

New insights in the groundwater species diversity of the isopod genus *Metastenasellus* in Benin and Cameroon

Gontran Sonet^a, Moïssou Lagnika^b, Raoul T. Kayo^c, Jean-François Flot^d, Patrick Martin^a

^a Royal Belgian Institute of Natural Sciences, Taxonomy and Phylogeny, 29 rue Vautier, B-1000 Brussels, Belgium

^b Université d'Abomey-Calavi, Faculté des Sciences et Techniques, Département de Zoologie, 01 BP: 526, République du Bénin

^c University of Bamenda, Department of Biological Sciences, Faculty of Science, PoBox: 39 Bambili-Cameroon

^d Université libre de Bruxelles, Ecological and Evolutionary genomics, 50 avenue F.-D. Roosevelt, B-1050 Brussels, Belgium

Corresponding author: gsonet@naturalsciences.be

Introduction

In tropical Africa, the Stenasellidae is a diverse family of isopods (Crustacea) that contains a large number of obligate groundwater species (stygobiontes). Within the Stenasellidae, the genus *Metastenasellus* Magniez, 1966 (Figure 1) is currently composed of nine species with a trans-Saharan distribution (Algeria, West and Central Africa).

Recently, studies documenting groundwater biodiversity in relation to water quality and vulnerability to pollution and local use have contributed to the descriptions of two new species of *Metastenasellus* in Cameroon → The diversity of this genus is probably underestimated due to a lack of studies and a deficit in taxonomic expertise.

Objective

Here, we further explore the diversity of *Metastenasellus* by sequencing the DNA barcode fragment of 57 Beninese and 27 Cameroonian specimens (from 24 and 29 localities respectively, cf. Figure 2).



Figure 1: *Metastenasellus* sp.

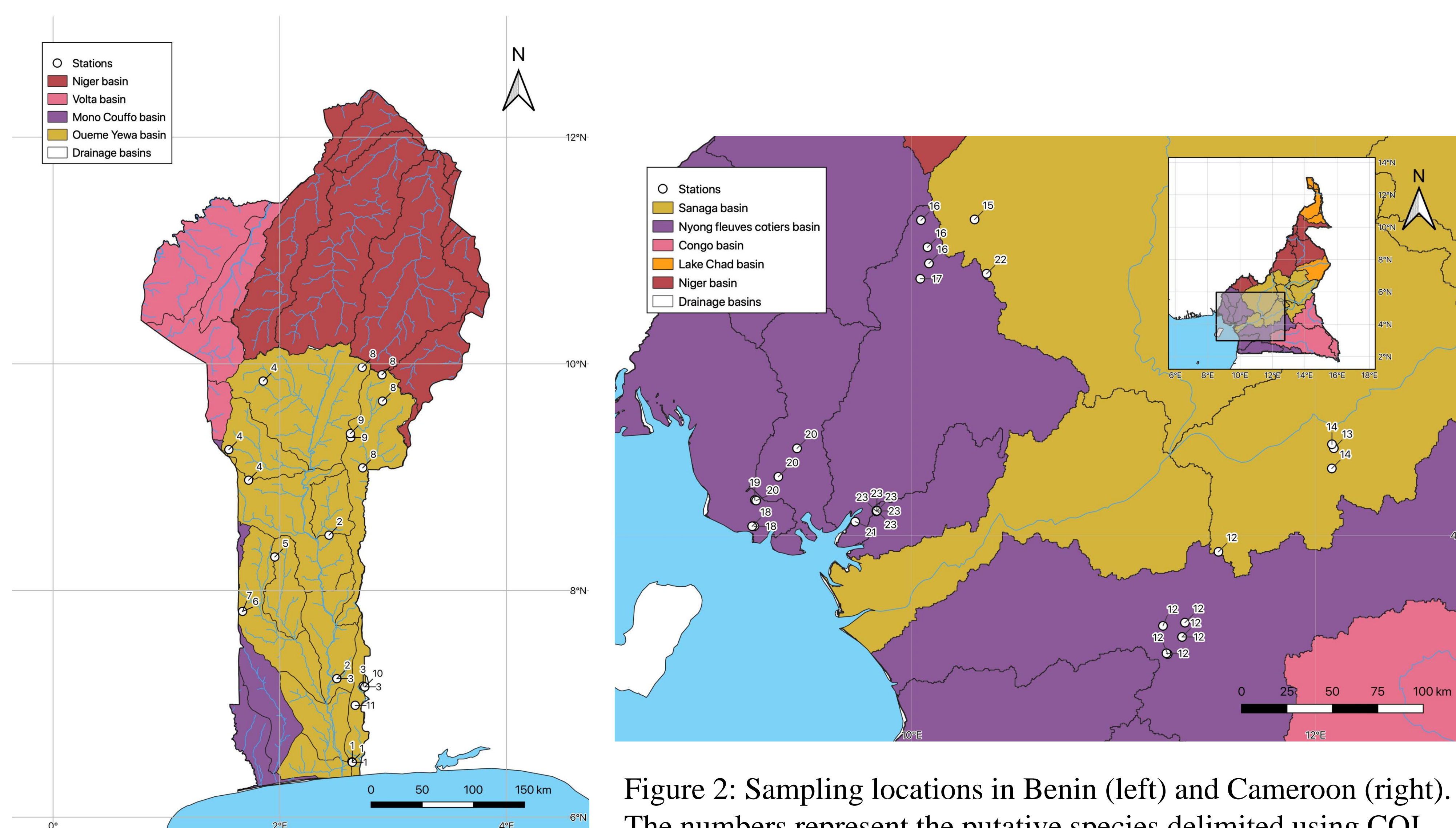


Figure 2: Sampling locations in Benin (left) and Cameroon (right). The numbers represent the putative species delimited using COI sequences and represented in Figure 3 (numbers under “Sp”).

Methods

The 5' end fragment of the COI gene was sequenced for 84 specimens using the Sanger method and species were delimited based on 4 methods: ABGD (automatic barcode gap delimitation), PTP (Poisson tree processes), GMYC (Generalized mixed Yule coalescent) and KoT (K over Theta).

Results and discussion

All methods agreed on a minimum of 23 putative species, 11 from Benin and 12 from Cameroon (Fig. 3).

Some of these putative species can coexist in some localities (Fig. 2) and others were already confirmed to correspond to distinct species in an ongoing morphological study of the male pleiopods.

Implications

Given the number of potential species currently observed per sampled station, it is to be expected that many new species could be discovered by increasing the sampling effort.

The geographical distribution of the 23 putative species suggests a restricted distribution and a low dispersal capacity of *Metastenasellus* species, as already observed for macro-stygobionts in Europe.

There also appears to be a decoupling between watersheds and species distribution, suggesting that watersheds are a rough approximation of water table boundaries or that the current distribution of *Metastenasellus* is more the result of historical factors than of dispersal constraints related to the current configuration of the catchment areas.

Acknowledgements: We thank the Global Taxonomic Initiative and the Belgian Science Policy (BELSPO) for their financial support.

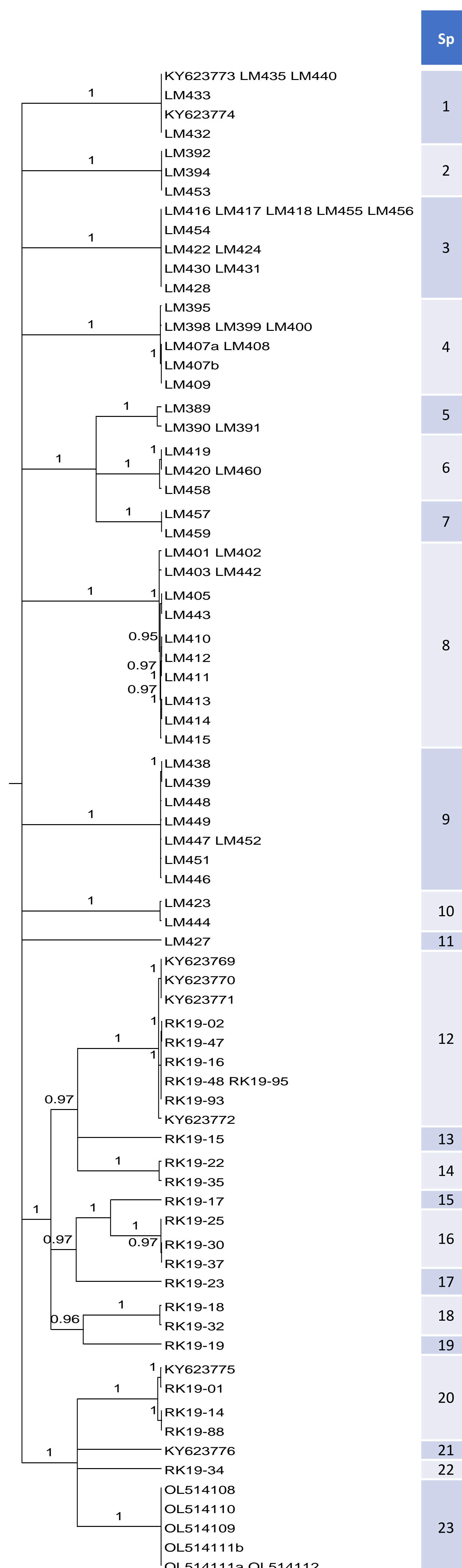


Figure 3: Phylogenetic tree (Bayesian inference) based on COI data (left), and COI-based species delimitation supported by all methods (right).