

Abstract

16S is a powerful genetic tool commonly used to evaluate the biodiversity of aquatic ecosystems. In this study, we used 16S analysis to evaluate the composition of heterotrophic bacteria in three northern peatlands, including a rich, moderate-rich and poor fen. Ordination analysis of the 16S results demonstrated that bacterial communities were distinct among the three peatlands. The poor fen showed high levels of denitrifying *Proteobacteria* (63.7%), specifically, the presence of the family *Pseudomonadaceae* (16.4%). Unlike the poor and rich fens, the moderate-rich fen showed high levels of *Firmicutes* (23.6%), particularly *Lachnospiraceae* (5.5%) and *Ruminococcaceae* (6.2%) and an unknown *Clostridiales* family (9.3%).

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