

KEAFish

The biodiversity, biogeography and evolutionary history of the northern basins of the Great African Lakes: the enigmatic fish faunas of Lakes Kivu, Edward and Albert revisited

DURATION
 15/12/2020 - 15/03/2025

BUDGET
 487 668€

PROJECT DESCRIPTION

The area of the northern East African rift-valley lakes Kivu, Edward and Albert (KEA) is one of the most enigmatic regions in terms of its biogeography. The region is situated at the intersection of three major ichthyo-geographic provinces (Nilo-Sudan, East Coast and Congo), features a turbulent tectonic history and likely acted as a species reservoir during recent climatic changes, such as the major drought some 15.000 years ago, which resulted in a nearly complete desiccation of Lake Victoria.

Recently, we have studied the taxonomy of several cichlid and non-cichlid groups and have produced some checklists for parts of the KEA region and adjacent areas in the Congo basin. It has become clear that there is a need to revise the biogeographical puzzle outlined above. Since a strong taxonomic basis is crucial to make biogeographic inferences, we will revise some key groups (cichlids and non-cichlids) based on a combined morphological and genetic approach.

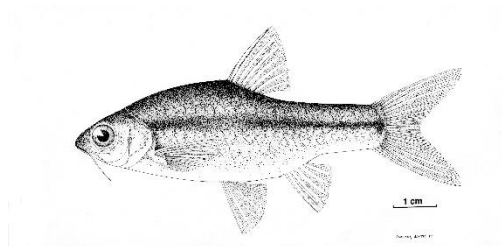
We will combine classical taxonomy with standard sequencing methods and state-of-the-art genomic techniques to provide a comprehensive characterisation of the understudied fish fauna of this region. This work will provide key insights into the region's bio-geographic history, evaluate its role as a species refuge, and test its previously suggested role as the origin of the about 600 species of the Lake Victoria haplochromine cichlid radiation. Our research hypothesis is that an out-of-Kivu origin for cichlids and non-cichlids and the role of refuges of the KEA lakes shaped to a large extent the ichthyodiversity of the region.

(1) We will perform a region-wide COI-scan of all fish groups of the region, except for the haplochromine cichlids (see below) and complement this with additional nuclear markers when necessary. All genetic data will be made freely available on GenBank.

We will then solve the taxonomic issues revealed, to create the necessary solid base to forward evolutionary and biogeographic scenarios. Collection data will be available in GBIF and new biological information will be put into FishBase.

(2) Because of the uninformative nature of the results of standard sequencing techniques, such as COI-barcoding, in haplochromines, we will concentrate on whole genome sequencing for this group. We will especially concentrate on Lake Albert and riverine habitats, because the Lake Edward fauna is already part of an ongoing FWO-PhD programme. For this, the samples need to be properly identified. Major obstacle here is the lack of knowledge of the Lake Albert haplochromines. Hence, a morphometric revision of this assemblage is included.

(3) We will use whole genome sequencing for selected non-haplochromines in order to acquire the necessary detail to fine-tune the evolutionary and ichthyogeographic scenarios. These include the species-rich cyprinid genus *Enteromius*, the widespread cichlid, *Oreochromis niloticus*, and the catfish species *Clarias liocephalus* and *Clarias gariepinus*. For the latter, a recent publication suggested the possible role of the Great lakes and particularly Lake Kivu as the centre of diversification from where the species spread over Africa. If this would also hold for *Oreochromis niloticus*, Lake Kivu would be the cradle of two of the most cultured tropical fish species in the world. The raw sequencing reads will be deposited on the NCBI Sequence Read Archive.



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The project is mainly a scientific project. Therefore the valorisation plan mainly targets a scientific audience, through peer-reviewed publications and presentations.

However, the impact of the project goes beyond this. The region studied is under considerable anthropogenic stress. Non-native fishes are introduced everywhere and form an increasing threat. Overfishing is ubiquitous. An inventory of the native species diversity and its genetic integrity is urgently needed for conservation and sustainable fisheries management

Whole-genome results for the two most important commercial African freshwater species, *Clarias gariepinus* and *Oreochromis niloticus*, may reveal important information about the genetic divergence of the various populations. Furthermore, signals about eventual hybridization events through human introduction will become available as baseline information for fisheries and aquaculture management.

The project will valorize the large historical and recent collections at the RMCA made in the region and at the same time, these collections form an essential prerequisite for the success of the research programme. It will contribute substantially to the role of the RMCA as one of the key players in the barcoding initiative on African fishes and for whole-genome analyses on non-haplochromine fishes. The project will supplement an ongoing FWO PhD programme and collaboration with the Joint Experimental Molecular Unit (JEMU) and the Svardal lab at Antwerp University.

We further valorise the project in terms of capacity building by training two members of the Ugandan and Congolese team in fish identification and morphometrics-based taxonomy. Additionally, we will link to the training component of the FishBase-for-Africa project at the RMCA in offering guided case studies linked to the species studied in the project. This win-win situation will provide extra training for and raising awareness in African scientists not directly involved in the project.



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