CLAIMS

WHAT IS CLAIMED IS:

1. A non-therapeutic method for improving gut microbiota population, comprising administering to a subject berberine or a berberine derivative,

wherein improving gut microbiota population is characterized by increasing a short-chain fatty acid (SCFA)-producing bacterium while simultaneously decreasing an endotoxin-producing bacterium in the gut microbiota population,

wherein the short-chain fatty acid (SCFA)-producing bacterium is *Blautia*, *Allobaculum*, *Prevotella, Bacterioides* or *Butyricimonas*; and /or

the endotoxin-producing bacterium is *Alistipes*, *Anaeroplasma, Barnesiella*, *Bifidobacterium*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Roseburia*, *Ruminococcus* or *TM7_genera_incertae_sedis.*

2. A non-therapeutic method for decreasing the serum level of lipopolysaccharide-binding protein, monocyte chemoattractant protein-1 or leptin and increasing the serum level of adiponectin, comprising administering to a subject berberine or a berberine derivative.

3. The method of claim 1 or 2, wherein the berberine or the berberine derivative is administered through oral administration or intestinal administration.

4. The method of claim 1 or 2, wherein the berberine or the berberine derivative is prepared as a suppository, tablet, pill, granule, film, microcapsule, drop pills, aerosol, medicated liquor, syrup or oral solution.

5. The method of claim 1, wherein the short-chain fatty acid (SCFA)-producing bacterium comprises a bacterium whose V3 region of 16S rRNA gene sequence is the same with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93, and the endotoxin-producing bacterium comprises a bacterium whose V3 region of 16S rRNA gene sequence is the same with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94 -268.

6. A non-therapeutic method for inhibiting food intake, comprising administering to a subject berberine or a berberine derivative.

7. The method of claim 6, wherein the berberine or the berberine derivative is administered through oral administration or intestinal administration.

8. The method of claim 6, wherein the berberine or the berberine derivative is prepared as a suppository, tablet, pill, granule, film, microcapsule, drop pills, aerosol, medicated liquor, syrup or oral solution.

9. Use of berberine or a berberine derivative in the manufacture of a medicament for improving gut microbiota population, wherein improving gut microbiota population is characterized by increasing a short-chain fatty acid (SCFA)-producing bacterium while simultaneously decreasing an endotoxin-producing bacterium in the gut microbiota population, and

wherein the short-chain fatty acid (SCFA)-producing bacterium is *Blautia*, *Allobaculum*, *Prevotella*, *Bacterioides* or *Butyricimonas*; and /or

the endotoxin-producing bacterium is *Alistipes*, *Anaeroplasma*, *Barnesiella*, *Bifidobacterium*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Roseburia*, *Ruminococcus* or *TM7_genera_incertae_sedis*.

10. The use of claim 9, wherein the berberine or the berberine derivative is administered through oral administration or intestinal administration.

11. The use of claim 9, wherein the berberine or the berberine derivative is prepared as a suppository, tablet, pill, granule, film, microcapsule, drop pills, aerosol, medicated liquor, syrup or oral solution.

CLAIMS

WHAT IS CLAIMED IS:

1. A composition for improving gut microbiota population, wherein the improving gut microbiota population comprises selectively increasing a first gut microbiota population while simultaneously decreasing a second gut microbiota population,

wherein the first gut microbiota population comprises, *Allobaculum*, *Bacteroides*, *Blautia, Butyricicoccus, Dorea, Holdemania*, Lawsonia, *Parabacteroides*, *Phascolarctobacterium*, *Sedimentibacter*, or a combination thereof;

wherein the second gut microbiota population comprises *Anaeroplasma*, *Bifidobacterium, Butyrivibrio, Coprococcus, Fastidiosipila, Marvinbryantia, Oribacterium, Roseburia, Ruminococcus, TM7_genera_incertae*_sedis, or a combination thereof; and

wherein the composition comprises *Berberis vulgaris*, *Coptis chinensis*, *Scutellaria baicalensis*, *Phellodendri Chinensis*, *Momordica* charantia, *Ilex kudingcha*, *Sophora flavescens*, *Gentiana scabra*, *Anemarrhena asphodeloides*, *Gardenia jasminoides*, *Rheum palmatum and Herba Taraxaci, or the* extract thereof.

2. The composition of Claim 1, wherein the composition is a food, a drink, a supplement, or a pharmaceutical formulation.

3. The composition of Claim 1, wherein the composition is to be administered at a dosage of from about 50 mg/kg body weight to about 400 mg/body weight and with once a day administration for at least two weeks.

4. The composition of Claim 1, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.

5. The composition of Claim 1, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.

6. The composition of Claim 1, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.

7. The composition of Claim 1, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.

8. The composition of Claim 1, wherein the composition decreases the serum level of a first cytokine and increase the serum level of a second cytokine, wherein the first cytokine comprises lipopolysaccharide-binding protein, monocyte chemoattractant protein-1, leptin, or a combination thereof, and wherein the second cytokine comprises adiponectin.

9. Use of the composition of any one of claims 1 to 8 in the manufacture of a medicament for prevention or treatment of metabolic syndrome including obesity, diabetes mellitus, insulin resistance, hyperlipoproteinemia, hyperuricemia, hepatic steatosis, hypercholesterolemia, hypertriglyceridemia, inflammation, and other disorders.

10. The use of claim 9, wherein the composition is to be administered at a dosage of from 50 mg/kg body weight to 400 mg/body weight and with once a day administration for at least two weeks.