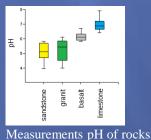


Phylogenetic relationships among *Klebsormidium* genotypes obtained in this study. The phylogenetic tree was inferred based on a Bayesian analysis of *rbcL* sequences. Values at the nodes indicate statistical support estimated by three methods: MP (left), ML bootstrap (middle), and MrBayes posterior node probability (right).

a-d: Bar chart graphs with standard dev.



Our results thus not only demonstrate a strong ecological differentiation of *Klebsormidium* clades, but also point to the existence of ecophysiological differences among the particular genotypes, even growing on the same habitats.

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