

ABSTRACT

Ciliates are known as a taxonomic group of highly diverse, globally distributed and intensively studied organisms. Being grazer of bacteria, harmful algal bloom species, smaller protist and primary source of metazoans, ciliates significantly influence population dynamics along with nutrient cycling within freshwater ecosystem. Objective of the current study was to investigate the dominant genera of ciliates present in Jallo Lake on the basis of morphological as well as molecular basis.

Sampling was done from April, 2017 to September, 2017. Samples taken along the littoral zone were found rich in diversity as well as in abundance when compared to the samples collected from limnetic zone. *Tetrahymena*, *Stylonychia* and *Paramecium* were found in multiple samples and identified by their shape, size and movement. *Tetrahymena* AR1 was recognized by their pear shaped body (pointed at one end while broader at other), presence of oral groove toward pointed end, centrally positioned nucleus and uniform lining of cilia. *Stylonychia* AR3 were recognized by their elongated oval shape dorso-ventrally flattened body and presence of distinct frontal and caudal cirri. *Paramecium* AR6 and AR12 were recognized by their characteristic shape and they differ in size (former being larger than later).

Isolates were grown in wheat grain, bold basal salt and modified neff's media at optimum temperature ($27\pm 2^{\circ}\text{C}$) and optimum pH (pH 7.5), to evaluate their growth rate. The order of growth rate observed as; Neff's medium > Bold-basal salt medium > wheat grain medium.

Phylogenetic analysis of all three samples based on 18srRNA gene sequence by constructing phylogenetic tree using neighbour-Joining method shows that *Stylonychia* AR3, *Paramecium* AR6 and AR12 have close evolutionary relationship with; *Stylonychia pustulata*, *Paramecium multimicronucleatum* and *Paramecium cilkinsi*, respectively.