

Neisseria meningitidis Serogroup W135, China

Technical Appendix

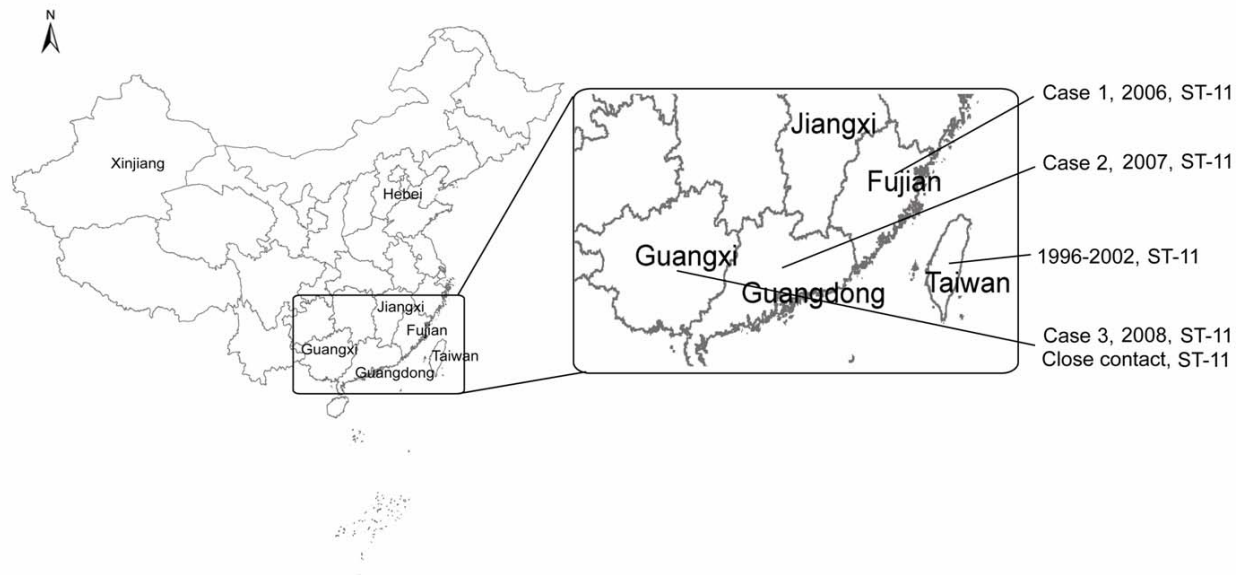


Figure 1. Distribution and molecular characterization of *Neisseria meningitidis* W135 isolates from 3 patients, People's Republic of China, and from Taiwan. ST, sequence type.

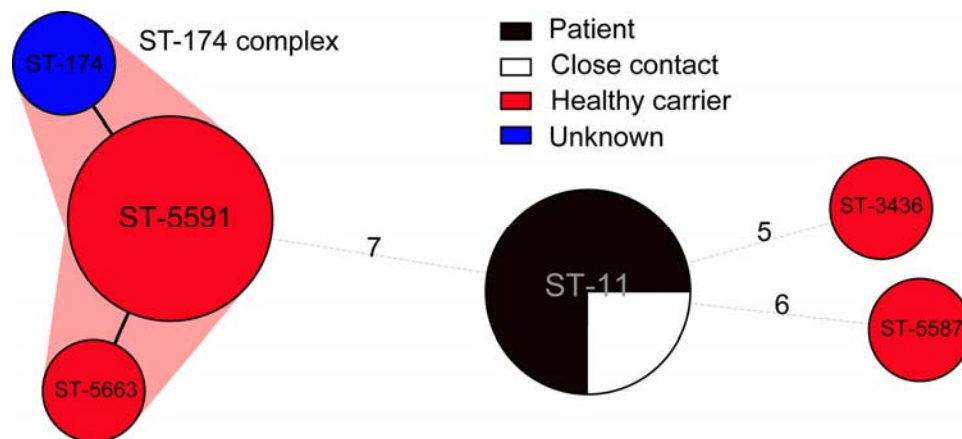


Figure 2. Distribution and molecular characterization of *Neisseria meningitidis* W135 isolates from case-patients, People's Republic of China. Minimum spanning tree of 12 W135 isolates typed by multilocus

sequence typing (MLST). Clustering of MLST profiles was performed by using a categorical coefficient. MLST types are indicated by circles. The size of each circle is proportional to the number of isolates with this particular type. Numbers (5, 6, and 7) indicate number of different loci between 2 MLST types. Thick solid lines connect types that differ at 1 locus and thin dotted lines connect types that differ at 2 loci. The color of each circle indicates types that belong to the same complex. MLST complexes were assigned if 2 neighboring types did not differ at >1 locus and if ≥ 2 types fulfilled this criterion. ST, sequence type.

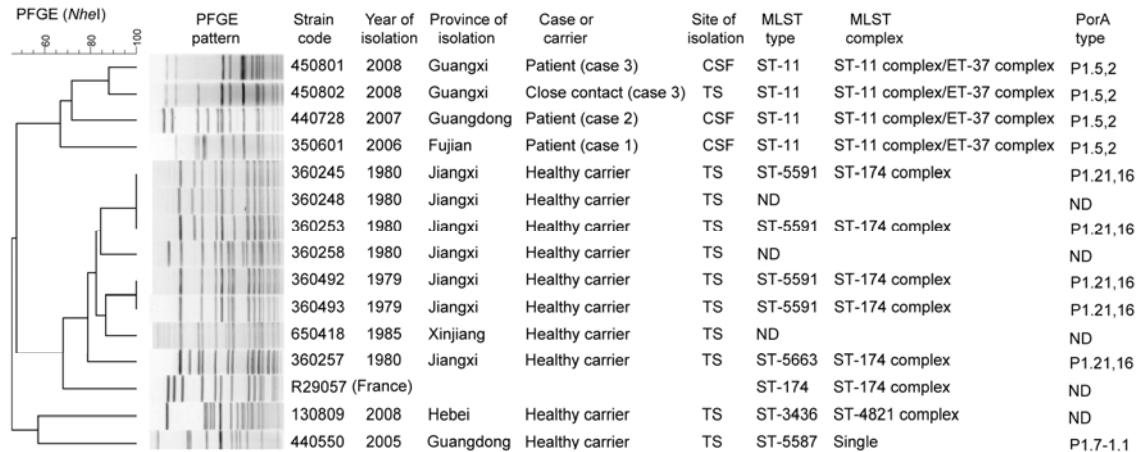


Figure 3. Distribution and molecular characterization of *Neisseria meningitidis* W135 isolates from case-patients, People's Republic of China. Cluster analysis of 15 strains base on pulsed-field gel electrophoresis (PFGE) patterns. Clustering was performed by using the Dice coefficient and a 1.2% optimization setting. The dendrogram was generated by using the unweighted pair group method using averages. MLST, multilocus sequence type; PorA, outer membrane protein; CSF, cerebrospinal fluid; ST, sequence type; TS, throat swab; ND, not determined.