Streptococcus pneumoniae Serotype 6C: an Intra- and Interclonal Complex Comparison

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We report the annotated draft genome sequences of four serotype 6C Streptococcus pneumoniae isolates of differing genetic backgrounds. Serotype 6C isolates are increasing in prevalence and becoming progressively more resistant to antibiotics. As a result, these strains are likely to become more important in the near future.

Streptococcus pneumoniae is a leading cause of meningitis, pneumonia, and otitis media globally, in addition to asymptomatically colonizing the upper respiratory tract of nearly half of all healthy children (2, 11, 16). Pneumococcal isolates express one of more than 90 distinct capsular polysaccharides (13). The introduction of a heptavalent pneumococcal conjugate vaccine (PCV7) has led to a decrease in invasive disease by isolates that express one of the targeted vaccine serotypes (14). However, during this period, nonvaccine serotypes have increased in prevalence (3, 9, 10), and novel serotypes such as 6C have recently been identified (13). The prevalence of serotype 6C isolates has increased in the United States over recent years (4, 12). Moreover, the proportion of serotype 6C isolates that are nonsusceptible to penicillin has also increased (8). While Gertz et al. (8) have determined several multilocus clonal complex pairwise comparisons revealed a mean of 136 gene differences. The genomes contained between 34 and 39 tRNA genes, comprising all amino acids. Further analysis of these genomes is currently being performed to determine genetic factors unique to these serotype 6C isolates.

Nucleotide sequence accession numbers. Whole-genome shotgun projects for each of the four isolates have been deposited at DDBJ/EMBL/GenBank under accession numbers AFBY00000000, AFBZ00000000, AFCB00000000, and AFBZ01000000, respectively.

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