

Abstract

Like all other ciliates, the genus *Paramecium* is considered to be of fundamental importance in aquatic ecosystems. These are being used in water quality assessment and the determination of saprobic levels. Based on the indicator values of representative species of *Paramecium*, the water quality of a particular water body may be determined. Due to these and other cytological and molecular applications, an unambiguous identification of these unicellular eukaryotes is very essential. Current knowledge of the variation and diversification of the species of this genus is limited especially in Asian countries. It is therefore need of the time to explore ecological diversity of *Paramecium* species in the local environment. For this purpose, eight waste water samples from four different localities (Lahore, Kasur, Sheikhpura and Mansehra) were collected. *Paramecium* species were isolated from these samples and designated as FT1, FT3, FT4, FT5, FT6, FT7, FT8 and FT9. The small subunit rRNA (SSrRNA) gene of all eight strains were amplified, cloned and get sequenced. Phylogenetic comparison of the sequences of these strains with 23 closely related *Paramecium* species from GenBank Database was performed. Three clades representing three different *Paramecium* species were supported by phylogenetic tree. One clade showed maximum similarities (97.8-98.4%) of FT1, FT3, FT5 and FT6 with *P. multimicronucleatum* and second with maximum affinities of FT4 (99.6%) with *P. jenningsi*. However, third one did not support the close association of FT7, FT8, and FT9 with any other species. This group fall at quite distance from other species showing its separate position in the tree, indicating that these species might be the new ones.