Phylogenetic trees were constructed with MEGA 7.0.26. Percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to branches. Numbers on the branches indicate bootstrap values obtained from a maximum likelihood analysis. The scale bar shows the estimated number of nucleotide substitutions per site.

The data from the present study were analyzed using the F-statistic approach of Nei et al. (1975) for assessing the genetic diversity. The genetic identity and distance (Nei 1978) were calculated using the software package POPGENE (Yeh et al. 1994). The genetic diversity (Hs) and Shannon diversity index (H′) were estimated using the formulae of Nei (1978). The statistical significance of the differences among the population groups was determined by the F-statistic analysis and AMOVA (analysis of molecular variance) analysis was performed by the software package ARLEQUIN (Excoffier et al. 1992). Genetic distance among the isolates was constructed using the Genetic Distance Matrix using the Nei’s unbiased genetic distances (Nei 1978). A UPGMA tree was constructed using the program TreeView. The images were prepared with the aid of Adobe Photoshop 6.0.