MAYO CLINIC LABORATORIES

Test Definition: BTWGS

Bacterial Typing, Whole Genome Sequencing, Varies

Overview

Useful For

Aiding in the investigation of a potential outbreak by a single bacterial species

May assist in identification of recurrent infection in an individual patient

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
BIORE	Bioinformatics Reanalysis	No, (Bill Only)	No
RMALD	Ident by MALDI-TOF mass spec	No, (Bill Only)	No
ISAE	Aerobe Ident by Sequencing	No, (Bill Only)	No
REFID	Additional Identification Procedure	No, (Bill Only)	No
RMALA	Id MALDI-TOF Mass Spec Anaerobe	No, (Bill Only)	No
ANAID	Anaerobe Ident	No, (Bill Only)	No
ISAN	Anaerobe Ident by Sequencing	No, (Bill Only)	No

Testing Algorithm

Organism identification is required prior to testing. All bacteria submitted will be tested. Organism identifications that are incorrect or incomplete may result in no results at final analysis. Laboratory may perform matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) or other testing as listed in Reflex Tests to confirm identification and report this finding at an additional charge.

When reanalysis of previously submitted isolates for comparison to new isolates is requested, bioinformatics reanalysis will be added by Mayo Clinic Laboratories. Original patient submission information (names and order numbers) must be provided.

Special Instructions

- Infectious Specimen Shipping Guidelines

Method Name

Whole Genome Sequencing

NY State Available

Yes

Specimen

Specimen Type
Varies

Ordering Guidance
Only the following bacteria are tested by this method: *Acinetobacter baumannii*, *Campylobacter jejuni/coli*, *Clostridioides difficile* (formerly *Clostridium difficile*), *Cutibacterium* (*Propionibacterium*) *acnes*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, and *Streptococcus pyogenes.*

Additional Testing Requirements
If uncertain of organism identification, concomitantly order IDENT / Organism Referred for Identification, Aerobic Bacteria or ANIDE / Organism Referred for Identification, Anaerobic Bacteria.

Shipping Instructions
1. For shipping information see Infectious Specimen Shipping Guidelines.
2. Place isolates in a large infectious container and label as an etiologic agent/infectious substance.
3. Place all isolates (all patients and/or sites to be compared) submitted for whole genome sequencing together in 1 large bag and send in the same shipping container. This is necessary for comparison of isolates by this method.

Necessary Information
1. Organism identification and specimen source (anatomical body site) **are required.**
2. *Acinetobacter baumannii*: Isolate must be *A baumannii*. Identifications of *A baumannii* complex and *A baumannii/calcoaceticus* complex are not acceptable.
3. *Enterobacter cloacae*: Isolate must be a member of the *E cloacae* complex (ie, *Enterobacter asburiae, Enterobacter bugandensis*, *E cloacae*, *E cloacae subspecies cloacae*, *E cloacae* subspecies *dissolvens*, *Enterobacter hormaechei* subspecies *hormaechei*, *Enterobacter kobei*, *Enterobacter ludwigii*, *Enterobacter xiangfangensis*).
4. *Klebsiella pneumoniae*: Isolate must be a member of the *K pneumoniae* complex (ie, *K pneumoniae*, *K pneumoniae* subspecies *pneumoniae*, *K pneumoniae* subspecies *ozaenae*, or *K pneumoniae* subspecies *rhinoscleromatis*).
5. *Staphylococcus aureus*: Isolate must indicate methicillin resistant *S aureus* (MRSA) or Methicillin Susceptible *S aureus* (MSSA).
6. An email address registered on the Mayo Clinic Laboratories website is required for report delivery.

Specimen Required
Aerobic Bacteria
Preferred:
Specimen Type: Bacterial isolate swab
Supplies:
E-swab (T853)
Infectious Container, Large (T146)
Container/Tube:

Preferred: E-Swab collection and transport system
Acceptable: Flocked swab and 1-mL liquid Amies transport medium in 12 x 80 mm tube.
Collection Instructions:
1. Perform isolation of infecting bacteria (must be *Acinetobacter baumannii*, *Campylobacter jejuni/coli*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus lugdunensis*, *Streptococcus agalactiae*, or *Streptococcus pyogenes)*.
2. Utilize the flocked swab to obtain an adequate sample of pure cultured isolate. **Do not submit mixed cultures**.
3. Place swab into the transport system containing 1-mL liquid Amies transport medium.
4. If needed, break off end of swab and close the transport tube.
5. Place the transport system into the secondary infectious container for shipment.
6. Each isolate must be submitted under a separate order.

Acceptable:
Specimen Type: Pure culture of organism from source cultured
Supplies: Infectious Container, Large (T146)
Container/Tube: Agar slant or other appropriate media
Collection Instructions:
1. Perform isolation of bacterial isolate.
2. Organism must be in pure culture, actively growing. **Do not submit mixed cultures**.
3. Place the agar slant or other appropriate media into the secondary infectious container for shipment
4. Each isolate must be submitted under a separate order.

Anaerobic Bacteria
Supplies:
Anaerobe Transport Tube (T588)
Infectious Container, Large (T146)
Container/Tube:
Preferred: Anaerobic transport tube
Acceptable: Thioglycollate broth or any other suitable anaerobic transport system
Specimen Volume: Isolates in separate transport tubes in pure culture
Collection Instructions:
1. Isolate the bacteria (must be *Clostridioides difficile* or *Cutibacterium* [*Propionibacterium*] *acnes*).
2. **Do not** submit growth directly from a CHROMagar plate; subculture to anaerobic media to obtain pure isolate and confirm identification prior to submission.
3. Bacterial isolate must be in pure culture, actively growing. **Do not submit mixed cultures.**
4. Each isolate must be submitted under a separate order.

Forms

If not ordering electronically, complete, print, and send a Microbiology Test Request (T244) with the specimen.

Reject Due To

Agar plate	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Ambient (preferred)		
	Refrigerated		

Clinical & Interpretive

Clinical Information

Bacterial strain typing may be useful for determining strain relatedness in the setting of possible nosocomial transmission or community outbreaks. Serial isolates obtained from the same patient may be typed to assess similarity. Typing may allow discrimination of 2 or more isolates of the same species, which can inform recognition of an outbreak, nosocomial transmission, or identify a potential source of infection in an individual patient.

Pulse-field gel electrophoresis (PFGE) has traditionally been used for strain typing but does not always discriminate between different bacterial strains (eg, 2 genetically dissimilar strains may have indistinguishable PFGE patterns). Whole genome sequencing offers a higher level of resolution of genetic relatedness of strains than PFGE does.

Reference Values

Reported as isolates are "related," "possibly related," or "unrelated."

Interpretation

The genomic sequence of individual isolates will be determined and compared to the genomic sequences of the other co-submitted isolates. The report will indicate the degree of relatedness between the isolates. A link to the interpretive report will be sent to the registered email address provided by the client.

Cautions

Genomic relatedness does not prove that tested bacterial isolates are epidemiologically related. Establishment of an epidemiologic relationship requires correlation with clinical and epidemiological information. An epidemiological link may be ascribed if a common contact can be established between patients with bacterial strains demonstrating a high degree of genetic relatedness. Similar to other types of stain typing (eg, pulse-field gel electrophoresis), sequence-based strain typing is most powerful in demonstrating genetic dissimilarity, decreasing the likelihood that the strains share a similar source.

Clinical Reference

1. Cunningham SA, Chia N, Jeraldo PR, et al. Comparison of whole-genome sequencing methods for analysis of three methicillin-resistant Staphylococcus aureus outbreaks. J Clin Microbiol. 2017;55(6):1946-1953. doi;10.1128/JCM.00029-17

2. Park KH, Greenwood-Quaintance KE, Uhl JR, et al. Molecular epidemiology of Staphylococcus aureus bacteremia in a single large Minnesota medical center in 2015 as assessed using MLST, core genome MLST and spa typing. PLoS ONE. 2017;12(6):e0179003. doi:10.1371/journal.pone.0179003

3. Madigan T, Cunningham SA, Patel R, et al. Whole-genome sequencing for methicillin-resistant Staphylococcus aureus (MRSA) outbreak investigation in a neonatal intensive care unit. Infect Control Hosp Epidemiol. 2018; 39(12):1412-1418. doi:10.1017/ice.2018.239

4. Trees E, Fei Fan Ng T, MacCannell D, et al. Molecular epidemiology. In: Carroll K, Pfaller M, eds. Manual of Clinical Microbiology. 12th ed. ASM Press; 2019:167-196

Performance

Method Description
Following whole genome sequencing of each submitted isolate on a MiSeq, sequences will be compared by core genome multilocus sequence typing analysis using SeqSphere+ Software (Ridom GmbH. Allelic profiles will be used to generate a phylogenetic tree showing isolate relatedness.(Leopold SR, Goering RV, Witten A, et al: Bacterial whole-genome sequencing revisited: portable, scalable, and standardized analysis for typing and detection of virulence and antibiotic resistance genes. J Clin Microbiol. 2014;52[7]:2365-2370)

PDF Report
No

Day(s) Performed
Once per week

Report Available
30 to 40 days

Specimen Retention Time
1 month

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

Test Classification
This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
0010U-Bacterial Typing, Whole Genome Seq
87900-Bioinformatics Reanalysis (if appropriate)

87077-Ident by MALDI-TOF mass spec (if appropriate)
87153-Aerobe ident by sequencing (if appropriate)
87077-Additional identification procedure (if appropriate)
87076-Id MALDI-TOF mass spec anaerobe (if appropriate)
87076-Anaerobe Ident (if appropriate)
87153-Anaerobe ident by sequencing (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
BTWGS	Bacterial Typing, Whole Genome Seq	90246-0

Result ID	Test Result Name	Result LOINC® Value
BTWGS	Bacterial Typing, Whole Genome Seq	90246-0