Dadheech, P.K., Glockner, G., Casper, P., Kotut, K., Mazzoni, C.J., Mbedi, S. & Krienitz, L. 2013. Cyanobacterial diversity in the hot spring, pelagic and benthic habitats of a tropical soda lake. FEMS Microbiol Ecol 85: 389 – 401.

Abstract

Hot springs and saline-alkaline lakes of East Africa are extreme habitats regarding temperature, or salinity and pH, respectively. This study examines whether divergent habitats of Lake Bogoria, Kenya, impacts cyanobacterial community structure. Samples from the hot springs, pelagic zone and sediment were analysed by light microscopy, multilocus 454-amplicons sequencing and metagenomics to compare the cyanobacterial diversity. Most of the phylogenetic lineages of Cyanobacteria occurred exclusively in the Bogoria hot springs suggesting a high degree of endemism. The prevalent phylotypes were mainly members of the Oscillatoriales (Leptolyngbya, Spirulina, Oscillatoria-like and Planktothricoides). The Chroococcales were represented by different clades of Synechococcus but not a single phylotype clustered with any of the lineages described earlier from different continents. In contrast, we found that the pelagic zone and the sediments were inhabited by only a few taxa, dominated by Arthrospira and Anabaenopsis. Arthrospira, the main food base of Lesser Flamingo, was detected in all three habitats by amplicons pyrosequencing, indicating its resilience and key role as a primary producer. Despite the close connection between the three habitats studied, the cyanobacterial communities in the hot springs and lake differed considerably, suggesting that they are unable to adapt to the extreme conditions of the neighbouring habitat.

KEYWORDS:

Cyanobacteria; Lake Bogoria; hot springs; metagenomics; pyrosequencing; soda lakes