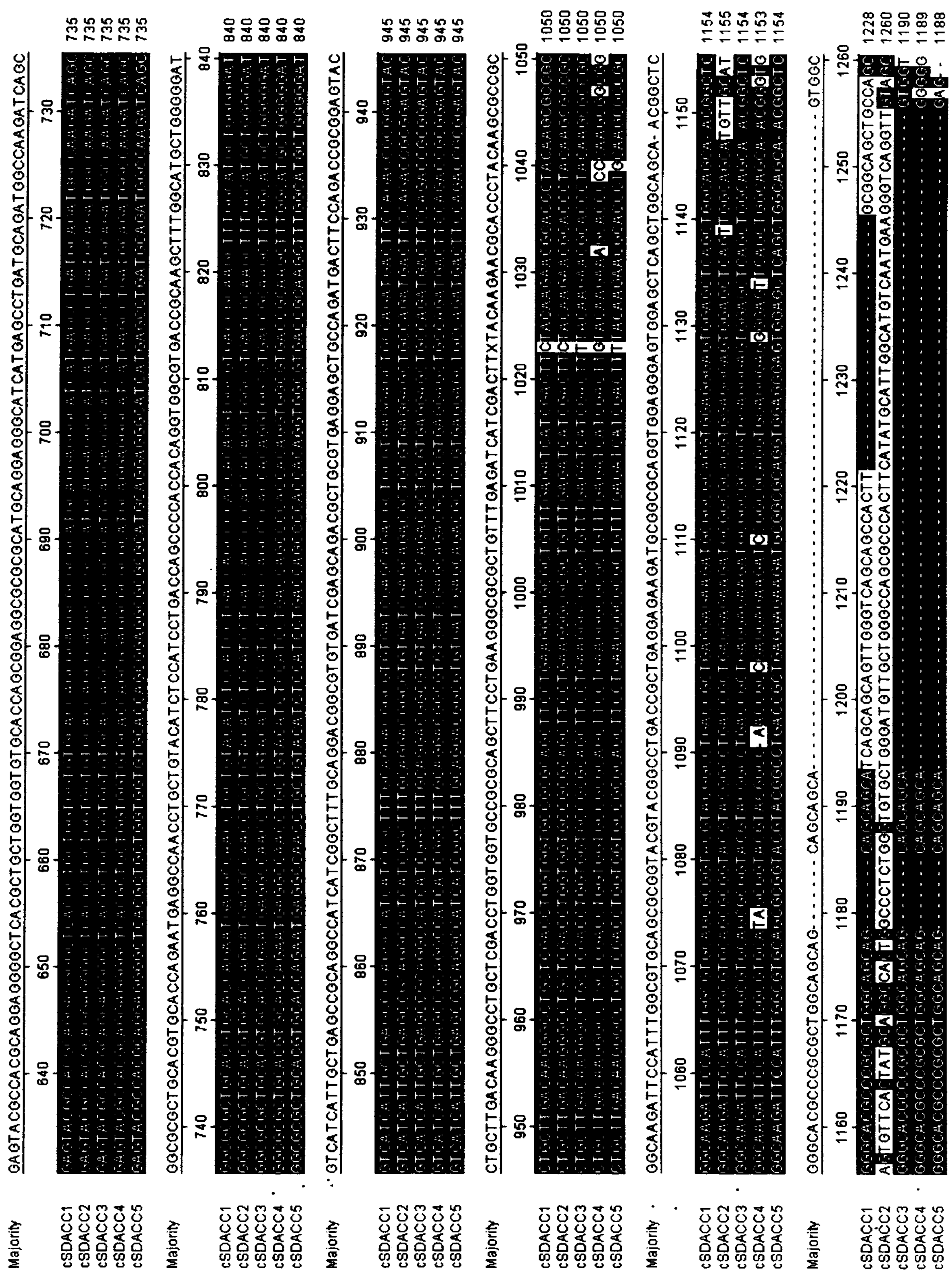

FIG. 23 (cont'd)

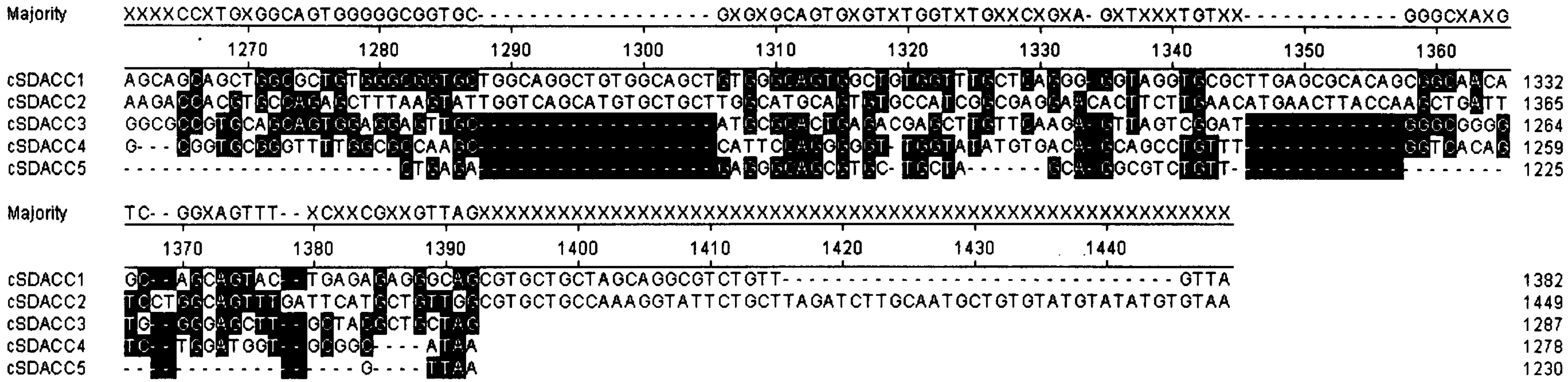

FIG. 23 (cont'd)

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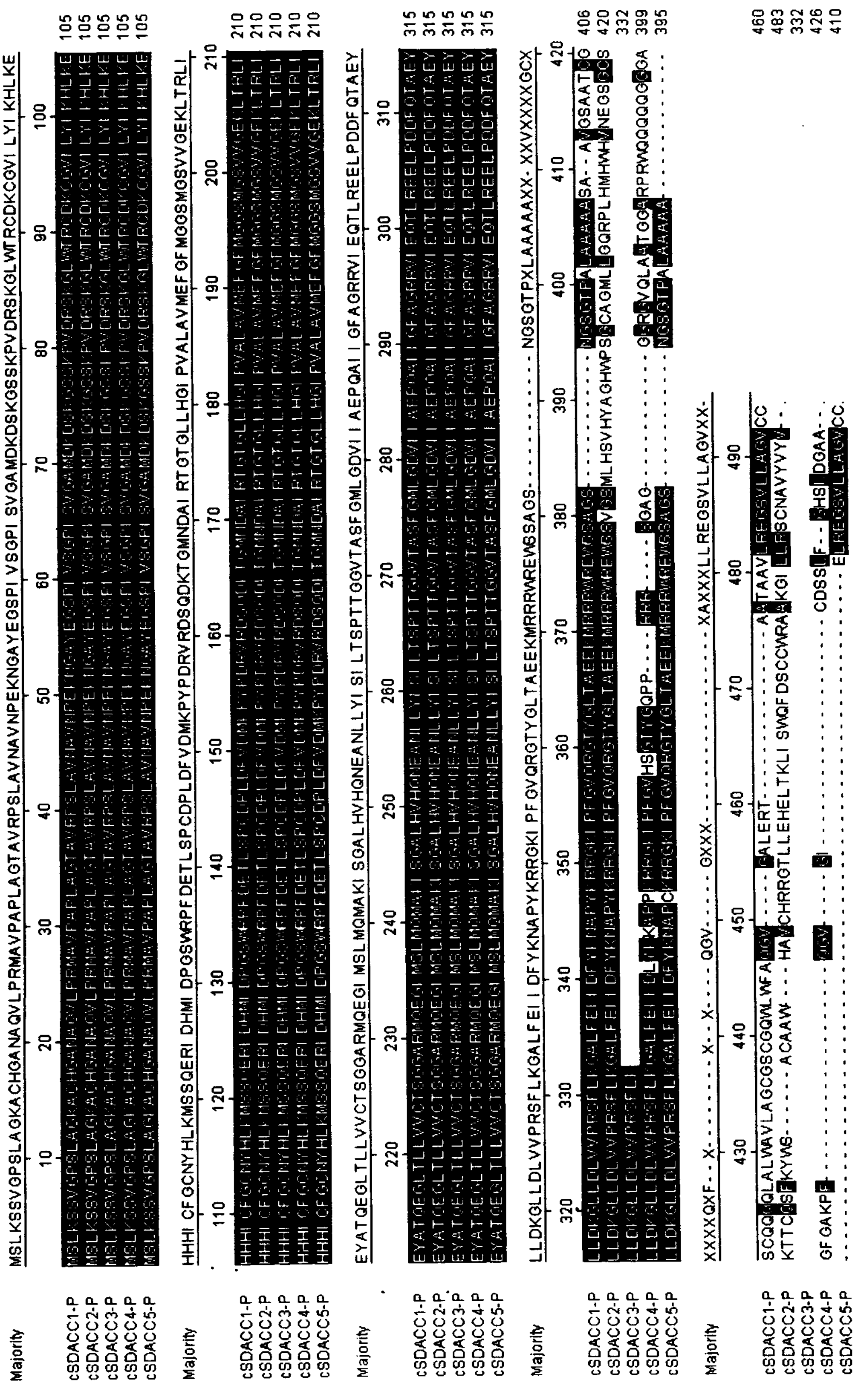

FIG. 24

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NOVEL ACETYL CoA CARBOXYLASES

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of United States Provisional Application Number 61/242,489, filed September 15, 2009, the entire contents of which are incorporated by reference for all purposes.

INCORPORATION BY REFERENCE

[0002] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BACKGROUND

[0003] Acetyl Coenzyme A carboxylase (ACCase) is the rate-limiting enzyme in the fatty acid biosynthesis pathway in plant, animal, yeast, and bacterial cells. Structurally, ACCases are biotinylated and are large enzymes consisting of two or more subunits. For example, most ACCases of animals, the cytoplasmic version in plants, and yeast are dimers of 420 to 700 kD native MW and contain subunits of 200 to 280 kD. Higher plant and algal plastid, and bacterial ACCases are 700 to 740 kD complexes 20 to 180 kD subunits.

[0004] Acetyl CoA Carboxylase (ACCase) catalyzes the formation of malonyl-CoA from acetyl-CoA and bicarbonate in animal, plant, and bacterial cells. Malonyl-CoA is an essential substrate for (i) de novo fatty acid (FA) synthesis, (ii) fatty acid elongation, (iii) synthesis of secondary metabolites such as flavonoids and anthocyanins, and (iv) malonylation of some amino acids and secondary metabolites. Synthesis of malonyl-CoA is the first committed step of flavonoid and fatty acid synthesis and current evidence suggests that ACCase catalyzes the rate-limiting step of fatty acid synthesis. Formation of malonyl-CoA by ACCase occurs via two partial reactions and requires a biotin prosthetic group:

(i) Enzyme-biotin+ATP+HCO_3 -> Enzyme-biotin-CO_2 +ADP+Pi

(ii) Enzyme-biotin-CO_2 +Acetyl-CoA ->Enzyme-biotin+malonyl CoA

The net reaction is:

Acetyl CoA+ATP+HCO_3 -> malonyl-CoA+ADP+Pi

[0005] In *E. coli*, these reactions are catalyzed by three distinct components; biotin carboxylase, biotin-acetyl CoA transcarboxylase, and biotin carboxyl carrier protein, which can be separated and yet retain partial activity. Plant and animal cytoplasmic ACCases contain all three activities on a single polypeptide.

[0006] Two different forms of the ACCase complex exist in plants (as described, for example, in Sasaki, Y. and Nagano, Y. (2004) *Biosci. Biotechnol. Biochem.* 68(6):1175-1184); the cytoplasmic enzyme, consisting of a very large single polypeptide chain, and the plastidic ACCase complex. The plastidic complex is a multi-enzyme complex composed of biotin carboxyl carrier protein (BCCP), biotin carboxylase, and a carboxyltransferase complex made up of two pairs of α and β subunits.

[0007] Several pieces of evidence indicate that, at least in higher plants, the chloroplast ACCase complex is subject to control via post-translational modification. Kozaki and Sasaki Biochem J., 339:541 (1999) describe light levels and the addition of reducing agent (dithiothreitol) as being able to increase chloroplast ACCase activity, while the amount of ACCase protein remained roughly unchanged.

[0008] Savage and Ohlrogge, Plant J., 18:521 (1999) described purification of pea chloroplast ACCase complex, and showed that the β-subunit of the complex was phosphorylated in vivo. Removal of the phosphates by phosphatase treatment dramatically reduced the ACCase activity in the sample.

[0009] Under certain physiological conditions, mammalian ACC activity is rapidly regulated by reversible phosphorylation (for example, as described in Kim, K.-H. (1983) *Curr. Top. Cell Regul.*, 22, 143-176; and Kim, K. -H., *et al.*, *FASEB J.* (1989) 3, 2250-2256) which involves specific protein kinases that phosphorylate and inactivate ACC (for example, as described in Kim, K. -H., *et al.*, *FASEB J.* (1989) 3, 2250-2256), and phosphatases that dephosphorylate and activate the enzyme.

[0010] Ha, J. *et al.* (The J. of Biol. Chem. (1994) 269 (35) pp. 22162-22168) created and expressed a cDNA of the entire coding region of the rat Acetyl-CoA carboxylase and identified eight different phosphorlyation sites on the carboxylase molecule. The sites were identified by comparing phosphopeptide sequences and the deduced amino acid sequences from rat ACC cDNA (for example, as described in Lopez-Casillas, F., *et al.* (1988) *Proc. Natl. Acad. Sci. U. S. A.*, 85, 5784-5788; Munday, M. R., *et al.* (1988) *Eur. J. Biochem.*, 175, 331-338; Haystead, T. A. J. and Hardie, D. G. (1988) *Eur. J. Biochem.*, 175, 339-345; and Haystead, T. A. J. *et al.* (1988) *Eur. J. Biochem.*, 175, 347-354). The identified sites are Ser 23, 25, 29, 77, 79, 95, 1200, and 1215. The roles of these phosphorylation sites on the activation of ACCase are not well understood.

[0011] Increasing the amount of ACCase activity in the cell has been proposed as a mechanism to increase the lipid content (for example, TAG, DAG, and other acyl lipids) in algae, higher plants, yeast, and mammals. Attempts have been made to increase ACCase activity by increasing the amount of protein present via upregulation of a native ACCase gene or by introduction of a transgene under a stronger promoter. These efforts have produced increased levels of ACCase protein in the target organisms, but have not significantly altered lipid level (for example, as described in Hu et al., The Plant J.,54:621 (2008)).

[0012] In order to increase fatty acid synthesis in a cell, what is needed is not simply to increase production of an ACCase protein, but rather to increase the level of ACCase activity in the cell, resulting in an increase in lipid production. The present disclosure meets that need.

SUMMARY

[0013] Provided herein are novel ACCases, and nucleotides encoding the same, that when introduced into a cell or organism result in an increase and/or accumulation of fatty acids, glycerol lipids, and/or oils. Also, provided herein are novel ACCases, and nucleotides encoding the same, that when introduced into a cell or organism result in a change in the types of fatty acids, glycerol lipids, and/or oils that are normally present in the cell or organism.