Figure. Evolutionary relationships of 22 taxa
The evolutionary history was inferred using the Minimum Evolution method [1]. The optimal tree with the sum of branch length = 1.09029457 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method [3] and are in the units of the number of base substitutions per site. The ME tree was searched using the Close-Neighbor-Interchange (CNI) algorithm [4] at a search level of 1. The Neighbor-joining algorithm [5] was used to generate the initial tree. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing alignment gaps and missing data were eliminated only in pairwise sequence comparisons (Pairwise deletion option). There were a total of 1137 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 [6].