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Genomic Strain Typing Report (NGSTYP)

Client Information

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Isolate Manifest

Accession	Name	Description	Collect Date
X1234	Patient A	Nares	01-20-2020
X1235	Patient B	Nares	01-25-2020
X1236	Patient C	Nares	02-20-2020
X1237	Patient D	Blood	12-27-2019
X1238	Patient E	Nares	01-27-2020
X1239	Patient F	Blood	01-26-2020
X1240	Patient G	Nares	01-22-2020

Results

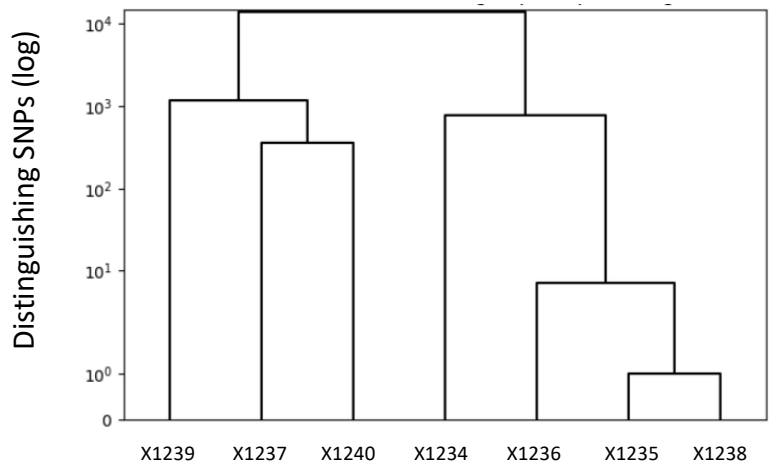
Isolates **X1238**, **X1235 and X1236** are closely related to one another:
Isolates **X1238** and **X1235** differ from each other by 1 SNP
Isolates **X1238** and **X1236** differ from each other by 8 SNPs
Isolates **X1235** and **X1236** differ from each other by 7 SNPs

All remaining isolate pairs differ by at least 358 SNPS and are unrelated to one another. Refer to the following distance table and dendrogram for additional information

Number of distinguishing SNPs:

	X1240	X1238	X1237	X1234	X1239	X1236
X1238	>2000					
X1237	358	2000+				
X1234	>2000	775	>2000			
X1239	1210	>2000	1180	>2000		
X1236	>2000	8	>2000	772	>2000	
X1235	>2000	1	>2000	775	>2000	7

The number of distinguishing SNPs between isolate pairs are approximated as a dendrogram and plotted on a log scale



Methods

Whole genome shotgun sequencing is performed using Illumina sequencing chemistries. Whole genome sequencing provides significantly greater resolution than conventional pulsed-field gel electrophoresis (PFGE) strain typing [1]. Single nucleotide polymorphisms (SNPs) distinguishing isolates from one another are identified using a reference free method which allows pairwise comparison of genomic sequences shared between isolates [2]. The number of distinguishing SNPs are counted in order to estimate the degree of relatedness among isolates. The number of polymorphisms which distinguish isolate pairs is proportional to their time of divergence from a common ancestor.

Additional Test Information

It is recommended that the results of strain characterization of epidemiologically associated bacteria be interpreted by an investigator familiar with the outbreak investigation and knowledgeable about the limitations of typing procedures. There are currently no standardized guidelines for interpretation of whole genome sequencing data for epidemiology investigations, although a working threshold of >50 SNPs has been defined for unrelated isolates (https://www.ncbi.nlm.nih.gov/pathogens/about/). Relationships among isolates should be considered with respect to the biology of the organism being analyzed and the number of genomic differences that distinguish among isolates. Assay is not intended to (1) identify all genomic differences distinguishing isolates, (2) detect genomic differences resulting from structural variation, gene acquisition or loss, gain or loss of extrachromosomal elements such as plasmids, or large sequence insertions or deletions. The results from this assay should be correlated with temporal, spatial, and clinical information. This test was developed by the Department of Laboratory Medicine, University of Washington.

References

1 Salipante, S. J. *et al.* Application of whole-genome sequencing for bacterial strain typing in molecular epidemiology. *J Clin Microbiol* **53**, 1072-1079, doi:10.1128/JCM.03385-14 (2015).

2 Uricaru, R. *et al.* Reference-free detection of isolated SNPs. *Nucleic Acids Res* **43**, e11, doi:10.1093/nar/gku1187 (2015).