Claims

1. A bacterium having a 16S rRNA gene comprising a nucleotide sequence having 97% or more identity to the nucleotide sequence represented by SEQ ID NO: 1, having at least one of the following characteristics a) to d), and having an ability to degrade a target microorganism;

a) no glucose fermentability

b) no mannitol fermentability

c) citric acid utilization

d) no nitrate reduction,

wherein, the target microorganism is at least one of the following microorganisms 1) to 5);

1) *Micrococcus lysodeikticus*

2) *Saccharomyces cerevisiae*

3) *Escherichia coli*

4) *Brevibacillus parabrevis*

5) *Gluconobacter oxydans*.

2. The bacterium according to claim 1, having a 16S rRNA gene comprising the nucleotide sequence represented by SEQ ID NO: 1.

3. The bacterium according to claim 2, wherein the bacterium satisfies at least one of

the 423rd base in SEQ ID NO: 1 being adenine,

the 441st base in SEQ ID NO: 1 being cytosine, and

the 1236th base in SEQ ID NO: 1 being guanine.

4. The bacterium according to any one of claims 1 to 3, wherein the target microorganism is at least killed bacterium of *Micrococcus lysodeikticus*.

5. A bacterium having a 16S rRNA gene comprising a nucleotide sequence represented by SEQ ID NO: 1, and satisfying at least one of

the 423rd base in SEQ ID NO: 1 being adenine,

the 441st base in SEQ ID NO: 1 being cytosine, and

the 1236th base in SEQ ID NO: 1being guanine.

6. A bacterium deposited under Accession number NITE BP-03020.

7. A microbial preparation for degrading sludge, comprising a bacterium (a1) or a culture thereof:

bacterium (a1): *Brevibacillus parabrevis* having a 16S rRNA gene comprising a nucleotide sequence having 90% or more identity to the nucleotide sequence represented by SEQ ID NO: 1.

8. The microbial preparation for degrading sludge according to claim 7, wherein the bacterium (a1) has a following characteristic: when 50 μL of the culture supernatant of the bacterium (a1) is added to 5.0 mL of a solution containing killed bacterium of the *Micrococcus lysodeikticus* and reacted at 25 °C, a turbidity (OD660) of the solution after addition of the supernatant is 80% or less of the turbidity (OD660) of the solution before addition of the supernatant.

9. The microbial preparation for degrading sludge according to claim 7 or 8, further comprising a microorganism (a2):

microorganism (a2): a microorganism different from bacterium (a1), wherein the percentage of the bacteria (a1) based on the total number of the bacteria (a1) and the microorganism (a2) is 0.1% or more and less than 100%.

10. The microbial preparation for degrading sludge according to claim 9,

wherein the microorganism (a2) has a 16S rRNA gene comprising a nucleotide sequence having 90% or more identity to the nucleotide sequence represented by SEQ ID NO: 7, and comprises at least one species selected from the group consisting of bacteria having an ability to degrade a target microorganism, bacteria of the genus *Bacillus* having an ability to degrade a target microorganism, and bacteria of the genus *Paenibacillus* having an ability to degrade a target microorganism,
wherein the target microorganism of the microorganism (a2) is at least one of the following microorganisms 1) to 7);

1) bacteria of the genus *Micrococcus*
2) bacteria of the genus *Bacillus*
3) bacteria of the genus *Staphylococcus*
4) bacteria of the genus *Lactobacillus*
5) bacteria of the genus *Paenibacillus*
6) bacteria of the genus *Escherichia*
7) bacteria of the genus *Acetobacter*.

11. A method for degrading sludge, comprising allowing the bacterium according to any one of claims 1 to 6 or the microbial preparation for degrading sludge according to any one of claims 7 to 10 to act on sludge.

12. A device for degrading sludge, wherein the bacterium according to any one of claims 1 to 6 or the microbial preparation for degrading sludge according to any one of claims 7 to 10 is used.