

What can parasites tell us about fish introductions in Congo?

Project title: Tracing fish Introductions and Lateral Parasite transfer to Indigenous Aquatic fauna (TILAPIA)

Detailed project information

The Nile Tilapia, *Oreochromis niloticus*, is the most commonly farmed tilapia species in the world. Native to Africa, this highly invasive species became established worldwide. With a yearly production of 20 million tonnes this species forms an essential part of food security. It is however a highly invasive species, being a strong competitor and fast grower. Its introduction resulted in the decline of endemics in e.g. Lakes Victoria and it by hybridizing with autochthonous cichlid species it threatens the genetic integrity of native fish resources. Fish introductions can also lead to the introduction of new parasite species that can threaten local fish species. This co-introduction is often overlooked despite the fact that it can strongly impact on the local fauna. Some parasite species can easily switch hosts and by doing so causing new epidemics. Introduction of a Monogenean *Gyrodactylus* parasite with live fish led to the decimation of the European salmon population in Norway, both in nature and in aquaculture. Other parasites are more host-specific and won't switch hosts after introduction. They can be used a biological tag of their host. Parasitic organisms usually have a much faster mutation rate than their hosts because of their faster generation time. By genetically characterizing the parasite population more information can be obtained on the migration history of the host it was isolated from. This is the so-called 'magnifying glass principle'.

Nile tilapia has also been introduced in the DR Congo. It started in the colonial times and was followed by natural and human-assisted dispersal throughout the Congo Basin. These fish introductions are not well documented and the consequences for the local fauna are unknown.

General objectives

Here we want to study the stocking history of the Nile Tilapia in the DRC by means of their monogenean parasites. More specifically we want to 1) test whether the introduction of Nile tilapia in the Congo basin has led to the introduction of new parasite species and 2) whether parasite genetics can help to decipher the complex stocking history.

Methodology

In this study we focus on monogenean flatworms. These are ectoparasites infecting fins and gills of teleost fish. They have a direct life cycle which means that they don't need an intermediate host to complete their lifecycle. Therefore they have a higher chance of being anthropogenically introduced with their hosts.

Work package 1: parasite community composition and detecting parasite introduction

The vast historical collection of the RMCA, the most extensive set of African freshwater fishes worldwide, is invaluable to define the baseline. Using pre-introduction historical specimens, the autochthonous tilapia parasite fauna of the Congo Basin will be reconstructed and compared with the present-day parasite fauna. To this end, three localities will be sampled (the Lower, Middle and Upper Congo) for local tilapia species and introduced Nile tilapia.

Monogenean parasites will be isolated from the gills and stored in ethanol while for each infected host individual a fin clip will be taken for molecular species identification. Each parasite individual will be identified by molecular and morphological methods.

Work package 2: tracing introduced Nile tilapia by means of fish genetics

Populations from both natural and introduced Nile tilapia from DRC will be studied by means of rapidly evolving molecular markers. Fin clips will be collected throughout the natural distribution range through our collaborative network. The phylogeographic and population genetic analyses of the Nile tilapia populations will allow to identify hybrid crosses between Nile tilapia and local tilapia species in addition to reconstructing the genetic population structure along the Congo basin in order to trace stocking events.

Work package 3: tracing introduced Nile tilapia by means of parasite genetics

The sampling campaigns will also serve a parasite-based assessment of the origins of introduced Nile tilapia populations. For a higher-resolution comparison with Nile tilapia populations than can be achieved using fish genetics, monogenean parasites from Nile tilapia introduced to the DRC will be sequenced. Sequences will be compared to those from the native range of Nile tilapia to determine the origins of the introduced populations. Population assignment will be compared to population genetic analysis of the introduced Nile tilapia populations. Rapidly evolving mitochondrial DNA markers will be developed for the monogenean parasites through a mitogenomic approach.