

Food resources and microbiome composition of the Lake Tanganyika sardines: A novel approach to investigate structure of overexploited *L. miodon* and *S. tanganicae* stocks.

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Lake Tanganyika (LT) is an ancient lake in the Great African Rift System, surrounded by the Central African countries Burundi, DR Congo, Tanzania and Zambia. *Limnothrissa miodon* and *Stolothrissa tanganicae* are two pelagic clupeid (sardine) species that are endemic to this lake (Coulter, 1991). They are very important for the local communities surrounding Lake Tanganyika since they comprise around 65% of the fish catches (De Keyzer et al., 2019). Over the last decades, fish stocks in the lake have been declining mainly due to overfishing and global warming (Nkotagu, 2008). To establish sustainable fisheries management, a good understanding of the ecology and population structure of these sardine species is needed. Knowing the precise food source of the sardines is important to analyse their role in the pelagic food web and study their ecological importance (Pikitch et al., 2004). Genetic studies on *S. tanganicae* and *L. miodon* did not show population structuring, suggesting some migration of these fish over the length of the lake (Hauser et al., 1998; De Keyzer et al., 2019). Here, we analyse the prey item and the gut microbiome composition of *L. miodon* and *S. tanganicae*. Until now, studies on the diet composition of the sardine species were mainly done visually. This technique is very time consuming, requires taxonomic specialists and is sensitive to degradation of food items (Jakubavičiute et al., 2017). In this study, we used metabarcoding to analyse stomach and gut content. Metabarcoding is a very effective way of detecting and identifying even small traces of DNA within a sample (Jakubavičiute et al., 2017). Our samples of *S. tanganicae* and *L. miodon* originate from five locations: Uvira (DR Congo) and Bujumbura (Burundi) in the North, Kalemie (DR Congo) in the centre, Mpulungu (Zambia) and Sumbu (Zambia) in the South. They were sampled during both wet (April, all locations) and dry (September, only Uvira) season. In this way, a comparison between different species, locations and seasons can be made. Findings from this study will give detailed information about the prey item and microbiome composition of sardines in LT. For the gut microbiome, we expect a difference over the north-south axis, since different bacteria phyla dominate in these basins (De Wever et al., 2005). A difference between seasons is not expected, because the microbiome of an individual is rather stable. For stomach content, we expect variation between species, since previous reports and differences in life cycles suggest different feeding habits. Furthermore, we expect a difference in diet composition between seasons due to a variation in abundance of certain prey species during the wet and the dry season. Since the composition of the plankton varies between the North and South, we also expect a variation in diet between locations.

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