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Oropharyngeal Gonorrhea in Absence of Urogenital Gonorrhea in Sexual Network of Male and Female Participants, Australia, 2018

Appendix

Supplementary Methods

DNA Extraction and Whole-Genome Sequencing

DNA extraction and whole-genome sequencing were performed at the Microbiological Diagnostic Unit Public Health Laboratory at the University of Melbourne (Carlton, Victoria, Australia). Genomic DNA was isolated from a single colony by using the QIAsymphony SP platform (QIAGEN, https://www.qiagen.com). Whole-genome sequencing was performed using the Illumina (https://www.illumina.com) NextSeq platform with 150-bp paired-end reads. All sequencing reads are available on the National Center for Biotechnology's Sequence Read Archive under BioProject no. PRJNA520805.

Bioinformatic Analysis

We analyzed sequences with Snippy version 4 (Seeman T, https://github.com/tseemann/snippy). In brief, reads were trimmed to remove adaptor sequences and low-quality bases with Trimmomatic (*1*), and Kraken (v0.10.5-β) was used to investigate for contamination (*2*). Reads were aligned to the NCCP11945 reference genome (*3*) with snippy v4. De novo assemblies were also performed with SPAdes (v.3.9.0) (*4*), as part of the Nullarbor pipeline, with genes annotated by using Prokka (v.1.12-β, Seemann T, https://github.com/tseemann/prokka). *Neisseria gonorrhoeae* multiantigen sequence type results were inferred in silico by using NGMASTER (*5*).

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