TEST ID: BTWGS
BACTERIAL TYPING BY WHOLE GENOME SEQUENCING

USEFUL FOR

- Aids in investigation of a potential outbreak by a single bacterial species
- May assist in identification of recurrent infection in an individual patient

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 does PFGE.

INTERPRETATION

The genomic sequence of individual isolates will be determined and compared to the genomic sequences of the other cosubmitted isolates. The report will indicate the degree of relatedness between the isolates. Results will be faxed to the client.

CLINICAL REFERENCE

2. Leopold SR: Bacterial whole-genome sequencing revisited: portable, scalable, and standardized analysis for typing and detection of virulence and antibiotic resistance genes. 2014;52:2365-2370

REFERENCE VALUES

Not applicable

ANALYTIC TIME

10 days