

concentration (MIC), or an MIC-like measurement, is to be determined. The inoculated medium is incubated for 18-24 hours and observed for visible growth, as measured by turbidity, pellet size, and/or release of the chromogenic or fluorogenic moiety. The lowest antibiotic concentration that completely inhibits visible growth of the isolated organism is recorded as the MIC.

[0006] The agar diffusion assay involves the placement of an antibiotic containing disc or an antibiotic gradient strip on the surface of an agar medium (typically, a Mueller Hinton agar plate) that has been inoculated with a pure isolate of the microorganism in question. The plates are incubated for 18-24 hours, during which time the antibiotic substance diffuses away from the disc or strip, such that the effective concentration of antibiotic varies as a function of the radius from the disc or strip. The diameter of the resulting area of no growth and/or no color (i.e., the zone of inhibition) around the disc or strip, if any, is directly proportional to the MIC.

[0007] Current FDA-approved methods for antibiotic susceptibility testing require inoculation of around 10^5 CFU/mL microorganisms. Because clinical samples generally contain substantially less than 10^5 CFU/mL, it is difficult to apply FDA-approved tests directly to clinical specimens. Typically, clinical samples are inoculated into culture medium and grown until the number of microorganisms reaches about 10^8 CFU/mL. Usually, the processes of microorganism identification and antibiotic susceptibility testing require 48 to 72 hours to be completed, during which time the microorganism continues to spread in the patient and in the environment.

[0008] Shortening the time necessary to identify the infectious microorganism and select an effective antibiotic regimen could significantly decrease morbidity and mortality rates, prevent epidemic outbreaks, and reduce the cost of treating patients with aggressive microorganism infections.

[0009] Accordingly, a primary object of the invention is to provide a method for rapid microorganism detection and drug susceptibility screening.

SUMMARY

[0010] Disclosed is a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria. The method includes steps of detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile and comparing the infection source profile to a control profile thereby

predicting the phenotypic antibiotic resistance of the bacteria. In embodiments, the bacteria may be obtained from a biological sample from a subject having or suspected of having a pathogenic bacterial infection or the bacteria may be collected from the environment.

[0010a] In one aspect, there is provided a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising: a. detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and b. comparing the infection source profile to a control profile thereby predicting the phenotypic antibiotic resistance of the bacteria.

[0011] Disclosed is a method for determining the minimal inhibitory concentration (MIC) of an antibiotic that treats a bacterial infection in a subject. The method includes steps of obtaining a biological sample (e.g., comprising pathogenic bacteria) from the subject, detecting in the biological sample the presence or absence of at least one antibiotic resistance gene to produce an infection source profile, and comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic that treats the bacterial infection. The method may further comprise choosing and administering the antibiotic to the subject at a dose based on the MIC. In embodiments, the subject has or is suspected of having a bacterial infection. In embodiments, the control profile is a database.

[0011a] In another aspect, there is provided a method for determining the minimal inhibitory concentration (MIC) of an antibiotic that treats a bacterial infection in a subject comprising: a. obtaining a biological sample from the subject; b. detecting in the biological sample the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and c. comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic that treats the bacterial infection.

[0012] Any of the above aspects or embodiments, the biological sample may be an anal swab, a rectal swab, a skin swab, a nasal swab, a wound swab, stool, blood, plasma, serum, urine, sputum, respiratory lavage, cerebrospinal fluid, or a bacterial culture.

[0013] Disclosed is a method for determining the minimal inhibitory concentration (MIC) of an antibiotic for a bacterial isolate. The method includes steps of detecting in the bacterial isolate the presence or absence of at least one antibiotic resistance gene to produce an infection source profile and comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic for the bacterial isolate. In embodiments, the

bacterial isolate may be obtained from a subject having or suspected of having a bacterial infection or the bacterial isolate may be collected from the environment.

[0013a] In another aspect, there is provided a method for determining the minimal inhibitory concentration (MIC) of an antibiotic for a bacterial isolate: a. detecting in the bacterial isolate the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and b. comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic for the bacterial isolate.

[0014] Disclosed is a method for determining whether an infection source will be susceptible to an antibiotic comprising. The method includes steps of obtaining a sample comprising the infection source, detecting in the sample the presence or absence of an antibiotic resistance gene thereby determining an infection source profile, and comparing the infection source profile to a control profile thereby determining whether an infection source will be susceptible to an antibiotic. In embodiments, the sample may be obtained from a subject having or suspected of having a bacterial infection or the sample may be collected from the environment.

[0014a] In another aspect, there is provided a method for determining whether an infection source will be susceptible to an antibiotic comprising: a. obtaining a sample comprising the infection source; b. detecting in the sample the presence or absence of an antibiotic resistance gene thereby determining an infection source profile; and c. comparing the infection source profile to a control profile thereby determining whether an infection source will be susceptible to an antibiotic.

[0015] Disclosed is a method for generating a database that correlates a genetic profile with a minimal inhibitory concentration (MIC) of an antibiotic. The method comprises steps of obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein the MIC of the antibiotic for each bacterial isolate in the plurality is known, determining a genetic profile for each bacterial isolate, wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes, and associating each genetic profile for each isolate with its known MIC of the antibiotic, thereby generating a database that correlates a genetic profile with a MIC of the antibiotic. The present disclosure also includes the database generated by this method. Also included is a non-transient computer readable medium containing the database.

[0015a] In another aspect, here is provided a method for generating a database that correlates a genetic profile with a minimal inhibitory concentration (MIC) of an antibiotic comprising: a. obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein the MIC of the antibiotic for each bacterial isolate in the plurality is known; b. determining a genetic profile for each bacterial isolate, wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes; and c. associating each genetic profile for each isolate with its known MIC of the antibiotic, thereby generating a database that correlates a genetic profile with a MIC of the antibiotic.

[0016] Disclosed is a method for generating a database that correlates a genetic profile with susceptibility to an antibiotic. The method comprises steps of obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein each bacterial isolate in the plurality has a known susceptibility to at least one antibiotic, determining a genetic profile for each isolate wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes, and associating each genetic profile for each isolate with its known susceptibility to the at least one antibiotic, thereby generating a database that correlates a genetic profile with susceptibility to at least one antibiotic. The present disclosure also includes the database generated by this method. Also included is a non-transient computer readable medium containing the database.

[0016a] In another aspect, there is provided a method for generating a database that correlates a genetic profile with susceptibility to an antibiotic comprising a. obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein each bacterial isolate in the plurality has a known susceptibility to at least one antibiotic; b.

determining a genetic profile for each isolate wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes; and c. associating each genetic profile for each isolate with its known susceptibility to the at least one antibiotic, thereby generating a database that correlates a genetic profile with susceptibility to at least one antibiotic.

[0016b] In another aspect, there is provided a database generated by the method as described herein.

[0016c] In another aspect, there is provided a non-transient computer readable medium containing the database as described herein.

[0017] Disclosed is a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria. The method comprises steps of detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile and comparing the infection source profile to a database as described herein, thereby predicting the phenotypic antibiotic resistance of the bacteria. In embodiments, the bacteria may be obtained from a subject having or suspected of having a pathogenic bacterial infection or the bacteria may be collected from the environment.

[0017a] In another aspect, there is provided a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising: a. detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and b. comparing the infection source profile to the database as described herein thereby predicting the phenotypic antibiotic resistance of the bacteria.

[0018] Disclosed is a method of identifying the bacterial species or bacterial strain in a sample. The method comprises steps of detecting in the sample the presence or absence of at least one antibiotic resistance gene to produce a sample

profile and comparing the sample profile to a control profile thereby identifying the bacterial strain in a sample. In embodiments, the sample may be obtained from a subject having or suspected of having a bacterial infection or the sample may be collected from the environment.

[0018a] In another aspect, there is provided a method of identifying the bacterial species or bacterial strain in a sample comprising: a. detecting in the sample the presence or absence of at least one antibiotic resistance gene to produce a sample profile; and b. comparing the sample profile to a control profile thereby identifying the bacterial strain in a sample.

[0019] Disclosed is a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria. The method comprises steps of assessing the expression of a plurality of antibiotic resistance genes in the bacteria and calculating a score from the expression the antibiotic resistance genes wherein the score indicates the phenotypic resistance of the bacteria. In embodiments, the bacteria may be obtained from a subject having or suspected of having a bacterial infection or the bacteria may be collected from the environment.

[0019a] In another aspect, there is provided a method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising: a. assessing the expression of a plurality of antibiotic resistance genes in the bacteria; and b. calculating a score from the expression the antibiotic resistance genes wherein the score indicates the phenotypic resistance of the bacteria.

[0020] In any of the above aspects or embodiments, when a sample, bacteria, or bacterial isolate is obtained from the environment, the method may further comprise making a contact precautions recommendation, e.g., one or more of isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

[0021] In any of the above aspects or embodiments, the antibiotic resistance gene may be aac(3)-Ia, aac(3)-Ic, aac(3)-Id/e, aac(3)-II(a-d), aac(3)-IV, aac(6')-Ia, aac(6')-Ib/Ib-cr, aac(6')-Ic, aac(6')-Ie, AAC(6')-IIa, aadA12-A24, aadA16, aadA3/A8, aadA5/A5, aadA6/A10/A11, aadA7, aadA9, ACC-1, ACC-3, ACT-1, ACT-5, ANT(2'')-Ia, ant(3'')-Ia, ant(3'')-II, aph(3')-Ia/c, aph(3')-IIb-A, aph(3')-IIb-B, aph(3')-IIb-C, aph(3')-IIIa, aph(3')-VIa, aph(3')-Vib, aph(3')-XV, aph(4)-Ia, aph(6)-Ic, armA, BEL-1, BES-1, CFE-1, CMY-1, CMY-2, CMY-41, CMY-70, CTX-M-1, CTX-M-2, CTX-M-8/25, CTX-M-9, dfr19/dfrA18, dfrA1, dfrA12, dfrA14, dfrA15, dfrA16, dfrA17, dfrA23, dfrA27, dfrA5, dfrA7, dfrA8, dfrB1/dfr2a, dfrB2, DHA, dhfrB5, E. cloacae GyrA, E. cloacae parC, E. coli GyrA, E. coli parC, ere(A), ere(B), erm(B), floR, FOX-1, GES-1, GIM-1, IMI-1, IMP-1, IMP-2, IMP-5, K. pneumoniae GyrA, K. pneumoniae parC, KPC-1, MCR-1, MIR-1, MOX-1, MOX-5, mph(A), mph(D), mph(E), msr(E), NDM-1, NMC-A, oqxA, oqxB, OXA-1, OXA-10, OXA-18, OXA-2, OXA-23, OXA-24, OXA-45, OXA-48, OXA-50, OXA-50, OXA-51, OXA-54, OXA-55, OXA-58, OXA-60, OXA-62, OXA-9, P. aeruginosa GyrA, P.

aeruginosa parC, PER-1, PSE-1, QnrA1, QnrA3, QnrB1, QnrB10, QnrB11, QnrB13, QnrB2, QnrB21, QnrB22, QnrB27, QnrB31, QnrD1, QnrS1, QnrS2, QnrVC1, QnrVC4, rmtB, rmtF, SFC-1, SHV- G238S & E240, SHV-G156 (WT), SHV-G156D, SHV-G238 & E240 (WT), SHV-G238 & E240K, SHV-G238S & E240K, SIM-1, SME-1, SPM-1, strA, strB, Sul1, Sul2, Sul3, TEM-E104 (WT), TEM-E104K, TEM-G238 & E240 (WT), TEM-G238 & E240K, TEM-G238S & E240, TEM-G238S & E240K, TEM-R164 (WT), TEM-R164C, TEM-R164H, TEM-R164S, tet(A), tetA(B), tetA(G), tetAJ, tetG, TLA-1, VanA, VEB-1, VIM-1, VIM-13, VIM-2, or VIM-5.

[0022] In any of the above aspects or embodiments, the antibiotic may be Amikacin, Amoxicillin/K Clavulanate, Ampicillin, Ampicillin/Sulbactam, Aztreonam, Cefazolin, Cefepime, Cefotaxime, Cefotaxime, Cefotaxime/K Clavulanate, Cefoxitin, Ceftazidime, Ceftazidime/K Clavulanate, Ceftriaxone, Cefuroxime, Ciprofloxacin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Nitrofurantoin, Piperacillin, Piperacillin/Tazobactam, Tetracycline, Ticarcillin/K Clavulanate, Tigecycline, Tobramycin, Trimethoprim/Sulfamethoxazole, Zerbaxa (ceftolozane and tazobactam), imipenem/cilastatin/relebactam, Amoxicillin / K Clavulanate, Ampicillin, Ampicillin / Sulbactam, Cefazolin, Ceftriaxone, Chloramphenicol, Clindamycin, Daptomycin, Erythromycin, Gentamicin, Gentamicin Synergy Screen, Imipenem, Levofloxacin, Linezolid, Meropenem, Moxifloxacin, Nitrofurantoin, Oxacillin, Penicillin, Rifampin, Streptomycin, Synercid, Tetracycline, Trimethoprim / Sulfamethoxazole, or Vancomycin.

[0023] In any of the above aspects or embodiments, the bacteria may be from the species *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Klebsiella oxytoca*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus salivarius*, *Enterobacter aerogenes*, *Serratia marcescens*, *Acinetobacter baumannii*, *Citrobacter freundii*, *Morganella morganii*, *Legionella pneumophila*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Haemophilus parainfluenzae*, *Mycoplasma pneumoniae*, *Chlamydomphila pneumoniae*, *Clostridium species*, or *Bacteroides fragilis*.

[0024] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice of the present disclosure, suitable methods and materials

are described below. All publications, patent applications, patents, and other references mentioned herein are expressly incorporated by reference in their entirety. In cases of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples described herein are illustrative only and are not intended to be limiting.

Other features and advantages of the disclosure will be apparent from and encompassed by the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] The above and further features will be more clearly appreciated from the following detailed description when taken in conjunction with the accompanying drawings.

[0026] **Figure 1** includes a decision tree for susceptibility to the antibiotic Cefepime. The decision tree includes positive/negative results for the antibiotic resistance genes *KPC*, *CTX-M-1*, *CTX-M-9*, *VEB*, and *NDM*.

[0027] **Figure 2** includes a decision tree for susceptibility to the antibiotic Levofloxacin. Levofloxacin minimum inhibitory concentration (MIC) values are based on genotypes for three genes.

[0028] **Figure 3** includes a comparison of measured minimum inhibitory concentration (MIC) values from phenotypic AST to predicted MIC values for isolates of *Klebsiella*. Cefepime minimum inhibitory concentration (MIC) values are based on genotypes for beta-lactamase genes.

[0029] **Figure 4** includes a comparison of resistance genes in *Klebsiella* that predict susceptibility to the antibiotic Cefepime.

[0030] **Figure 5** includes predicted non-susceptibility of *Klebsiella* and *E. coli* to the antibiotics Ceftazidime, Cefepime, Etrapanem, Meropenem, and Imipenem.

[0031] **Figure 6** includes a comparison of measured minimum inhibitory concentration (MIC) values from phenotypic AST to predicted MIC values for isolates of *Pseudomonas aeruginosa*. Levofloxacin predicted minimum inhibitory concentration (MIC) values are based on mutation of *P. aeruginosa* DNA gyrase.

[0032] **Figure 7** includes a comparison of gyrase genotypes in *P. aeruginosa* that predict susceptibility to the antibiotic Levofloxacin.

[0033] **Figure 8** includes predicted non-susceptibility of *P. aeruginosa*, *E. coli*, and *Klebsiella pneumonia* to Levofloxacin and Ciprofloxacin.

Claims

We claim:

1. A method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising:
 - a. detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and
 - b. comparing the infection source profile to a control profile thereby predicting the phenotypic antibiotic resistance of the bacteria.
2. The method of claim 1, wherein the pathogenic bacteria is obtained from a biological sample from a subject having or suspected of having a pathogenic bacterial infection.
3. The method of claim 1, wherein the pathogenic bacteria is collected from the environment.
4. The method of claim 3, further comprising making a contact precautions recommendation.
- 5 The method of claims 4, wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.
6. A method for determining the minimal inhibitory concentration (MIC) of an antibiotic that treats a bacterial infection in a subject comprising:
 - a. obtaining a biological sample from the subject;
 - b. detecting in the biological sample the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and
 - c. comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic that treats the bacterial infection.
7. The method of claim 6, wherein the subject has or is suspected of having a bacterial infection.
8. The method of claim 6, wherein the biological sample comprises pathogenic bacteria.

9. The method of claim 1 or 8, wherein the pathogenic bacteria is *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Klebsiella oxytoca*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus salivarius*, *Enterobacter aerogenes*, *Serratia marcescens*, *Acinetobacter baumannii*, *Citrobacter freundii*, *Morganella morganii*, *Legionella pneumophila*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Haemophilus parainfluenzae*, *Mycoplasma pneumoniae*, *Chlamydia pneumoniae*, *Clostridium* species, or *Bacteroides fragilis*.

10. The method of claim 1 or 6, wherein the antibiotic resistance gene is aac(3)-Ia, aac(3)-Ic, aac(3)-Id/e, aac(3)-II(a-d), aac(3)-IV, aac(6')-Ia, aac(6')-Ib/Ib-cr, aac(6')-Ic, aac(6')-Ie, AAC(6')-IIa, aadA12-A24, aadA16, aadA3/A8, aadA5/A5, aadA6/A10/A11, aadA7, aadA9, ACC-1, ACC-3, ACT-1, ACT-5, ANT(2'')-Ia, ant(3'')-Ia, ant(3'')-II, aph(3')-Ia/c, aph(3')-IIb-A, aph(3')-IIb-B, aph(3')-IIb-C, aph(3')-IIIa, aph(3')-VIa, aph(3')-Vib, aph(3')-XV, aph(4)-Ia, aph(6)-Ic, armA, BEL-1, BES-1, CFE-1, CMY-1, CMY-2, CMY-41, CMY-70, CTX-M-1, CTX-M-2, CTX-M-8/25, CTX-M-9, dfr19/dfrA18, dfrA1, dfrA12, dfrA14, dfrA15, dfrA16, dfrA17, dfrA23, dfrA27, dfrA5, dfrA7, dfrA8, dfrB1/dfr2a, dfrB2, DHA, dhfrB5, E. cloacae GyrA, E. cloacae parC, E. coli GyrA, E. coli parC, ere(A), ere(B), erm(B), floR, FOX-1, GES-1, GIM-1, IMI-1, IMP-1, IMP-2, IMP-5, K. pneumoniae GyrA, K. pneumoniae parC, KPC-1, MCR-1, MIR-1, MOX-1, MOX-5, mph(A), mph(D), mph(E), msr(E), NDM-1, NMC-A, oqxA, oqxB, OXA-1, OXA-10, OXA-18, OXA-2, OXA-23, OXA-24, OXA-45, OXA-48, OXA-50, OXA-50, OXA-51, OXA-54, OXA-55, OXA-58, OXA-60, OXA-62, OXA-9, P. aeruginosa GyrA, P. aeruginosa parC, PER-1, PSE-1, QnrA1, QnrA3, QnrB1, QnrB10, QnrB11, QnrB13, QnrB2, QnrB21, QnrB22, QnrB27, QnrB31, QnrD1, QnrS1, QnrS2, QnrVC1, QnrVC4, rmtB, rmtF, SFC-1, SHV- G238S & E240, SHV-G156 (WT), SHV-G156D, SHV-G238 & E240 (WT), SHV-G238 & E240K, SHV-G238S & E240K, SIM-1, SME-1, SPM-1, strA, strB, Sul1, Sul2, Sul3, TEM-E104 (WT), TEM-E104K, TEM-G238 & E240 (WT), TEM-G238 & E240K, TEM-G238S & E240, TEM-G238S & E240K, TEM-R164 (WT), TEM-R164C, TEM-R164H, TEM-R164S, tet(A), tetA(B), tetA(G), tetAJ, tetG, TLA-1, VanA, VEB-1, VIM-1, VIM-13, VIM-2, or VIM-5.

11. The method of claim 1 or 6, wherein the antibiotic is Amikacin, Amoxicillin/K Clavulanate, Ampicillin, Ampicillin/Sulbactam, Aztreonam, Cefazolin, Cefepime, Cefotaxime, Cefotaxime, Cefotaxime/K Clavulanate, Cefoxitin, Ceftazidime, Ceftazidime/K Clavulanate, Ceftriaxone, Cefuroxime, Ciprofloxacin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Nitrofurantoin, Piperacillin, Piperacillin/Tazobactam, Tetracycline, Ticarcillin/K Clavulanate, Tigecycline, Tobramycin, Trimethoprim/Sulfamethoxazole, Zerbaxa (ceftolozane and tazobactam), imipenem/cilastatin/relebactam, Amoxicillin / K Clavulanate, Ampicillin, Ampicillin / Sulbactam, Cefazolin, Ceftriaxone, Chloramphenicol, Clindamycin, Daptomycin, Erythromycin, Gentamicin, Gentamicin Synergy Screen, Imipenem, Levofloxacin, Linezolid, Meropenem, Moxifloxacin, Nitrofurantoin, Oxacillin, Penicillin, Rifampin, Streptomycin, Synercid, Tetracycline, Trimethoprim / Sulfamethoxazole, or Vancomycin.

12. The method of claim 1 or 6, wherein the control profile is a database.

13. The method of claim 1 or 6, wherein the biological sample is an anal swab, a rectal swab, a skin swab, a nasal swab, a wound swab, stool, blood, plasma, serum, urine, sputum, respiratory lavage, cerebrospinal fluid, or a bacterial culture.

14. A method for determining the minimal inhibitory concentration (MIC) of an antibiotic for a bacterial isolate:

- a. detecting in the bacterial isolate the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and
- b. comparing the infection source profile to a control profile thereby identifying the MIC of the antibiotic for the bacterial isolate.

15. The method of claim 14, wherein the bacterial isolate is obtained from a subject having or suspected of having a bacterial infection.

16. The method of claim 14, wherein the bacterial isolate is collected from the environment.

17. The method of claim 16, further comprising making a contact precautions recommendation.

18. The method of claims 17 wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

19. The method of claim 14, wherein the bacterial isolate is from the species *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Klebsiella oxytoca*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus salivarius*, *Enterobacter aerogenes*, *Serratia marcescens*, *Acinetobacter baumannii*, *Citrobacter freundii*, *Morganella morganii*, *Legionella pneumophila*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Haemophilus parainfluenzae*, *Mycoplasma pneumoniae*, *Chlamydophila pneumoniae*, *Clostridium species*, or *Bacteroides fragilis*.

20. The method of claim 14, wherein the antibiotic resistance gene is aac(3)-Ia, aac(3)-Ic, aac(3)-Id/e, aac(3)-II(a-d), aac(3)-IV, aac(6')-Ia, aac(6')-Ib/Ib-cr, aac(6')-Ic, aac(6')-Ie, AAC(6')-IIa, aadA12-A24, aadA16, aadA3/A8, aadA5/A5, aadA6/A10/A11, aadA7, aadA9, ACC-1, ACC-3, ACT-1, ACT-5, ANT(2'')-Ia, ant(3'')-Ia, ant(3'')-II, aph(3')-Ia/c, aph(3')-Iib-A, aph(3')-Iib-B, aph(3')-Iib-C, aph(3')-IIIa, aph(3')-VIa, aph(3')-Vib, aph(3')-XV, aph(4)-Ia, aph(6)-Ic, armA, BEL-1, BES-1, CFE-1, CMY-1, CMY-2, CMY-41, CMY-70, CTX-M-1, CTX-M-2, CTX-M-8/25, CTX-M-9, dfr19/dfrA18, dfrA1, dfrA12, dfrA14, dfrA15, dfrA16, dfrA17, dfrA23, dfrA27, dfrA5, dfrA7, dfrA8, dfrB1/dfr2a, dfrB2, DHA, dhfrB5, E. cloacae GyrA, E. cloacae parC, E. coli GyrA, E. coli parC, ere(A), ere(B), erm(B), floR, FOX-1, GES-1, GIM-1, IMI-1, IMP-1, IMP-2, IMP-5, K. pneumoniae GyrA, K. pneumoniae parC, KPC-1, MCR-1, MIR-1, MOX-1, MOX-5, mph(A), mph(D), mph(E), msr(E), NDM-1, NMC-A, oqxA, oqxB, OXA-1, OXA-10, OXA-18, OXA-2, OXA-23, OXA-24, OXA-45, OXA-48, OXA-50, OXA-50, OXA-51, OXA-54, OXA-55, OXA-58, OXA-60, OXA-62, OXA-9, P. aeruginosa GyrA, P. aeruginosa parC, PER-1, PSE-1, QnrA1, QnrA3, QnrB1, QnrB10, QnrB11, QnrB13, QnrB2, QnrB21, QnrB22, QnrB27, QnrB31, QnrD1, QnrS1, QnrS2, QnrVC1, QnrVC4, rmtB, rmtF, SFC-1, SHV- G238S & E240, SHV-G156 (WT), SHV-G156D, SHV-G238 & E240 (WT), SHV-G238 & E240K, SHV-G238S & E240K, SIM-1, SME-1, SPM-1, strA, strB, Sul1, Sul2, Sul3, TEM-E104

(WT), TEM-E104K, TEM-G238 & E240 (WT), TEM-G238 & E240K, TEM-G238S & E240, TEM-G238S & E240K, TEM-R164 (WT), TEM-R164C, TEM-R164H, TEM-R164S, tet(A), tetA(B), tetA(G), tetAJ, tetG, TLA-1, VanA, VEB-1, VIM-1, VIM-13, VIM-2, or VIM-5.

21. The method of claim 14, wherein the antibiotic is Amikacin, Amoxicillin/K Clavulanate, Ampicillin, Ampicillin/Sulbactam, Aztreonam, Cefazolin, Cefepime, Cefotaxime, Cefotaxime, Cefotaxime/K Clavulanate, Cefoxitin, Ceftazidime, Ceftazidime/K Clavulanate, Ceftriaxone, Cefuroxime, Ciprofloxacin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Nitrofurantoin, Piperacillin, Piperacillin/Tazobactam, Tetracycline, Ticarcillin/K Clavulanate, Tigecycline, Tobramycin, Trimethoprim/Sulfamethoxazole, Zerbaxa (ceftolozane and tazobactam), imipenem/cilastatin/relebactam, Amoxicillin / K Clavulanate, Ampicillin, Ampicillin / Sulbactam, Cefazolin, Ceftriaxone, Chloramphenicol, Clindamycin, Daptomycin, Erythromycin, Gentamicin, Gentamicin Synergy Screen, Imipenem, Levofloxacin, Linezolid, Meropenem, Moxifloxacin, Nitrofurantoin, Oxacillin, Penicillin, Rifampin, Streptomycin, Synercid, Tetracycline, Trimethoprim / Sulfamethoxazole, or Vancomycin.

22. A method for determining whether an infection source will be susceptible to an antibiotic comprising:

- a. obtaining a sample comprising the infection source;
- b. detecting in the sample the presence or absence of an antibiotic resistance gene thereby determining an infection source profile; and
- c. comparing the infection source profile to a control profile thereby determining whether an infection source will be susceptible to an antibiotic.

23. The method of claim 22, wherein the sample is obtained from a subject having or suspected of having a bacterial infection.

24. The method of claim 22, wherein the sample is collected from the environment.

25. The method of claim 24, further comprising making a contact precautions recommendation.

26. The method of claim 25, wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

27. A method for generating a database that correlates a genetic profile with a minimal inhibitory concentration (MIC) of an antibiotic comprising:

- a. obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein the MIC of the antibiotic for each bacterial isolate in the plurality is known;
- b. determining a genetic profile for each bacterial isolate, wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes; and
- c. associating each genetic profile for each isolate with its known MIC of the antibiotic, thereby generating a database that correlates a genetic profile with a MIC of the antibiotic.

28. A method for generating a database that correlates a genetic profile with susceptibility to an antibiotic comprising

- a. obtaining a plurality of bacterial isolates of a bacterial species or a bacterial strain wherein each bacterial isolate in the plurality has a known susceptibility to at least one antibiotic;
- b. determining a genetic profile for each isolate wherein the genetic profile comprises the presence or absence of one or more antibiotic resistance genes; and
- c. associating each genetic profile for each isolate with its known susceptibility to the at least one antibiotic, thereby generating a database that correlates a genetic profile with susceptibility to at least one antibiotic.

29. The method of claim 27 or 28, wherein the bacterial isolates are selected from the group consisting of *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Klebsiella oxytoca*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus salivarius*, *Enterobacter aerogenes*, *Serratia marcescens*, *Acinetobacter baumannii*, *Citrobacter freundii*, *Morganella morganii*, *Legionella pneumophila*, *Moraxella*

catarrhalis, *Haemophilus influenzae*, *Haemophilus parainfluenzae*, *Mycoplasma pneumoniae*, *Chlamydophila pneumoniae*, *Clostridium species*, and *Bacteroides fragilis*.

30. The method of any one of claims 27 to 29, wherein the antibiotic resistance gene is aac(3)-Ia, aac(3)-Ic, aac(3)-Id/e, aac(3)-II(a-d), aac(3)-IV, aac(6')-Ia, aac(6')-Ib/Ib-cr, aac(6')-Ic, aac(6')-Ie, AAC(6')-IIa, aadA12-A24, aadA16, aadA3/A8, aadA5/A5, aadA6/A10/A11, aadA7, aadA9, ACC-1, ACC-3, ACT-1, ACT-5, ANT(2'')-Ia, ant(3'')-Ia, ant(3'')-II, aph(3')-Ia/c, aph(3')-IIb-A, aph(3')-IIb-B, aph(3')-IIb-C, aph(3')-IIIa, aph(3')-VIa, aph(3')-Vib, aph(3')-XV, aph(4)-Ia, aph(6)-Ic, armA, BEL-1, BES-1, CFE-1, CMY-1, CMY-2, CMY-41, CMY-70, CTX-M-1, CTX-M-2, CTX-M-8/25, CTX-M-9, dfr19/dfrA18, dfrA1, dfrA12, dfrA14, dfrA15, dfrA16, dfrA17, dfrA23, dfrA27, dfrA5, dfrA7, dfrA8, dfrB1/dfr2a, dfrB2, DHA, dhfrB5, E. cloacae GyrA, E. cloacae parC, E. coli GyrA, E. coli parC, ere(A), ere(B), erm(B), floR, FOX-1, GES-1, GIM-1, IMI-1, IMP-1, IMP-2, IMP-5, K. pneumoniae GyrA, K. pneumoniae parC, KPC-1, MCR-1, MIR-1, MOX-1, MOX-5, mph(A), mph(D), mph(E), msr(E), NDM-1, NMC-A, oqxA, oqxB, OXA-1, OXA-10, OXA-18, OXA-2, OXA-23, OXA-24, OXA-45, OXA-48, OXA-50, OXA-50, OXA-51, OXA-54, OXA-55, OXA-58, OXA-60, OXA-62, OXA-9, P. aeruginosa GyrA, P. aeruginosa parC, PER-1, PSE-1, QnrA1, QnrA3, QnrB1, QnrB10, QnrB11, QnrB13, QnrB2, QnrB21, QnrB22, QnrB27, QnrB31, QnrD1, QnrS1, QnrS2, QnrVC1, QnrVC4, rmtB, rmtF, SFC-1, SHV- G238S & E240, SHV-G156 (WT), SHV-G156D, SHV-G238 & E240 (WT), SHV-G238 & E240K, SHV-G238S & E240K, SIM-1, SME-1, SPM-1, strA, strB, Sul1, Sul2, Sul3, TEM-E104 (WT), TEM-E104K, TEM-G238 & E240 (WT), TEM-G238 & E240K, TEM-G238S & E240, TEM-G238S & E240K, TEM-R164 (WT), TEM-R164C, TEM-R164H, TEM-R164S, tet(A), tetA(B), tetA(G), tetAJ, tetG, TLA-1, VanA, VEB-1, VIM-1, VIM-13, VIM-2, or VIM-5.

31. The method of any one of claims 27 to 30, wherein the antibiotic is Amikacin, Amoxicillin/K Clavulanate, Ampicillin, Ampicillin/Sulbactam, Aztreonam, Cefazolin, Cefepime, Cefotaxime, Cefotaxime, Cefotaxime/K Clavulanate, Cefoxitin, Ceftazidime, Ceftazidime/K Clavulanate, Ceftriaxone, Cefuroxime, Ciprofloxacin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Nitrofurantoin, Piperacillin, Piperacillin/Tazobactam, Tetracycline, Ticarcillin/K Clavulanate, Tigecycline, Tobramycin, Trimethoprim/Sulfamethoxazole, Zerbaxa (ceftolozane and tazobactam),

imipenem/cilastatin/relebactam, Amoxicillin / K Clavulanate, Ampicillin, Ampicillin / Sulbactam, Cefazolin, Ceftriaxone, Chloramphenicol, Clindamycin, Daptomycin, Erythromycin, Gentamicin, Gentamicin Synergy Screen, Imipenem, Levofloxacin, Linezolid, Meropenem, Moxifloxacin, Nitrofurantoin, Oxacillin, Penicillin, Rifampin, Streptomycin, Synercid, Tetracycline, Trimethoprim / Sulfamethoxazole, or Vancomycin.

32. A database generated by the method of any one of claims 27 to 31.

33. A non-transient computer readable medium containing the database of claim 32.

34. A method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising:

- a. detecting in the bacteria the presence or absence of at least one antibiotic resistance gene to produce an infection source profile; and
- b. comparing the infection source profile to the database of claim 32 thereby predicting the phenotypic antibiotic resistance of the bacteria.

35. The method of claim 34, wherein the pathogenic bacteria is obtained from a subject having or suspected of having a pathogenic bacterial infection.

36. The method of claim 34, wherein the pathogenic bacteria is collected from the environment.

37. The method of claim 36, further comprising making a contact precautions recommendation.

38. The method of claims 37, wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

39. A method of identifying the bacterial species or bacterial strain in a sample comprising:
a. detecting in the sample the presence or absence of at least one antibiotic resistance gene to produce a sample profile; and

b. comparing the sample profile to a control profile thereby identifying the bacterial strain in a sample.

40. The method of claim 39, wherein the sample is obtained from a subject having or suspected of having a bacterial infection.

41. The method of claim 39, wherein the sample is collected from the environment.

42. The method of claim 41, further comprising making a contact precautions recommendation.

43. The method of claim 42, wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

44. A method for predicting phenotypic antibiotic resistance of a pathogenic bacteria comprising:

- a. assessing the expression of a plurality of antibiotic resistance genes in the bacteria; and
- b. calculating a score from the expression the antibiotic resistance genes wherein the score indicates the phenotypic resistance of the bacteria.

45. The method of claim 44, wherein the bacteria is obtained from a subject having or suspected of having a bacterial infection.

46. The method of claim 44, wherein the bacteria is collected from the environment.

47. The method of claim 46, further comprising making a contact precautions recommendation.

48. The method of claim 47, wherein the contact precautions includes one or more of the following: isolating the patient to a quarantine area or ward, providing a private room for said patient, donning personal protective apparel upon entering the patient's room, limiting

patient mobility, limiting or restricting access of non-colonized or non-infected patients or medical personnel to the patient, or providing dedicated patient care equipment.

49. The method of claim 44, wherein the antibiotic resistance gene is *aac(3)-Ia*, *aac(3)-Ic*, *aac(3)-Id/e*, *aac(3)-II(a-d)*, *aac(3)-IV*, *aac(6')-Ia*, *aac(6')-Ib/Ib-cr*, *aac(6')-Ic*, *aac(6')-Ie*, *AAC(6')-IIa*, *aadA12-A24*, *aadA16*, *aadA3/A8*, *aadA5/A5*, *aadA6/A10/A11*, *aadA7*, *aadA9*, *ACC-1*, *ACC-3*, *ACT-1*, *ACT-5*, *ANT(2'')-Ia*, *ant(3'')-Ia*, *ant(3'')-II*, *aph(3')-Ia/c*, *aph(3')-IIb-A*, *aph(3')-IIb-B*, *aph(3')-IIb-C*, *aph(3')-IIIa*, *aph(3')-VIa*, *aph(3')-Vib*, *aph(3')-XV*, *aph(4)-Ia*, *aph(6)-Ic*, *armA*, *BEL-1*, *BES-1*, *CFE-1*, *CMY-1*, *CMY-2*, *CMY-41*, *CMY-70*, *CTX-M-1*, *CTX-M-2*, *CTX-M-8/25*, *CTX-M-9*, *dfr19/dfrA18*, *dfrA1*, *dfrA12*, *dfrA14*, *dfrA15*, *dfrA16*, *dfrA17*, *dfrA23*, *dfrA27*, *dfrA5*, *dfrA7*, *dfrA8*, *dfrB1/dfr2a*, *dfrB2*, *DHA*, *dhfrB5*, *E. cloacae GyrA*, *E. cloacae parC*, *E. coli GyrA*, *E. coli parC*, *ere(A)*, *ere(B)*, *erm(B)*, *floR*, *FOX-1*, *GES-1*, *GIM-1*, *IMI-1*, *IMP-1*, *IMP-2*, *IMP-5*, *K. pneumoniae GyrA*, *K. pneumoniae parC*, *KPC-1*, *MCR-1*, *MIR-1*, *MOX-1*, *MOX-5*, *mph(A)*, *mph(D)*, *mph(E)*, *msr(E)*, *NDM-1*, *NMC-A*, *oqxA*, *oqxB*, *OXA-1*, *OXA-10*, *OXA-18*, *OXA-2*, *OXA-23*, *OXA-24*, *OXA-45*, *OXA-48*, *OXA-50*, *OXA-50*, *OXA-51*, *OXA-54*, *OXA-55*, *OXA-58*, *OXA-60*, *OXA-62*, *OXA-9*, *P. aeruginosa GyrA*, *P. aeruginosa parC*, *PER-1*, *PSE-1*, *QnrA1*, *QnrA3*, *QnrB1*, *QnrB10*, *QnrB11*, *QnrB13*, *QnrB2*, *QnrB21*, *QnrB22*, *QnrB27*, *QnrB31*, *QnrD1*, *QnrS1*, *QnrS2*, *QnrVC1*, *QnrVC4*, *rmtB*, *rmtF*, *SFC-1*, *SHV-G238S & E240*, *SHV-G156 (WT)*, *SHV-G156D*, *SHV-G238 & E240 (WT)*, *SHV-G238 & E240K*, *SHV-G238S & E240K*, *SIM-1*, *SME-1*, *SPM-1*, *strA*, *strB*, *Sul1*, *Sul2*, *Sul3*, *TEM-E104 (WT)*, *TEM-E104K*, *TEM-G238 & E240 (WT)*, *TEM-G238 & E240K*, *TEM-G238S & E240*, *TEM-G238S & E240K*, *TEM-R164 (WT)*, *TEM-R164C*, *TEM-R164H*, *TEM-R164S*, *tet(A)*, *tetA(B)*, *tetA(G)*, *tetAJ*, *tetG*, *TLA-1*, *VanA*, *VEB-1*, *VIM-1*, *VIM-13*, *VIM-2*, or *VIM-5*.

50. The method of claim 44, wherein the antibiotic is Amikacin, Amoxicillin/K Clavulanate, Ampicillin, Ampicillin/Sulbactam, Aztreonam, Cefazolin, Cefepime, Cefotaxime, Cefotaxime/K Clavulanate, Cefoxitin, Ceftazidime, Ceftazidime/K Clavulanate, Ceftriaxone, Cefuroxime, Ciprofloxacin, Ertapenem, Gentamicin, Imipenem, Levofloxacin, Meropenem, Nitrofurantoin, Piperacillin, Piperacillin/Tazobactam, Tetracycline, Ticarcillin/K Clavulanate, Tigecycline, Tobramycin, Trimethoprim/Sulfamethoxazole, Zerbaxa (ceftolozane and tazobactam),

imipenem/cilastatin/relebactam, Amoxicillin / K Clavulanate, Ampicillin, Ampicillin / Sulbactam, Cefazolin, Ceftriaxone, Chloramphenicol, Clindamycin, Daptomycin, Erythromycin, Gentamicin, Gentamicin Synergy Screen, Imipenem, Levofloxacin, Linezolid, Meropenem, Moxifloxacin, Nitrofurantoin, Oxacillin, Penicillin, Rifampin, Streptomycin, Synercid, Tetracycline, Trimethoprim / Sulfamethoxazole, or Vancomycin.