CLAIMS

The following is claimed:

1. A modified microorganism capable of butyl acetate (BA) production, the microorganism capable of expressing an alcohol acyl transferase (AAT); and comprising a butanol synthesis pathway.
2. The modified microorganism of claim 1, wherein the AAT is selected from one or more of: Vaat, Saat, Atf1, Eht1, and a functional homolog of any of the foregoing.
3. ~~The modified microorganism of claim 1, capable of expressing all of: Vaat, Saat, Atf1, and Eht1.~~
4. ~~The modified microorganism of claim 1, wherein the AAT is Vaat having at least 70% sequence identity with SEQ ID NO: 1.~~
5. ~~The modified microorganism of claim 1, wherein the AAT is Saat having at least 70% sequence identity with SEQ ID NO: 2.~~
6. ~~The modified microorganism of claim 1, wherein the AAT is Atf1 having at least 70% sequence identity with SEQ ID NO: 3.~~
7. ~~The modified microorganism of claim 1, wherein the AAT is Eht1 having at least 70% sequence identity with SEQ ID NO: 4.~~

~~8.~~3. The modified microorganism of claim 1 or 2, comprising an acetyl CoA synthesis pathway.

~~9.~~4. The modified microorganism of any one of claims 1-3, comprising multiple nucleic acid sequences each encoding Atf1 or a functional homolog of Atf1.

10. ~~A modified microorganism capable of butyl butyrate (BB) production, the microorganism capable of expressing an alcohol acyl transferase (AAT); and comprising a butanol synthesis pathway and a butyryl coenzyme A synthesis pathway.~~
11. ~~The microorganism of claim 10, wherein the AAT is Eht1 or a functional homolog of Eht1.~~
12. ~~The microorganism of claim 10, wherein the AAT is Saat or a functional homolog of Saat.~~
13. ~~Any one of the microorganisms of claims 1 and 10, wherein the microorganism is a prokaryote.~~

14. Any one of the microorganisms of claims 1 and 10, wherein the microorganism is fermentative.

15. Any one of the microorganisms of claims 1 and 10, wherein the microorganism is a bacterium of genus *Clostridium.*

16.5. Any one of tThe modified microorganisms of any one of claims 1-4 and 10, wherein the microorganism is selected from *Clostridium saccharoperbutylacetonicum, Clostridium beijerinckii, Clostridium pasteurianum,* and *Clostridium tyrobutyricum.*

17.6. Any one of tThe modified microorganisms of any one of claims 1-5 and 10, capable of expressing Lipase B or a functional homolog of Lipase B.

18. Any one of the microorganisms of claims 1 and 10, capable of expressing a functional homolog of Lipase B having at least 70% sequence identity with SEQ ID NO: 5.

19. Any one of the microorganisms of claims 1 and 10, capable of expressing Lipase B or a functional homolog of Lipase B, and comprising an acetic acid synthesis pathway.

20. Any one of the microorganisms of claims 1 and 10, capable of expressing Lipase B or a functional homolog of Lipase B, and comprising a butyric acid synthesis pathway.

21.7. Any one of tThe modified microorganisms of any one of claims 1-6 and 10, having reduced or eliminated NuoG activity.

22.8. Any one of tThe modified microorganisms of any one of claims 1-7 and 10, capable of expressing a heterologous Sadh or a functional homolog thereof.

23. Any one of the microorganisms of claims 1 and 10, comprising a *sadh-hydG* gene cluster.

24.9. Any one of tThe modified microorganisms of any one of claims 1-8 and 10, comprising an exogenous AAT gene operatively linked to promoter P_{adh}.

25. Any one of the microorganisms of claims 1 and 10, comprising an exogenous AAT gene operatively linked to promoter P_{ald}.

26.10. Any one of tThe modified microorganisms of any one of claims 1-9 and 10, comprising an wherein the AAT that is localized at the cell membrane.

27. Any one of the microorganisms of claims 1 and 10, wherein the AAT is fused to a C-terminal membrane-targeting sequence of MinD.

28. Any one of the microorganisms of claims 1 and 10, wherein the AAT is fused to a C-terminal membrane-targeting sequence of MinD encoded by SEQ ID NO: 6.

29. Any one of the microorganisms of claims 1 and 10, wherein the AAT is fused to an 8-12 residue C-terminal membrane-targeting sequence of MinD.

30. Any one of the microorganisms of claims 1 and 10, wherein the microorganism has been cured of a prophage.

31.11. Any one of tThe modified microorganisms of any one of claims 1-10 and 10, wherein the microorganism has been cured of all native prophages.

32. Any one of the microorganisms of claims 1 and 10, wherein the microorganism has been cured of one or more prophages by deletion of the one or more prophages.

33.12. Any one of tThe modified microorganisms of any one of claims 1-11 and 10, wherein the microorganism is a bacterium of genus *Clostridium,* and wherein the microorganism has been cured of one or more of prophages P1, P2, P3, P4, and P5.

34. Any one of the microorganisms of claims 1 and 10, wherein the microorganism is a bacterium of genus *Clostridium,* and wherein the microorganism has been cured of all of prophages P1, P2, P3, P4, and P5.

35.13. Any one of tThe modified microorganisms of any one of claims 1-12 and 10, wherein said microorganism does not express a functional redox-sensing transcriptional repressor Rex.

36.14. Any one of tThe modified microorganisms of any one of claims 1-13 and 10, capable of expressing soluble pyridine nucleotide transhydrogenase (SthA) or a functional homolog thereof.

37. Any one of the microorganisms of claims 1 and 10, capable of expressing soluble pyridine nucleotide transhydrogenase (SthA) having at least 70% sequence identity with SEQ ID NO: 7.

38.15. Any one of tThe modified microorganisms of any one of claims 1-14 and 10, wherein said microorganism does not express a functional *cftA1-ctfB1* gene cluster.

39. Any one of the microorganisms of claims 1 and 10, wherein the functional homolog has only preferred substitutions from Table 1 compared to the AAT, Lipase B, SthA, or Sadh.

40.16. A genetically modified microorganism that is a *Clostridium saccharoperbutylacetonicum* having improved BA production and designated YM028P, having NCMA designation number 202012116, deposited on 16 December 2020 at the National Center for Marine Algae and Microbiota at Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544 USA.

41. A genetically modified *Clostridium saccharoperbutylacetonicum* having improved BB production and designated YM016PB, having NCMA designation number 202012115, deposited on 16 December 2020 at the National Center for Marine Algae and Microbiota at Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544 USA.

42.17. A genetically modified microorganism that is a *Clostridium saccharoperbutylacetonicum* having improved BA production and designated FJ-1301, having NCMA designation number 202012114, deposited on 16 December 2020 at the National Center for Marine Algae and Microbiota at Bigelow Laboratory for Ocean Sciences, 60 Bigelow Drive, East Boothbay, ME 04544 USA.

43.18. A method of ester BA production, comprising culturing any one of the modified microorganisms of any one of claims 1-17, 10, and 40-42 under conditions suitable to produce an esterBA.

44. The method of claim 43, comprising culturing any one of the microorganisms above in a medium containing glucose.

45.19. The method of claim 4318, comprising culturing any one of the modified microorganisms above in a medium containing a biomass hydrolysate.

46. The method of claim 43, comprising culturing any one of the microorganisms above in a medium containing a corn stover hydrolysate.

47. The method of claim 43, wherein the ester is at least one of BA and BB.

48.20. The method of claim 4318 or 19, producing at least 1.5 g BA/L of culture.

49. The method of claim 43, producing at least 25 g BA/L of culture.

50. The method of claim 43, producing at least 0.1 g BB/L of culture.

51. The method of claim 43, producing at least 1.6 g BB/L of culture.