Draft Genome Sequence of a Dominant, Multidrug-Resistant *Neisseria gonorrhoeae* Strain, TCDC-NG08107, from a Sexual Group at High Risk of Acquiring Human Immunodeficiency Virus Infection and Syphilis

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*Neisseria gonorrhoeae* infection is the second major cause of sexually transmitted diseases worldwide. Development of resistance to multiple classes of antimicrobials in *N. gonorrhoeae* has compromised treatment and disease control. Herein, we report the availability of the draft genome sequence of a multidrug-resistant *N. gonorrhoeae* isolate, TCDC-NG08107, which spread in groups of men who have sex with men (MSM) in Taiwan.

The *Neisseria gonorrhoeae* isolate TCDC-NG08107 was obtained from a 17-year-old male patient in May 2008. The isolate was identified as sequence types ST2253 and ST7363 by multiantigen sequence typing (NG-MAST) and multilocus sequence typing (MLST), respectively. NG-MAST ST2253 is closely related to a worldwide-prevalent ST835 clone (9), and furthermore, MLST ST7363 has been reported to be a dominant ST with reduced susceptibility to cefixime in Japan (6). Interestingly, TCDC-NG08107 belongs to a dominant NG-MAST *N. gonorrhoeae* sequence type prevalent in groups of men who have sex with men (MSM), with an 11.1% syphilis and 38.9% HIV coinfection rate during 2006 to 2009 in Taiwan. The isolate was resistant to cefixime (MIC, 0.5 mg/liter) and had reduced susceptibility to ceftriaxone (0.19 mg/liter) (10).

The genome of TCDC-NG08107 was sequenced with an Illumina genome analyzer II. The sequence coverage was about 700×. Automated DNA sequencing chromatograms were analyzed by the CLC bio software package. In particular, the order of 180 contigs was predicted by comparison with the chromosome sequences of *N. gonorrhoeae* FA1090 (GenBank accession no. AE004969) and NCCP11945 (GenBank accession no. CP001050) (1) and then confirmed by optical mapping (8). The length of the draft sequence of the TCDC-NG08107 circular chromosome is 2,154,835 bp. By MUMmer (5), the overall chromosome sequence identities are 94.5 and 97.7% to FA1090 and NCCP11945, respectively. We also isolated a 39,054-bp circular plasmid, pNGTCDC08107, whose sequence was ~3 kb shorter than but nearly identical to that of pEP5289 (GenBank accession no. GU479466), which has a Dutch-type backbone (7).

In the TCDC-NG08107 genome, the most abundant repeat type is the DNA uptake sequence (5′-GCCGTTCTGAA-3′), comprising 1,931 copies (FA1090, 1,965 copies; and NCCP11945, 1,966 copies). Open reading frame (ORF) prediction and functional assignment of genes were performed with GLIMMER (2), BioNumerics software (version 6.5; Applied Maths), and BLAST. The chromosome and the plasmid have 2,151 and 45 predicted ORFs, respectively. In addition, there are 46 tRNAs and 4 copies between the *N. gonorrhoeae* genomes.

The deduced or putative protein sequence accession numbers. The draft genome sequence of *N. gonorrhoeae* TCDC-NG08107 has been assigned GenBank accession no. CP002440 and CP002441.

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