Figure S1: Neighbor-joining phylogenetic tree based on the alignment of **cps**A-**cps**D regions of the 35 reference strains and 78 isolates used in the study. The unrooted tree was constructed using the nucleotide sequence from the start of the coding region of **cps**A to the end of the coding region of **cps**D. The confidence values were obtained using 1,000 nonparametric bootstrap replicates. 35 serotype reference strains are marked in blue. 78 isolates are marked in red. Bar, sequence dissimilarity.