letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 5.

[0051] FIGS. 5A-ARU: Features of the bacteriophage F170/08 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-213 listed in FIG. 5 encode the amino acid sequences of SEQ ID NO:131-343, respectively.

[0052] FIGS. 6A-B: The host range of F170/08 as determined by the spot test in 105 *Enterococcus faecalis* (EFS) (6A) and 56 *Enterococcus faecium* (EFM) (6B) strains isolated from clinical samples. Each spot contained 5 μl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0053] FIG. 7: Schematic of the organization of the F770/05 genome, comprising the nucleic acid sequence of SEQ ID NO:3. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 8.

[0054] FIGS. 8A-AEE: Features of the bacteriophage F770/05 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded

coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 14.

[0060] FIGS. 14A-~~S~~U: Features of the bacteriophage F86/06 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid sequence, (iii) a listing of homologous proteins and conserved domains within its encoded polypeptide and (iv) an assignment of putative function. ORFs 1-63 listed in FIG. 14 encode the amino acid sequences of SEQ ID NO:554-616, respectively.

[0061] FIG. 15: The host range of F86/06 as determined by the spot test in 100 *Staphylococcus aureus* (STA) strains isolated from clinical samples. Each spot contained 5 µl bacteriophage suspension with indicated titers (prepared from CsCl purified lysate). Sensitivity of each strain to the phage was evaluated based on a relative scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

[0062] FIG. 16: Schematic of the organization of the F87s/06 genome, comprising the nucleic acid sequence of SEQ ID NO:6. The ORFs predicted in the genome are represented by arrows and numbered in black. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for which products a functional assignment could be made based on the known functions of homologous proteins (ORFs encoding products exhibiting homology to the same or similar proteins are indicated using the same number and differentiated by lowercase letter); Gray - ORFs coding for products that are similar to proteins of unknown function; White or Empty – ORFs coding for proteins that share no significant homology with proteins in available databases. Functionally assigned ORFs are also listed in the figure. The information in the figure is also included in tabular form in FIG. 17.

[0063] FIGS. 17A-~~U~~V: Features of the bacteriophage F87s/06 genome, including gene products and assignment of putative functions. The figure includes a listing of the ORFs of the genome and provides for each ORF (i) its position within the genome, (ii) the encoded amino acid

arrows and numbered in black. For the ORFs functionally assigned, the number is substituted by the predicted function. The direction of an arrow indicates the direction of transcription. Color coding: Black – ORFs for whose products a functional assignment could be made based on homologous proteins; Gray - ORFs coding for products that are similar to proteins of unknown function; Striped – ORFs with an assigned function based on its relative genome position and on the presence of putative transmembrane domains in the encoded product; Empty arrows – ORFs coding for proteins that share no significant homology with proteins in databases.

[0069] FIGS. 23A-~~I~~O: Features of bacteriophage F1245/05 genome, including gene products and assignment of putative functions are provided.

[0070] FIGS. 24A-E: The host range of F1245/05 as determined by the spot test in 100 *Acinetobacter baumannii* strains isolated from clinical samples is provided. Each spot contained 5 µl bacteriophage suspensions with indicated titers (prepared from CsCl purified lysate). Sensitivity to the phage is presented as a scale ranging from turbid (+) to clear (++++) lysis halos. Resistance to phage infection is indicated as (-).

6. DETAILED DESCRIPTION

[0071] The present invention is directed to isolated bacteriophages, and their isolated polypeptide products, having antibacterial activity against one or more species or strains of the nosocomial pathogens *A. baumannii, E. faecalis*, *E. faecium*, *P. aeruginosa* and *S. aureus*. In one embodiment, isolated bacteriophages or polypeptides are provided that exhibit antimicrobial and/or antibacterial activity against methicillin resistant strains of *S. aureus* (MRSA). In addition, the bacteriophages and polypeptides of the invention may exhibit antibacterial or antimicrobial activity against one or more species or strains of pathogenic bacteria including, but not limited to, S. *epidermidis, S. auricularis, S. capitis, S. haemolyticus, S. hominis, S. saprophyticus, S. simulans, S. xylosis, Micrococcus luteus, Bacilus subtilis, B. pumilus, E. hirae* and *E. avium*.

[0072] In one embodiment, the invention provides a bacteriophage having a genome comprising or consisting of the nucleic acid sequence of SEQ ID NO:1. A specific example in accordance with this embodiment is the isolated bacteriophage F168/08, which targets a number of strains of *E. faecalis* and *E. faecium*. Open reading frames (ORFs) in the F168/08 genome, the amino acid sequences encoded by the ORFs and the assignment of putative functions of the encoded amino

WHAT IS CLAIMED IS:

1. A purified bacteriophage comprising the nucleic acid sequence of SEQ ID NO:2.

2. A pharmaceutical composition comprising the bacteriophage of claim 1 and a pharmaceutically acceptable carrier.

3. The pharmaceutical composition of claim 2, further comprising one or more additional bacteriophages effective against *Enterococcus faecalis* or *Enterococcus faecium.*

4. The pharmaceutical composition of claim 2, further comprising one or more additional bacteriophages effective against bacteria other than *Enterococcus faecalis* or *Enterococcus faecium.*

5. An isolated lysin protein from bacteriophage F170/08, having the amino acid sequence of SEQ ID NO:184 or SEQ ID NO:203, or a fragment thereof having antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*, wherein said bacteriophage F170/08 comprises the nucleic acid sequence of SEQ ID NO:2.

6. The fragment of claim 5, wherein said fragment is a CHAP domain isolated from a polypeptide having the amino acid sequence of SEQ ID NO:184 or SEQ ID NO:203.

7. An isolated tail tape measure protein or tail protein from bacteriophage F170/08, having the amino acid sequence of SEQ ID NO:204 or a fragment thereof having antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*, wherein said bacteriophage F170/08 comprises the nucleic acid sequence of SEQ ID NO:2.

8. A pharmaceutical composition comprising the isolated protein or fragment of any one of claims 5-7 and a pharmaceutically acceptable carrier.

9. The pharmaceutical composition of claim 8, comprising the isolated protein having the amino acid sequence of SEQ ID NO:184, SEQ ID NO:203 or SEQ ID NO:204, or a fragment thereof, having antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*.

10. The pharmaceutical composition of claim 9, further comprising one or more bacteriophages or additional proteins effective against *Enterococcus faecalis* or *Enterococcus faecium* and/or effective against bacteria other than *Enterococcus faecalis* or *Enterococcus faecium*.

11. An isolated nucleic acid comprising a nucleotide sequence encoding the protein or fragment of any one of claims 5-7.

12. Use of a therapeutically effective amount of the pharmaceutical composition of any one of claims 2-4 or 8-10 in the manufacture of a medicament for treating or reducing the incidence of a bacterial infection in a subject in need thereof.

13. The use of claim 12 wherein said bacterial infection is an infection by *Enterococcus faecalis* or *Enterococcus faecium*.

14. The use of claim 12, wherein the infection is a nosocomial infection.

15. The use of claim 12, wherein the composition is administered topically.

16. The use of claim 12, wherein the subject is a mammal.

17. The use of claim 16, wherein the mammal is a human.

18. The use of claim 12, wherein the infection treated is an infection of the skin.

19. The use of claim 18, wherein said infection of the skin is an infection associated with an ulcer or a skin structure infection.

20. The use of claim 18, wherein said infection of the skin is an infection associated with a diabetic foot ulcer.

21. A method for diagnosing *Enterococcus faecalis* or *Enterococcus faecium* as the causative agent of a bacterial infection comprising:

(i) culturing a tissue sample from a patient;

(ii) contacting the culture of step (i) with the bacteriophage of claim 1, or the protein or fragment of any one of claims 5-7; and

(iii) monitoring for evidence of growth or lysis of the culture;

wherein evidence of lysis of the culture indicates that the culture comprises *Enterococcus faecalis* or *Enterococcus faecium*.

22. The method of claim 21, wherein the tissue sample is a sample of blood, fluid, tissue biopsy or swab collected from said patient.

23. A method for reducing or inhibiting colonization or growth of *Enterococcus faecalis* or *Enterococcus faecium* bacteria on a solid surface comprising contacting said solid surface with the bacteriophage of claim 1, or the protein or fragment of any one of claims 5-7.

24. The method of claim 23, wherein said solid surface is the surface of a hospital apparatus or a piece of hospital equipment.

25. The method of claim 24, wherein said apparatus of equipment is a surgical apparatus or a piece of surgical equipment.

26. Use of the bacteriophage of claim 1, or the protein or fragment of any one of claims 5-7, in the manufacture of a medicament for reducing or inhibiting an infection associated

with colonization or growth of *Enterococcus faecalis* or *Enterococcus faecium* on a biological surface of a mammal that is contacted therewith.

27. The use of claim 26, wherein said surface is the skin or a mucus membrane of a mammal.

28. The use of claim 27, wherein said mammal is a human.

29. The use of claim 12, wherein said medicament further comprises

(i) an antibiotic for treating infection by *Enterococcus faecalis* or *Enterococcus faecium*;

(ii) one or more additional bacteriophage known to have antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*; and/or

(iii) one or more additional bacteriophage known to have antibacterial or antimicrobial activity against bacteria other than *Enterococcus faecalis* or *Enterococcus faecium*.

~~WHAT IS CLAIMED IS:~~

1. An isolated bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:760.

2. A pharmaceutical composition comprising the bacteriophage of claim 1 and a pharmaceutically acceptable carrier.

3. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:2 further comprising one or more additional bacteriophages effective against *Enterococcus faecalis* or *Enterococcus faecium.*

4. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:2 further comprising one or more additional bacteriophages effective against bacteria other than *Enterococcus faecalis* or *Enterococcus faecium.*

5. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:3 further comprising one or more additional bacteriophages effective against *Pseudomonas aeruginosa.*

6. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:3 further comprising one or more additional bacteriophages effective against bacteria other than *Pseudomonas aeruginosa.*

7. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7 further comprising one or more additional bacteriophages effective against *Staphylococcus aureus.*

8. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 or SEQ ID NO:7 further comprising one or more additional bacteriophages effective against bacteria other than *Staphylococcus aureus.*

9. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:760 further comprising one or more additional bacteriophages effective against *Acinetobacter baumannii.*

10. The pharmaceutical composition of claim 2, comprising a bacteriophage having a genome which comprises the nucleic acid sequence of SEQ ID NO:760 further comprising one or more additional bacteriophages effective against bacteria other than *Acinetobacter baumannii.*

11. An isolated lysin protein from bacteriophage F1245/05, F170/08, F197/08, F86/06, F87s/06 or F91a/06, or a fragment thereof having antibacterial or antimicrobial activity against one or more of *Acinetobacter baumanii, Enterococcus faecalis*, *Enterococcus faecium* and *Staphylococcus aureus*.

12. The isolated lysin protein of claim 11, said protein having the amino acid sequence of SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641, SEQ ID NO:712, SEQ ID NO: 797, or a fragment thereof, which fragment has antibacterial or antimicrobial activity against one or more of *Enterococcus faecalis*, *Enterococcus faecium*, *Staphylococcus aureus* and *Acinetobacter baumanii.*

13. An isolated first protein having at least 85% sequence identity to a second protein of the same size, wherein said first protein has antibacterial or antimicrobial activity against one or more of *Acinetobacter baumanii, Enterococcus faecalis*, *Enterococcus faecium* and *Staphylococcus aureus* and said second protein has the amino acid sequence of SEQ ID NO: 797, SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641, SEQ ID NO:712 or a fragment thereof.

14. The isolated first protein of claim 13 having at least 95% sequence identity to said second protein.

15. The fragment of claim 11, wherein said fragment is a CHAP domain isolated from a polypeptide having the amino acid sequence of SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:575, SEQ ID NO:641 or SEQ ID NO:712.

16. The fragment of claim 15, wherein said fragment has the amino acid sequence of SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758 or SEQ ID NO:759.

17. An isolated tail tape measure protein or tail protein from bacteriophage, F170/08, F770/05, F197/08, F86/06, F87s/06, F91a/06, or F1245/05, or a fragment thereof having antibacterial or antimicrobial activity against one or more of *Acinetobacter baumanni, Enterococcus faecalis, Enterococcus faecium, Pseudomonas aeruginosa* and *Staphylococcus aureus*.

18. The isolated tail tape measure protein or tail protein of claim 17, said protein having the amino acid sequence of SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:795, or a fragment thereof, which fragment has antibacterial or antimicrobial activity against one or more of *Acinetobacter baumanni, Enterococcus faecalis, Enterococcus faecium, Pseudomonas aeruginosa* and *Staphylococcus aureus*.

19. An isolated first protein having at least 85% sequence identity to a second protein of the same size, wherein said first protein has a biological activity associated with bacteriophage F170/08, F770/05, F197/08, F86/06, F87s/06, F91a/06, or F1245/05 and said second protein has the amino acid sequence of SEQ ID NO:204, SEQ ID NO:214, SEQ ID NO:435, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:795, or a fragment thereof.

20. The isolated first protein of claim 19 having at least 95% sequence identity to said second protein.

21. A pharmaceutical composition comprising the isolated protein of claim 11 or 17 and a pharmaceutically acceptable carrier.

22. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204 or SEQ ID NO:214, or a fragment thereof, having antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*, further comprising one or more bacteriophages or additional proteins effective against *Enterococcus faecalis* or *Enterococcus faecium.*

23. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:184, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204 or SEQ ID NO:214, or a fragment thereof, having antibacterial or antimicrobial activity against *Enterococcus faecalis* or *Enterococcus faecium*, further comprising one or more bacteriophages or additional proteins effective against bacteria other than *Enterococcus faecalis* or *Enterococcus faecium.*

24. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:435 or SEQ ID NO:438, or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Pseudomonas aeruginosa*, further comprising one or more bacteriophages or additional proteins effective against *Pseudomonas aeruginosa.*

25. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:435 or SEQ ID NO:438, or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Pseudomonas aeruginosa*, further comprising one or more bacteriophages or additional proteins effective against bacteria other than *Pseudomonas aeruginosa.*

26. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID

NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632,SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704 or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Staphylococcus aureus*, further comprising one or more bacteriophages or additional proteins effective against *Staphylococcus aureus.*

27. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NO:440, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:632,SEQ ID NO:633, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Staphylococcus aureus*, further comprising one or more bacteriophages or additional proteins effective against bacteria other than *Staphylococcus aureus.*

28. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NOS:761-816, or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Acinetobacter baumannii*, further comprising one or more bacteriophages or additional proteins effective against *Acinetobacter baumannii.*

29. The pharmaceutical composition of claim 21, comprising an isolated protein having the amino acid sequence of SEQ ID NOS:761-816, or a fragment, variant or derivative thereof having antibacterial or antimicrobial activity against *Acinetobacter baumannii*, further comprising one or more bacteriophages or additional proteins effective against bacteria other than *Acinetobacter baumannii.*

30. An isolated nucleic acid comprising a nucleotide sequence encoding the protein of claim 11 or 17.

31. Use of the pharmaceutical composition of claim 2 or 21 in the manufacture of a medicament for treating or preventing a bacterial infection in a subject in need thereof.

32. The use of claim 31 wherein said bacterial infection is an infection by one or more of *Acinetobacter baumanni, Enterococcus faecalis*, *Enterococcus faecium*, *Pseudomonas aeruginosa* and *Staphylococcus aureus*.

33. The use of claim 31 wherein said bacterial infection is an infection by a bacterium other than *Acinetobacter baumanni, Enterococcus faecalis*, *Enterococcus faecium*, *Pseudomonas aeruginosa* and *Staphylococcus aureus*.

34. The use of claim 31, wherein the infection is a nosocomial infection.

35. The use of claim 31, wherein the composition is administered topically.

36. The use of claim 31, wherein the subject is a mammal.

37. The use of claim 36, wherein the mammal is a human.

38. The use of claim 31, wherein the infection treated is an infection of the skin.

39. The use of claim 38, wherein said infection of the skin is an infection associated with a diabetic foot ulcer.

40. A method for diagnosing the causative agent of a bacterial infection comprising:

(i) culturing a tissue sample from a patient;

(ii) contacting the culture of step (i) with the bacteriophage of claim 1, or protein of claim 11 or 17; and

(iii) monitoring for evidence of growth or lysis of the culture;

wherein evidence of lysis of the culture indicatives that the culture comprises a species or strain of bacteria that is known to be susceptible to the bacteriophage or protein used in step (ii).

41. The method of claim 40, wherein the tissue sample is a sample of blood, fluid, tissue biopsy or swab collected from said patient.

42. A method for reducing or inhibiting the colonization or growth of bacteria on a solid surface comprising contacting said solid surface with the bacteriophage of claim 1, or protein of claim 11 or 17.

43. The method of claim 42, wherein said solid surface is the surface of a hospital apparatus or a piece of hospital equipment.

44. The method of claim 43, wherein said apparatus or equipment is a surgical apparatus or piece of surgical equipment.

45. Use of a bacteriophage of claim 1, or protein of claim 11 or 17, in the manufacture of a medicament for reducing or inhibiting an infection associated with the colonization or growth on a biological surface of a mammal of one or more of *Acinetobacter baumanni, Enterococcus faecalis, Enterococcus faecium, Pseudomonas aeruginosa* and *Staphylococcus aureus*.

46. The use of claim 45, wherein said surface is the skin or a mucus membrane of a mammal.

47. The use of claim 46, wherein said mammal is a human.