



Fig. 4. Phylogenetic trees generated by the neighbor-joining method for the four regions sequenced. F, Flexneri; B, *Boydii*; D, *Dysenteriae*; SS, *Sonnei*, followed by the serotype number. The three major clusters are identified. Bootstrap values are percentages of 1,000 replications and are indicated at the nodes. LT2 is used as the outgroup.