# Taxonomic re-evaluation of African anuran trypanosomes with the morphological, morphometric, and molecular diagnosis of *Trypanosoma nelspruitense* Laveran, 1904

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### Background

### **Results & Discussion**

- Trypanosoma spp. are extracellular blood parasites, infecting all vertebrate classes globally.
- Several species can cause dangerous diseases in humans and livestock.
- Aquatic trypanosomes' ecological interactions and phylogeny are not well-understood, due to their complex life cycles and a lack of molecular data.
- All 13 species of the African anuran trypanosomes were described in the 20th century.
- Only one species has currently been described from South Africa, *T. nelspruitense* Laveran, 1904.
- The aim of this study was to provide a basis for future taxonomic work on amphibian trypanosomes.

### Methods

#### **Specimen Collection**

- Six of the seven frogs collected in Mbombela were found to be infected with *Trypanosoma* spp. None of the 13 tadpole samples were infected. The samples from a previous study in Potchefstroom were known to be infected with trypanosomes.
- Morphological analysis is notoriously unreliable with *Trypanosoma* specimens, therefore it is used in combination with molecular analyses.
- The morphological and morphometric analyses showed three distinct species, which are supported with the phylogeny.
- Possible different forms of the same species were also observed.
- No morphological measurements of closely related species are currently available for comparison.
- *T. nelspruitense, Trypanosoma* sp. 2 and sp. 3 from this study were placed in new subclades within the aquatic trypanosome phylogeny.
- Academic trypanosomatid phylogenies can often be misleading due to the multi-host life cycles causing overlap of the clades.
- Blood samples from the type host, Amietia delalandii (Common River Frog), were collected from various sites in South Africa, including the type locality.

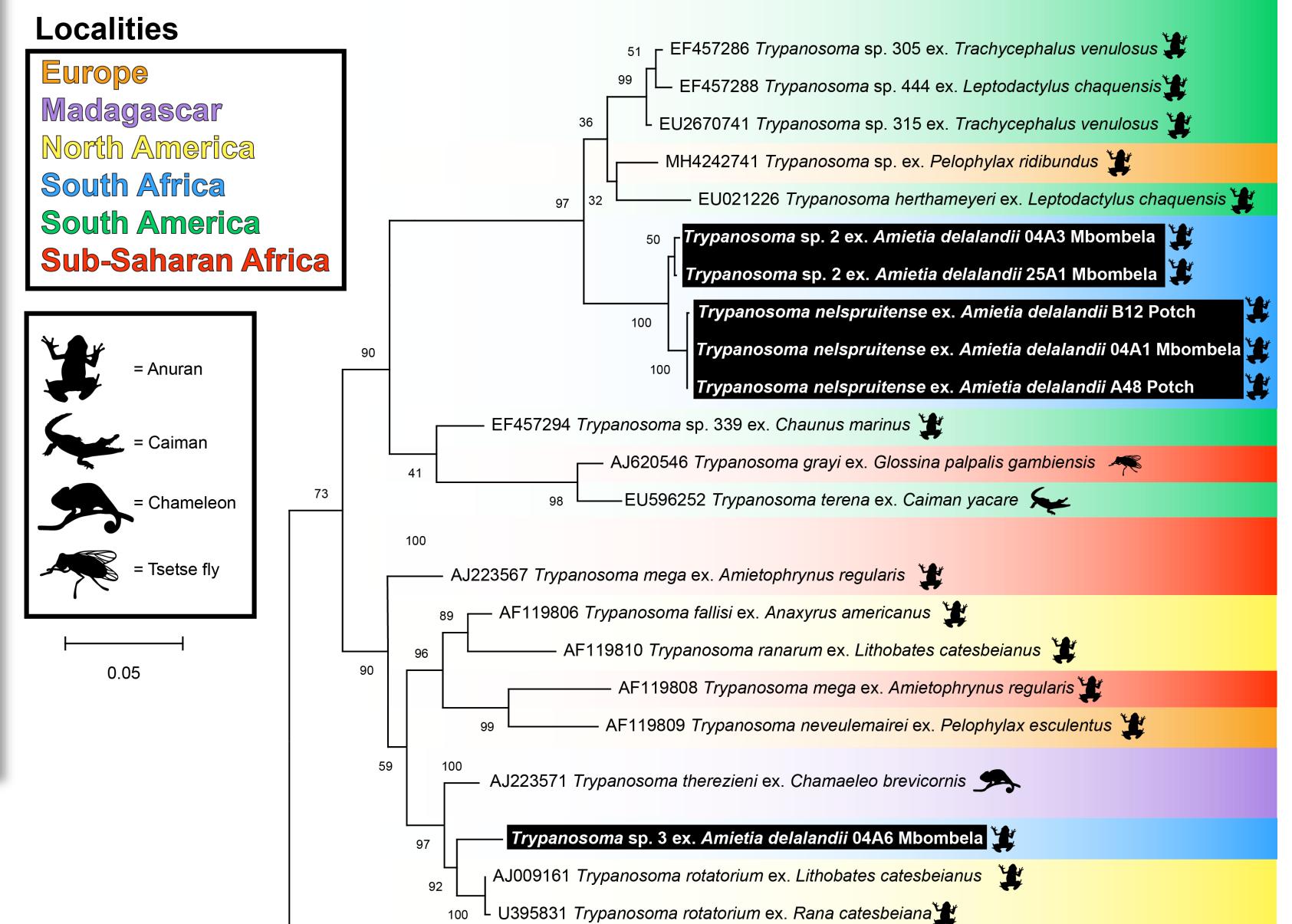
#### **Morphological characterisation**

- Blood smear slides were stained with a Giemsa solution and microscopically screened.
- Trypanosome specimens were morphologically measured.

#### Molecular analysis

- Two overlapping fragments of the 18S rRNA gene were targeted for amplification, using a nested PCR method.
- A maximum likelihood (ML) phylogeny was constructed using sequences from current literature and GenBank for comparison.





*T. nelspruitense Trypanosoma* sp. 2

*Trypanosoma* sp. 3

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– M84225 Leishmania tarentolae | X53915 Leishmania major 100

Nodal bootstrap values are indicated as a percentage. Scale shown is nucleotide substitutions per site.



- Morphological, morphometric and molecular data of three species of Trypanosoma (including T. nelspruitense) is presented in this study.
- This is the first study to provide molecular data for species of *Trypanosoma* from South African anurans, setting a platform for future research.