

CLAIMS

1. A method of identifying, partially identifying or classifying at least one bacterium, yeast organism or filamentous fungi in a sample, said method comprising analysing at least a portion of a bacterial 16S rRNA gene or gene product from the sample, or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product from the sample, for the presence or absence of at least one single nucleotide polymorphism (SNP),

wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or gene product is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1;

wherein the at least one bacterium, yeast organism or filamentous fungi in the sample is identified, partially identified or classified based on the presence or absence of the at least one SNP.

2. A method of identifying, partially identifying, classifying or diagnosing a bacterial, yeast organism or filamentous fungi infection in a subject, said method comprising analysing the presence or absence of at least one single nucleotide polymorphism (SNP) in at least a portion of a bacterial 16S rRNA gene or gene product or in at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product in a sample from the subject;

wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or gene product is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1;

wherein the presence or absence of said at least one SNP in the at least a portion of the 16S rRNA gene or gene product or in the at least a portion of the 18S rRNA gene or gene product is used to identify, partially identify, classify or diagnose the bacterial, yeast organism or filamentous fungi infection in the subject.

3. A method of treating a subject having a bacterial, yeast organism or filamentous fungi infection, said method comprising:

identifying, partially identifying, classifying or diagnosing a bacterial, yeast organism or filamentous fungi infection in a subject according to the method of claim 2, to identify, partially identify, classify or diagnose the bacterial, yeast organism or filamentous fungi infection in the subject;

administering to the subject a therapy or treatment agent for treating the bacterial, yeast organism or filamentous fungi infection in the subject.

4. The method of any one of claims 1 to 3, wherein the sample is a biological sample

comprising sputum, blood, cerebrospinal fluid or urine.

5. The method of any one of claims 1 to 4, wherein the step of analysing comprises determining the presence or the absence of the at least one SNP using high resolution melt analysis, 5' nuclease digestion, molecular beacons, oligonucleotide ligation, microarray, restriction fragment length polymorphism, antibody detection methods, direct sequencing or any combination thereof.

6. The method of any one of claims 1 to 5, wherein said method further comprises the step of determining whether the at least one bacteria, yeast organism or filamentous fungi is resistant to a therapeutic agent.

7. A method of identifying at least one bacterium in a sample, said method comprising analysing nucleic acid from the sample for at least one SNP in a bacterial 16S rRNA gene at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, and 653 of the 16S rRNA gene set forth in SEQ ID NO: 1, wherein the at least one bacterium is identified based on the presence of the at least one SNP.

8. The method of any one of claims 1 to 6, wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or gene product is at a position corresponding to at least one of positions 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1.

9. The method of any one of claims 1 to 6, wherein the at least one SNP in the at least a portion of the yeast organism or filamentous fungi 18S rRNA gene or gene product is at a position corresponding to at least one of positions 343, 371, 388, 416, and 467 of the 18S rRNA gene or gene product set forth in SEQ ID NO: 37.

10. The method of any one of claims 1 to 6, wherein said method comprises analysing at least a portion of a bacterial 16S rRNA gene or gene product from the sample, or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product from the sample, for the presence or absence of:

single nucleotide polymorphisms in the at least a portion of the bacterial 16S rRNA gene or gene product at a position corresponding to at least four of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1; or

single nucleotide polymorphisms in the at least a portion of the yeast organism or filamentous fungi 18S rRNA gene or gene product at a position corresponding to positions 343, 371, 388, 416, and 467 of the 18S rRNA gene set forth in SEQ ID NO: 37.

11. The method of any one of claims 1 to 6, wherein the bacterium is or the bacterial infection is caused by at least one of the group consisting of: *Acinetobacter calcoaceticus*; *Enterobacter aerogenes*; *Enterobacter cloacae*; *Enterococcus faecalis*; *Enterococcus faecium*;

Escherichia coli; *Klebsiella pneumoniae*; *Proteus mirabilis*; *Pseudomonas aeruginosa*; *Serratia marcescens*; *Staphylococcus aureus*; *Staphylococcus epidermidis*; *Streptococcus agalactiae*; *Streptococcus pneumoniae*; *Streptococcus pyogenes*; *Listeria monocytogenes*; *Clostridium perfringens*; *Corynebacterium jeikeium*; *Bacteroides fragilis*; *Neisseria meningitidis*; *Haemophilus influenzae*; *Salmonella sp.*; and *Staphylococcus epidermidis*.

12. The method of any one of claims 1 to 6, wherein the bacterium is or the bacterial infection is caused by at least one of the group consisting of: *Bacillus anthracis*, *Clostridium botulinum*, *Yersinia pestis*, *Francisella tularensis*, *Vibrio cholerae*, and *Burkholderia pseudomallei*.

13. The method of any one of claims 1 to 6, wherein the yeast organism or filamentous fungi is at least one of the group consisting of: *Candida albicans*, *Candida tropicalis*, *Candida parapsilosis*, *Candida glabrata*, *Fusarium sp.*, *Aspergillus fumigatus*, and *Cryptococcus neoformans*.

14. A method of identifying, partially identifying, classifying or diagnosing an infection in a subject, wherein said infection is a bacterial, yeast organism or filamentous fungi infection, said method comprising assaying a biological sample obtained from the subject for a property of at least one bacterial 16S rRNA gene or gene product or a portion thereof or at least one yeast organism or filamentous fungi 18S rRNA gene or gene product or a portion thereof, wherein said assay comprises detecting at least one single nucleotide polymorphism (SNP) in the at least one bacterial 16S rRNA gene or gene product or a portion thereof or the at least one yeast organism or filamentous fungi 18S rRNA gene or gene product or a portion thereof,

wherein the at least one SNP in the bacterial 16S rRNA gene or gene product or a portion thereof is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1;

wherein the at least one bacteria, yeast organism or filamentous fungi in the sample is identified, partially identified, classified or diagnosed based on the presence or absence of the at least one SNP.

15. At least one isolated probe, tool or reagent capable of identifying, partially identifying, or classifying at least one bacteria, yeast organism or filamentous fungi in a sample, wherein the probe, tool or reagent is capable of binding, detecting or identifying the presence or absence of at least one single nucleotide polymorphism (SNP) in at least a portion of a bacterial 16S rRNA gene or gene product or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product,

wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or

gene product is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1.

16. The at least one isolated probe, tool or reagent of claim 15, wherein the at least one probe, tool or reagent comprises an oligonucleotide having a nucleotide sequence as set forth in at least one of SEQ ID NOs: 16-35 and 53-57.

17. A method of identifying, partially identifying, or classifying at least one bacterium, yeast organism or filamentous fungi in a sample, said method comprising:

combining with the sample the at least one isolated probe, tool or reagent of claim 15 or claim 16; and

identifying, partially identifying, or classifying the at least one bacterium, yeast organism or filamentous fungi based on the presence or absence of at least one at least one single nucleotide polymorphism (SNP) in at least a portion of a bacterial 16S rRNA gene or gene product or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product,

wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or gene product is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1.

18. An array comprising more than one said isolated probe, tool or reagent of claim 15 or claim 16.

19. A biochip comprising a solid substrate and at least one isolated probe, tool or reagent of claim 15 or claim 16.

20. A kit or assay for classifying or identifying at least one bacterium or at least one yeast organism or filamentous fungi in a sample, said kit or assay comprising: the at least one probe, tool or reagent of claim 15 or claim 16; the array of claim 18; and/or the biochip of claim 19.

21. At least one single nucleotide polymorphism (SNP) in at least a portion of a bacterial 16S rRNA gene or gene product or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product for use as an indicator for classifying, identifying or partially identifying at least one bacterium, yeast organism or filamentous fungi in a sample;

wherein the at least one SNP in the at least a portion of the bacterial 16S rRNA gene or gene product is at a position corresponding to at least one of positions 273, 378, 412, 440, 488, 647, 653, 737, 755, 762 and 776 of the 16S rRNA gene set forth in SEQ ID NO: 1.

22. Use of at least one single nucleotide polymorphism (SNP) in at least a portion of a bacterial 16S rRNA gene or gene product or at least a portion of a yeast organism or filamentous fungi 18S rRNA gene or gene product as defined in claim 1, or the at least one

isolated probe, tool or reagent of claim 15 or claim 16 in identifying, partially identifying or classifying at least one bacterium, yeast organism or filamentous fungi in a sample, wherein said at least one bacterium, yeast organism or filamentous fungi is identified, partially identified or classified based on the presence or absence of at least one SNP in at least a portion of the 16S rRNA gene or gene product or of at least a portion of the 18S rRNA gene or gene product from the sample.