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Characterization of ciliate diversity in bromeliad tank waters from the Brazilian Atlantic Forest

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Abstract

Bromeliads are a diverse group of plants that includes many species whose individuals are capable of retaining water, forming habitats called phytotelmata. These habitats harbor a diversity of organisms including prokaryotes, unicellular eukaryotes, metazoans, and fungi. Among single-celled eukaryotic organisms, ciliates are generally the most abundant. In the present study, we used Illumina DNA sequencing to survey the eukaryotic communities, especially ciliates, inhabiting the tanks of the bromeliads *Aechmea gamosepala* and *Vriesea platynema* in the Atlantic Forest of southern Brazil. Filtered sequences were clustered into distinct OTUs using a 99% identity threshold, and then assigned to phylum and genus using a BLAST-based approach (implemented in QIIME) and the SILVA reference database. Both bromeliad species harbored very diverse eukaryotic communities, with Arthropoda and Ciliophora showing the highest abundance (as estimated by the number of sequence reads). The ciliate genus *Tetrahymena* was the most abundant among single-celled organisms, followed by apicomplexan gregarines and