

predicting the phenotypic antibiotic resistance of the bacteria. In examples, 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 example, 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 examples, the subject has or is suspected of having a bacterial infection. In examples, the control profile is a database.

[0011a] In one aspect, the present disclosure refers to a method for determining the minimal inhibitory concentration (MIC) of an antibiotic that treats a bacterial infection in a subject, the method comprising: a. providing a biological sample obtained 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, wherein the comparison is performed using a predictive algorithm for susceptibility, and wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in the biological sample.

[0012] Any of the above aspects or examples, 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 examples, 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, the present disclosure refers to a method for determining the minimal inhibitory concentration (MIC) of an antibiotic for a bacterial isolate, the method comprising: 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, wherein the comparison is performed using a predictive algorithm for susceptibility, and wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in 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 examples, 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 example, 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 example, 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, the present disclosure refers to a method for generating a database that correlates a genetic profile with a minimal inhibitory concentration (MIC) of an antibiotic, the method 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 in genomic DNA of each bacterial isolate; 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.

[0016b] In another aspect, the present disclosure refers to a database generated by the method as described herein.

[0016c] In another aspect, the present disclosure refers to 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 examples, 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 example, 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 examples, 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 example, 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 examples, 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 example, 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.

[0019b] In another aspect, the present disclosure refers to use of an antibiotic in the manufacture of a medicament for treating a bacterial infection in a subject, wherein the antibiotic is chosen and to be administered to the subject at a dose based on the MIC, and wherein the MIC is determined by a method comprising: a. providing a biological sample obtained 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, wherein the comparison is performed using a predictive algorithm for susceptibility, and wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in the biological sample.

[0020] In any of the above aspects or examples, 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 examples, 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 examples, 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 examples, 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*, *Chlamydophila 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

Claims

We claim:

1. A method for determining the minimal inhibitory concentration (MIC) of an antibiotic that treats a bacterial infection in a subject, the method comprising:
 - a. providing a biological sample obtained 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,wherein the comparison is performed using a predictive algorithm for susceptibility, and

wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in the biological sample.
2. The method of claim 1, wherein the biological sample comprises pathogenic bacteria.
3. The method of claim 1, wherein the control profile is a database.
4. The method of claim 1, 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.
5. A method for determining the minimal inhibitory concentration (MIC) of an antibiotic for a bacterial isolate, the method comprising:
 - 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,wherein the comparison is performed using a predictive algorithm for susceptibility, and

wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in the bacterial isolate.

6. The method of claim 1 or claim 5, wherein the subject has or is suspected of having a bacterial infection, or wherein the bacterial isolate is obtained from a subject having or suspected of having a bacterial infection.
7. The method of claim 5, wherein the bacterial isolate is collected from the environment.
8. The method of claim 7, further comprising making a contact precautions recommendation; optionally 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.
9. A method for generating a database that correlates a genetic profile with a minimal inhibitory concentration (MIC) of an antibiotic, the method 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 in genomic DNA of each bacterial isolate; 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.
10. The method of any one of claims 2, 5, or 9, wherein the pathogenic bacteria or bacterial isolate(s) 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*.

11. A database generated by the method of claim 9.

12. A non-transient computer readable medium containing the database of claim 11.

13. The method of any one of claims 1, 5, and 9, 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.

14. The method of any one of claims 1, 5, and 9, 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.

15. Use of an antibiotic in the manufacture of a medicament for treating a bacterial infection in a subject, wherein the antibiotic is chosen and to be administered to the subject at a dose based on the MIC, and wherein the MIC is determined by a method comprising:

- a. providing a biological sample obtained 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,
- wherein the comparison is performed using a predictive algorithm for susceptibility, and
- wherein the presence or absence of at least one antibiotic resistance gene is detected in genomic DNA in the biological sample.