Outbreak analysis of Shigella sonnei using **1928 SNP analysis**

A white paper describing
how to use the 1928 platform
for outbreak analysis

www.**1928diagnostics**.com

Introduction

1928 Diagnostics offers a platform for analysis of NGS sequenced bacterial genome data for resistance predictions and outbreak surveillance in a clinical routine setting.

For outbreak analysis, two different methods can be used: cgMLST and SNP analysis.

For cgMLST, 1928 Diagnostics support a wide range of bacteria through predefined and manually curated schemas. In this whitepaper, we are looking at data from a previously published study and re-create the phylogeny presented in the article, by performing SNP analysis.

Article and raw data

The Shigella sonnei outbreak in focus in this whitepaper is:

First report of sexually transmitted multi-drug resistant Shigella sonnei infections in Switzerland, investigated by whole genome sequencing

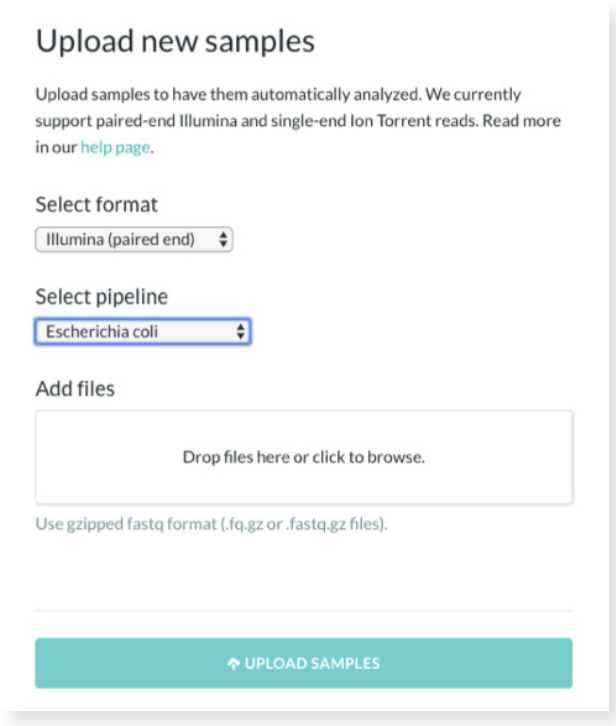
Hinic Vladimira, Seth-Smith Helena, Stöckle Marcel, Goldenberger Daniel, Egli Adrian

doi:10.4414/smw.2018.14645
Swiss Med Wkly. 2018;148:w14645

The article describes the first report of 3 cases of sexually acquired Shigella sonnei infections in Switzerland. The data from the article can be found in the Bioprojects PRJEB23646 and PRJNA315192.

Data analysis

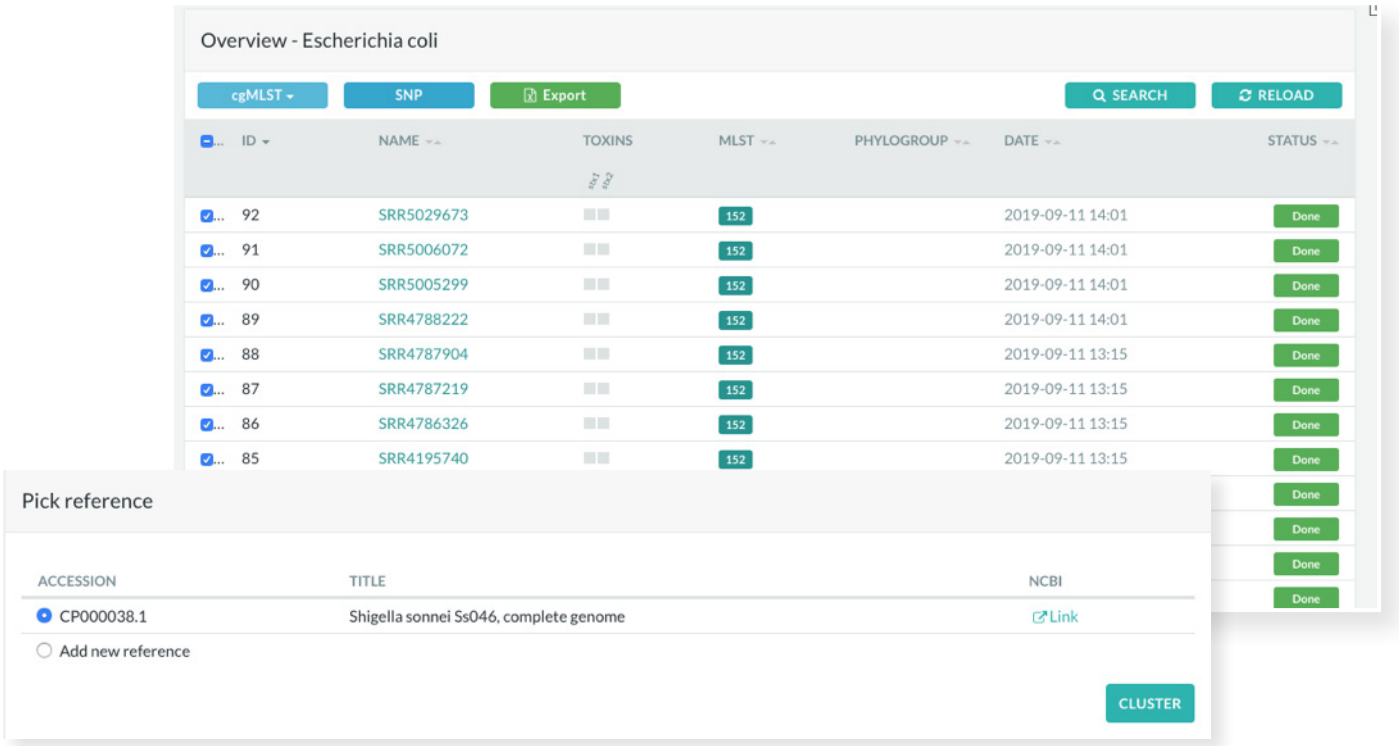
The raw FASTQ files for each sample from the Bioprojects were uploaded to the 1928 platform using the Escherichia coli pipeline. The analysis starts automatically once the upload is complete and will perform de-novo assembly as well as identifying resistance markers.



Once the analysis is done, the sample index shows an overview:

One of the samples failed to pass the 1928 Quality Control with an estimated coverage depth of 24x and was subsequently excluded from further analysis. This sample is shown in red in the screenshot above, sample ID SRR3530422.

To perform the SNP analysis – the sample set is selected, and the SNP button is pressed.

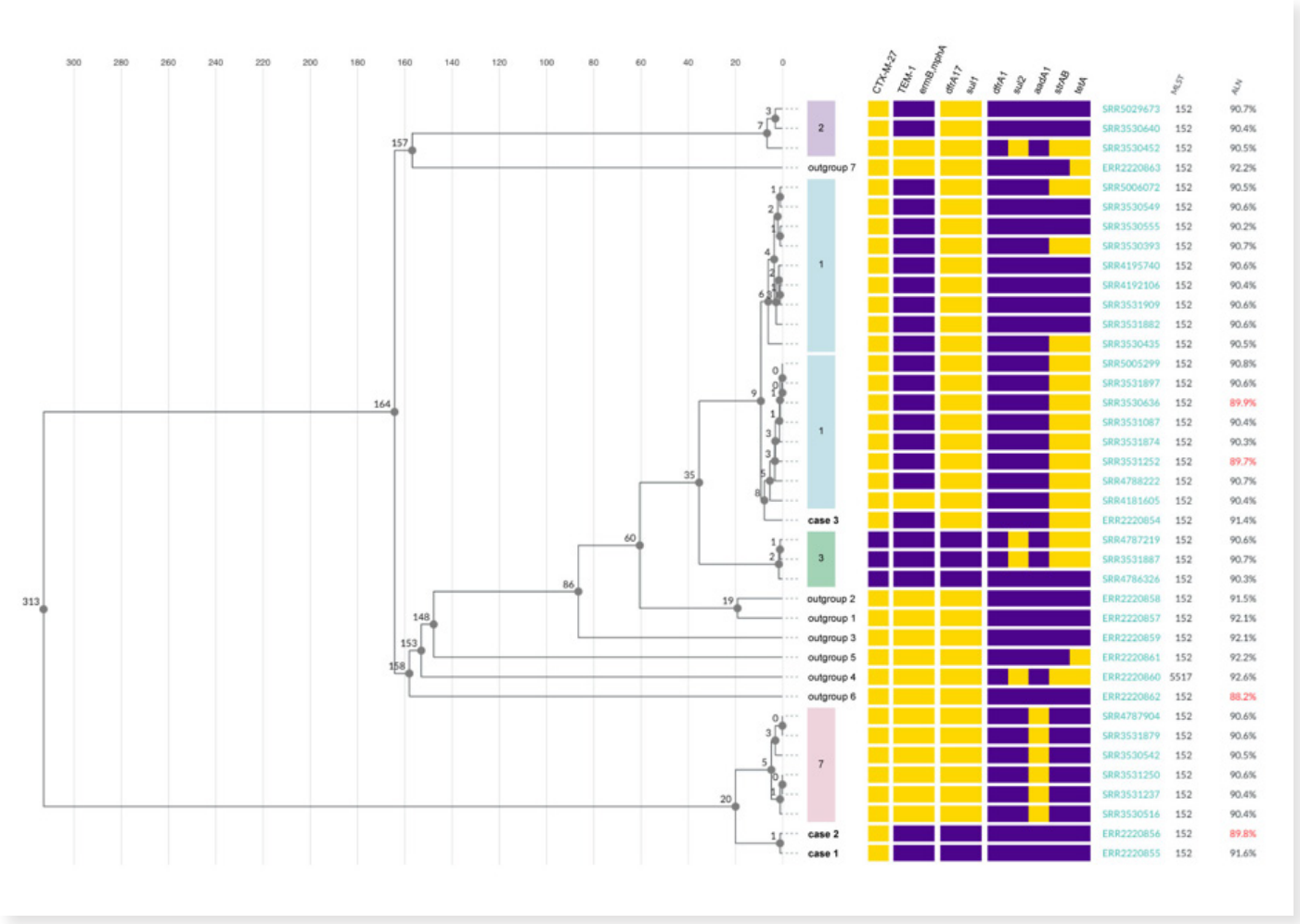


The SNP analysis pipeline is based on read alignment against a reference, and in the analysis, the same reference genome was selected as in the original article, namely the Shigella sonnei Ss064, NCBI accession number CP000038. The dendrogram tree generated from the SNP output is created from the distance matrix using the UPGMA algorithm.

In addition, the resistance genes found in the samples were exported to an Excel document, where the presence of genes were combined into a presence/absence table and overlayed on the dendrogram, together with the UK MSM cluster numbering.

Results

The 1928 SNP analysis is able to re-create the phylogeny from the original article with great detail. The topology of the original tree is preserved, including the two cluster groups within the UK MSM cluster 1.



Conclusions

SNP analysis is a powerful tool for outbreak surveillance to use as a complement to cgMLST, for pathogens where no cgMLST schemas exist, or where additional resolution might be needed.

To learn more about the 1928 platform visit

www.1928diagnostics.com

For resources about using the platform and other articles:
https://1928diagnostics.com/product_resources/index.html

Scientific support

Need to complete your research with a nice-looking typing schema or an AMR profiling? 1928 offers to open the platform for research samples. Just connect with us at:
support@1928diagnostics.com

Schedule a meeting or book a demo?
Email us at: **sales@1928diagnostics.com**

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