Intraspecific diversification and mitonuclear discordance in the monogenean parasite *Dolicirroplectanum lacustre*, co-introduced with the invasive Nile perch <u>Kelly J. M. Thys</u>¹, Maarten M. P. Vanhove¹, Maarten Van Steenberge^{1,2}, Nikol Kmentová¹ ¹Hasselt University, Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Diepenbeek, Belgium ²Royal Belgian Institute of Natural Sciences, Operational Directorate Taxonomy and Phylogeny, Brussels, Belgium

1. INTRODUCTION

Parasites typically speciate faster, and might be even more species-rich than their hosts. African lates perches (Latidae), some of the largest freshwater fishes, host only a single monogenean flatworm: *Dolicirroplectanum lacustre*^{*a, b*}. This parasite has 'failed to diverge', but displays high morphological variability, with two morphotypes identified: slender and gravid ^{*a, b*}. The latid Nile perch (*Lates niloticus*) is a notorious invader which has caused the extinction of 500+ species of endemic haplochromine cichlids in Lake Victoria ^{*c*}. Along with the introductions of the Nile perch, its parasites were possibly co-introduced. Lake Albert, type locality of *D. lacustre*, is one of the source localities of introduced *L. niloticus* in Lake Victoria.



General hypotheses

(1) A founder effect has taken place in Lake

(2) *D. lacustre* displays high phenotypic variation and low genetic differentiation in Lake Albert, as supported by the presence of distinct morphotypes

Fig. 1 Sampling localities of *Lates niloticus* at Lake Albert and Lake Victoria: Kaiso Landing site, Lake Albert, Uganda (n=8) and Kikondo rocky shore, Lake Victoria, Uganda (n = 7). Triangles depict localities sampled in another study ^a, for which the generated data was combined with this study. Victoria, hence *D. lacustre* displays reduced genetic and morphological diversity within its introduced range in comparison with its native population.

2. MATERIALS AND METHODS

To investigate the pattern of parasite co-introduction, we studied the intraspecific diversification of *D. lacustre* in Lake Albert (n = 90) and Lake Victoria (n = 34) (Fig. 1).



Morphological characterisation morphometrics of the hard structures in the haptor and copulatory organs



Microscopic examination of hard structures

Genetic characterisation barcoding, genetic diversity measures, and haplotype networks



Parasite extraction from gill filaments

Cut individuals in three parts

DNA extraction

mitochondrial COI, nuclear ITS-1, 18S and 28S DNA

3. RESULTS

- Two morphotypes (Fig. 2) are genetically distinct in COI (Fig. 3)
- Two morphotypes display mitonuclear discordance (Fig. 3)
- Only the slender morphotype introduced in Lake Victoria, with reduced genetic diversity







Fig. 2 Morphometric variation in *Dolicirroplectanum lacustre* summarised in a PCA biplot. Drawings from the dorsal view with: whole mount; haptoral structures; copulatory organs.

4. CONCLUSIONS

- Monogenean gill parasite D. lacustre was co-introduced into Lake Victoria
- Reduced genetic and morphological diversity in Lake Victoria indicates a founder effect
- Mitonuclear discordance indicates an incomplete reproductive barrier between the morphotypes, and ongoing diversification



Fig. 3 Haplotype networks of *Dolicirroplectanum lacustre* based on sequences of mitochondrial COI mtDNA (n=45), and nuclear ITS1 rDNA (n=11), 28S rDNA (n=12), 18S rDNA (n=11) using the Median-Joining Networks approach.

References

^a Kmentová et al. (2020). J. Great Lakes Res., 46, 1113-1130.

^b Thurston & Paperna (1969). Proc. Helminthol. Soc. Wash., 36, 214-218.

^c Pringle (2005). BioScience, 55, 780.

kelly.thys@uhasselt.be

Instagram: @bitelab_uhasselt

Twitter: @BiTE_UHasselt

