
5 Conclusions

This study showed that:

1. Due to mass developments and production of cyanotoxins the cyanobacteria are those organisms with the most impact on the water quality of Kenyan freshwater and alkaline-saline habitats.
2. The investigated freshwater lakes are dominated by the gas-vacuolate cyanobacteria *Microcystis aeruginosa* or *Anabaena flos-aquae* and *Anabaena discoidea*. The dominance of these cyanobacterial species can be related to high turbidity, high water temperatures and high nutrient concentrations of the water bodies. *Anabaena discoidea* found 2002 in L. Victoria was only known from classical studies, conducted at the beginning of the 20th century in this lake, and is now rediscovered.
3. The studied alkaline-saline lakes were dominated by mass developments of *Arthrospira fusiformis*, *Anabaenopsis abijatae*, *Anabaenopsis arnoldii* and *Anabaena* sp. in different compositions and with changing dominances. *Anabaenopsis abijatae* and *Anabaena* sp. are reported for the first time from Kenyan lakes. This is a clear change from the persistent unialgal blooms of *Arthrospira* which were described in many earlier studies from East African alkaline-saline lakes.
4. The investigation of cyanobacterial mats from hot springs revealed four dominant species: *Phormidium* cf. *terebriformis*, *Spirulina subsalsa*, *Oscillatoria willei*, and *Synechococcus bigranulatus*. Members of the genera *Phormidium* and *Synechococcus* are common cyanobacteria in thermal habitats worldwide. *Spirulina subsalsa* has a wide ecological distribution and is found in thermal springs and in brackish and marine habitats. *Oscillatoria willei* is a pantropical species.
5. Cyanobacterial toxins (hepatotoxic microcystins and neurotoxic anatoxin-a) were for the first time investigated and detected in cyanobacterial samples from Kenyan freshwater and alkaline-saline lakes. The findings of cyanotoxins in hot springs were the first evidence worldwide for these kind of habitats. The cyanotoxins in freshwater and alkaline habitats can have harmful effects on public health, livestock and wildlife. Water from freshwater lakes is used for hygienic purposes and washing by the local human population or as

drinking water for livestock and people. The detection of microcystins and anatoxin-a in gut contents and liver samples of dead Lesser Flamingos (*Phoeniconaias minor*), ingested with cyanobacteria from alkaline lakes and hot springs, suggest that cyanotoxins are a further contributory cause to occurring mass deaths of these birds, beside infectious diseases and poisoning by pesticides and heavy metals.

6. Sources for the toxin production in the investigated Kenyan freshwater habitats are mass developments of *Microcystis aeruginosa*, *Anabaena flos-aquae*, and *Anabaena discoidea*. Several potential sources for the toxins exist in the alkaline water bodies. In *Arthrospira fusiformis* strains from different lakes microcystins and anatoxin-a were found. This is the first evidence of toxicity in strains of *Arthrospira fusiformis*. The cyanobacterial mat community of hot springs is another source of toxins. Further possible producers of cyanotoxins are toxic strains of *Anabaenopsis abijatae*, *Anabaenopsis arnoldii*, and *Anabaena* sp. which have invaded the alkaline-saline lakes.
7. Despite morphological and habitat differences *Arthrospira fusiformis*, *Arthrospira indica*, and *Phormidium* cf. *terebriformis* strains from several Kenyan and Indian water bodies showed high similarities in sequences of the 16S rRNA gene, the internally transcribed spacer region, and phycocyanin operon. The uniform clusters of the *Arthrospira* strains in calculated phylogenetic trees suggest that the strains of *Arthrospira fusiformis* and *Arthrospira indica* are members of the same species. It is likely that the investigated *Phormidium* cf. *terebriformis* strain from L. Nakuru is closely related to the genus *Arthrospira*. The investigated *Phormidium* cf. *terebriformis* strains from L. Nakuru and the hot springs near L. Bogoria had a 16S rDNA sequence similarity of 92% only. The clear separation of *Spirulina* strains from *Arthrospira* strains supports the separation of these two genera. Different salinity tolerance of *Spirulina* strains coincides with low similarities in sequences of 16S rDNA and phycocyanin operon and results in a separation in the *Spirulina* cluster in calculated phylogenetic trees.