New distribution records and molecular data for species of *Macrogyrodactylus* Malmberg, 1957 (Monogenea: Gyrodactylidae) from *Clarias gariepinus* (Burchell) (Siluriformes: Clariidae) in southern Africa

Marlieese Truter¹, ², Aline A Acosta¹, Olaf LF Weyl², Nico J Smit¹

¹ Water Research Group, Unit for Environmental Sciences and Management, North-West University, Private Bag X6001, Potchefstroom, 2520, South Africa
² DSI/NRF Research Chair in Inland Fisheries and Freshwater Ecology, South African Institute for Aquatic Biodiversity, Makhanda, South Africa

Introduction

Of the nine known species in the genus *Macrogyrodactylus* Malmberg, three species: *Macrogyrodactylus clarii* Gussев, *M. congolensis* (Prudhoe) and *M. karibae* (Douillé et Chishawa) are predominantly known to parasites the skin and gills of the African sharp-tooth catfish *Clarias gariepinus* (Burchell) throughout Africa (Fig. 1). These three species are also well studied with ample publications consisting of species descriptions and elaborative information on their anatomy, pathogenicity and co-occurrence with other monogeneans in various freshwater systems on the continent. Their well-studied host *C. gariepinus* occurs naturally throughout Africa as well as in the northern regions of South Africa and was introduced into the Eastern and Western Cape Provinces of South Africa from the Zambezi and northern Southern Cape Ichthyofaunal regions. No studies have been conducted on their co-introduced or potential co-invasive parasitic communities in these regions.

This study presents partial data obtained from an extensive metazoan parasitological study on *C. gariepinus* in southern Africa that includes:

- A summary on the distribution of *Macrogyrodactylus* spp. in Africa;
- Novel distribution records, morphological and molecular data for the genus.

Methods

During the present study, 184 individuals of *C. gariepinus* were collected from various localities in South Africa and Zambia (Fig. 2) and subjected to a parasitological screening. Monogeneans found on the fins, skin and gills were cleared in glycerin ammonium picrate for morphological identification and select individuals were fixed in 96% molecular grade ethanol for molecular characterisation of the ITS1-5.8S-ITS2 region.

Results

Host individuals from five of the sampled localities were infected with any combination of the three species, *M. clarii*, *M. congolensis* and *M. karibae* primarily known from *C. gariepinus* (Fig. 2). Prevalence, intensity of infestation and co-occurrence of the three species varied across localities with *M. clarii* as the dominant species when in co-occurrence with *M. karibae* or *M. congolensis*.

No clinical signs such as greyish-white patches on the skin were observed when intensities of *M. congolensis* were as high as 109 parasites per individual host.

No infestation with *Macrogyrodactylus* spp. were found on *C. gariepinus* in its invasive range in South Africa.

Morphometrics and molecular characterisation of the ITS1-5.8S-ITS2 region corroborated the identity of all three species. All the sequences obtained grouped in the respective subclades for each species, except for *M. congolensis* from the Vaal River in South Africa (Fig. 3). This species’ position in the subclade in relation to its congeners from Kenya and Senegal are inconclusive.

The literature search yielded a total of 57 accessible publications for all nine species of *Macrogyrodactylus* of which 46 were exclusively on the three species found from *C. gariepinus*. These publications were grouped into main research focus areas for the genus (Fig. 4).

Conclusions

All records of the three species from the present study represent new distribution records. The first sequence data from South Africa and Zambia are available for the respective species.

Despite the success in identification of the three species using a widely used gene region, the resolution on the interspecific relationships with basal clades are low.

Host specificity of *M. clarii*, *M. congolensis* and *M. karibae* is confirmed with 80% of all records of *Macrogyrodactylus* spp. being from *C. gariepinus*.

Disparity in knowledge on the true community composition and distribution of the species parasitising *C. gariepinus* (or even other hosts) is evident with few ecological studies in natural systems throughout the wide distribution range of the host in Africa.

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