

Patient: [REDACTED]
DOB: Not Provided Age: N/A Sex: U
Patient Identifiers: [REDACTED]
[REDACTED]
Visit Number (FIN): [REDACTED]

Client: [REDACTED]
Physician: [REDACTED]

ARUP Test Code: 3002528
Collection Date: 11/22/2023
Received in lab: 11/23/2023
Completion Date: 12/12/2023

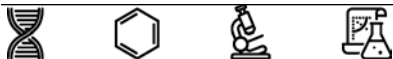
COMMENT:

Clinical Information: 3 isolates of *Stenotrophomonas maltophilia* compared.

1,23-320-06888
2,23-320-10330
3,23-320-09538

STRAIN RELATIONSHIPS:

GROUPS OR STRAINS NOT RELATED TO OTHER ISOLATES:
23-320-06888, 23-320-09538, 23-320-10330

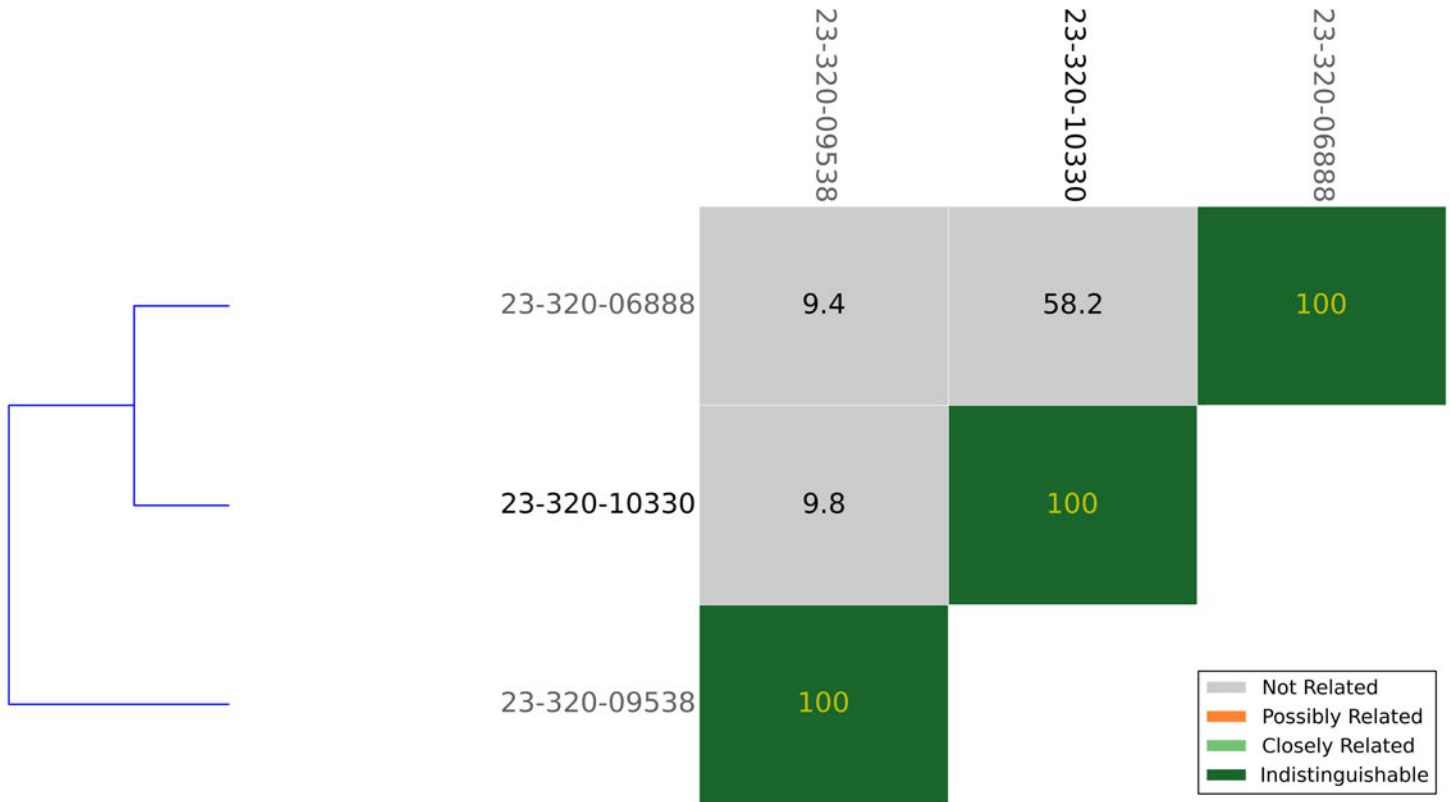


Patient: [REDACTED]
ARUP Accession: 23-326-400526

Bacterial Strain Typing by Next Generation Sequencing

Patient: [REDACTED] | Date of Birth: Not Provided | Sex: U | Physician: [REDACTED]
Patient Identifiers: [REDACTED] | Visit Number (FIN): [REDACTED]

Dendrogram and Identity Matrix



INTERPRETIVE DATA: Bacterial Strain Typing by NGS

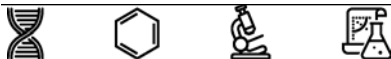
Method

Whole Genome Sequencing (WGS) is performed using Ion Torrent sequencing chemistry. Reference-free pairwise comparisons are performed using short, overlapping sequence matching (kmer) analysis. Relationships are determined by the percent of kmers that match between isolate pairs.

Interpretation

Predicted relatedness is based on the total number of differences between the isolates, applying the thresholds shown in the table. The dendrogram and relationship matrix (see enhanced report) illustrate isolate relatedness. Interpretation of strain relatedness should be performed by an investigator knowledgeable about whole genome strain typing procedures and based on all available epidemiological evidence. Inferred relationships based on any strain typing method should not be used for individual patient management.

WGS Strain Typing provides substantial improvements in resolution and reproducibility when compared to pulsed-field gel electrophoresis (PFGE) and can be performed on a broad range of microorganisms. Test was validated for *Staphylococcus*, *Acinetobacter*, *Enterococcus*, *Escherichia*, *Pseudomonas*, *Stenotrophomonas*, *Serratia*, and *Klebsiella* species.



Patient: [REDACTED]
ARUP Accession: 23-326-400526

Bacterial Strain Typing by Next Generation Sequencing

Patient: [REDACTED] | Date of Birth: Not Provided | Sex: U | Physician: [REDACTED]
Patient Identifiers: [REDACTED] | Visit Number (FIN): [REDACTED]

Category	Kmer Identity	Epidemiological Interpretation
Indistinguishable	≥ 99.9	Part of the outbreak
Closely related	99.8 - 99.2	Probably part of the outbreak
Possibly related	99.1 - 95.0	Possibly part of the outbreak
Unrelated	< 95	Not part of the outbreak

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

