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# Exploring the molecular diversity of ant venoms reveals conserved toxin precursors and distinctive mature peptides features among phylogenetic subfamilies

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## Context

Comprehensive venom studies previously conducted on:

- *Myrmecia gulosa*<sup>1</sup>
- *Odontomachus monticola*<sup>2</sup>
- *Tetramorium bicarinatum*<sup>3</sup>

Purpose

- To study several phylogenetic subfamilies of ants

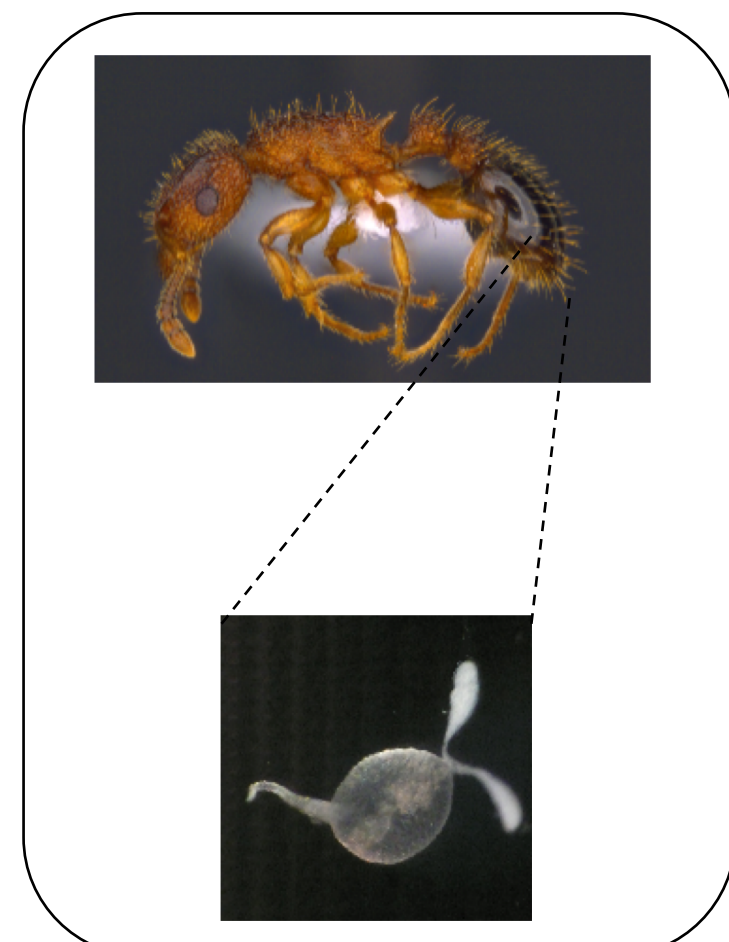
→ Improvement of our understanding about peptide toxins diversification

This presentation

- Novel venom peptidome characterization of *Tetraponera aethiops* (Pseudomyrmecinae) and *Manica rubida* (Myrmicinae)

- Comparison with recently characterized ants venoms peptidomes

## Venomics methodology



Dissection

Venom  
Venom glands

### Proteomics

LC-MS/MS

- Masses lists
- Peptide abundance
- Peptidic sequences

Bioinformatics

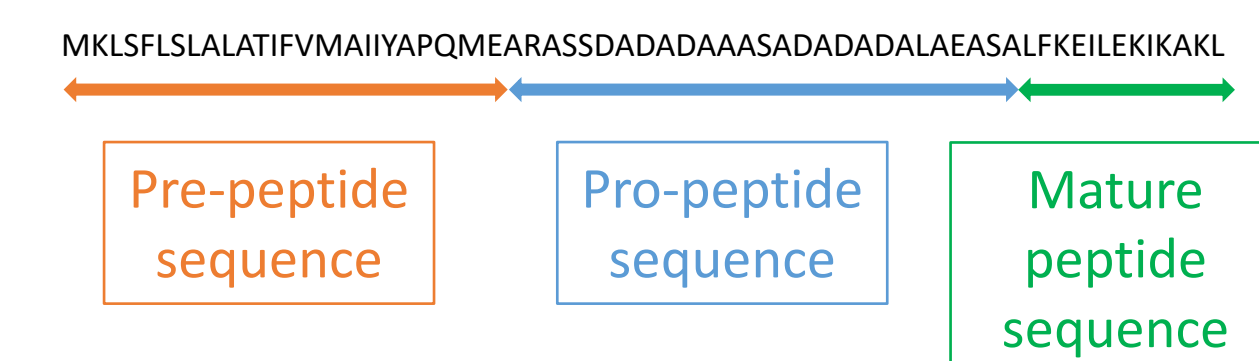
### RNA sequencing

- Contigs expressed by venom glands
- Nucleotide sequences

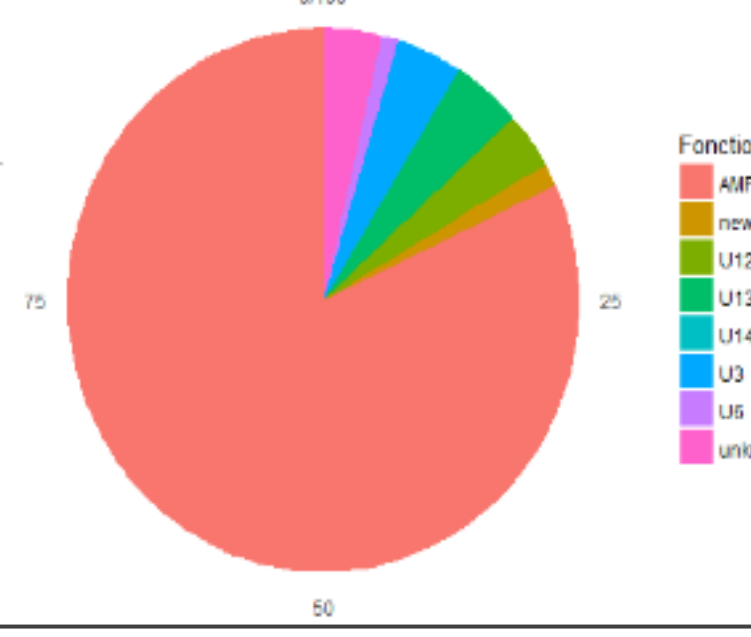
Transcriptomics

### Peptidomes

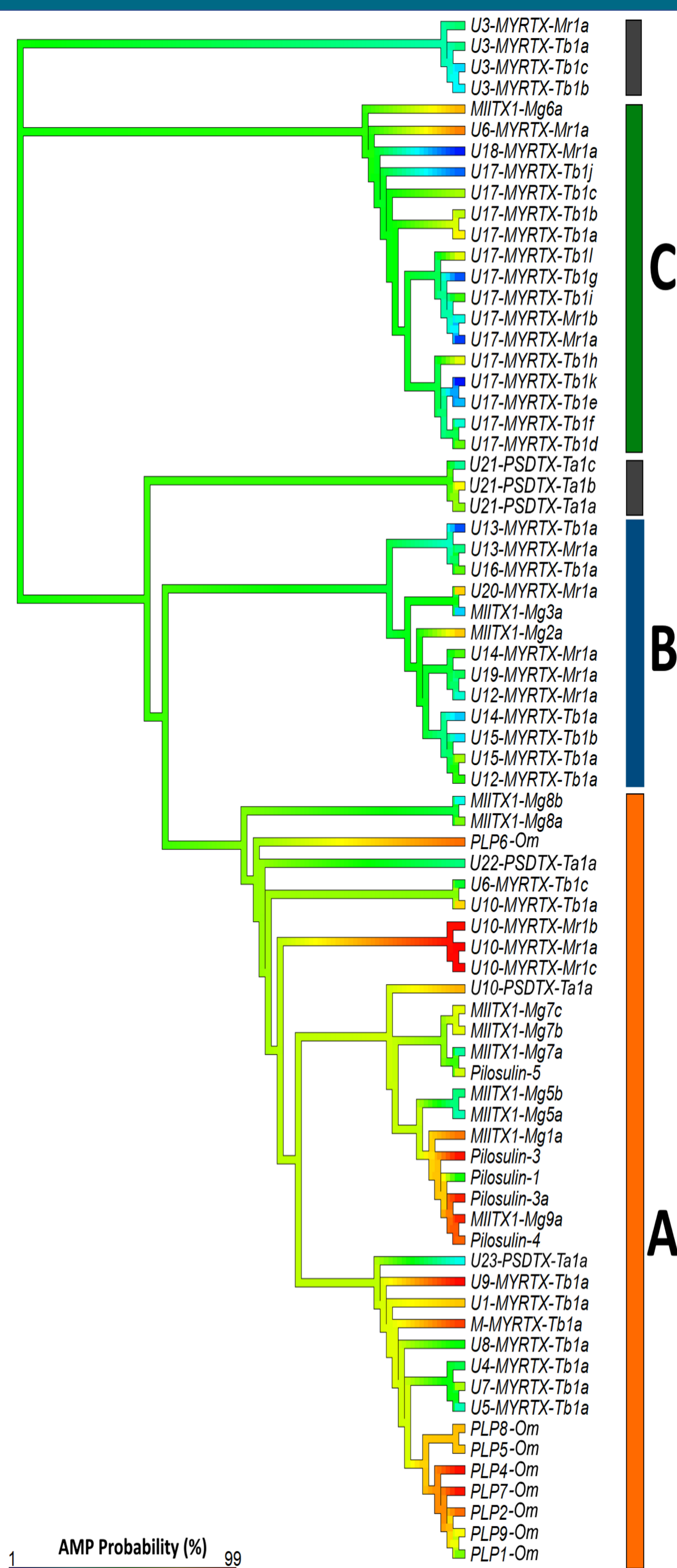
- Peptides sequences



- Peptides abundances



## Superfamilies of ant venom peptide precursors



- Three main superfamilies of precursors: A, B and C.
- Superfamily A: mature peptides mainly predicted to be membrane disruptors

- Homologies of mature peptide sequences between different ant species.
- U10 peptides predicted to be amphiphilic and polycationic  $\alpha$ -helical peptides
- U10-MIITX1-Mg1a activates mammalian sensory neurons and incapacitates arthropods<sup>1</sup>

Fig 1: Cladogram of ant venom peptides based on prepro peptide sequences alignments – *Tetramorium bicarinatum* (Tb), *Manica rubida* (Mr), *Tetraponera aethiops* (Ta), *Odontomachus monticola* (Om), *Myrmecia gulosa* (Mg), *Myrmecia pilosula* (Mp), *Myrmecia banksi* (Mb). Branches color represent the probability that mature peptides sequences exhibit antimicrobial activities by interaction with cells membranes.

## Sequences and structures homologies

A

% ID	Species
-	<i>Manica rubida</i>
57	<i>Manica rubida</i>
76	<i>Manica rubida</i>
28	<i>Tetraponera aethiops</i>
41	<i>Myrmecia gulosa</i>
24	<i>Tetramorium bicarinatum</i>

B

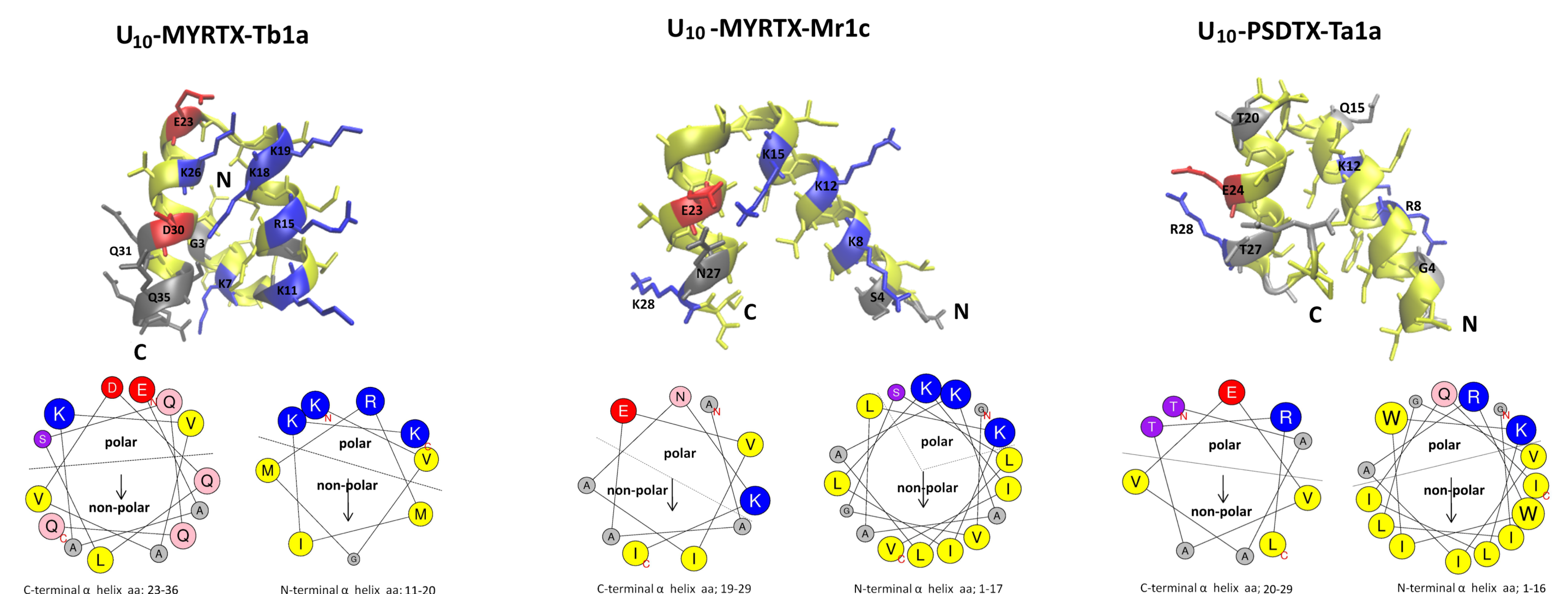


Fig. 2: (A) Alignment of mature peptides sequences from the U10 family and associated percentage identity. (B) Predicted structures of linear peptides from *Tetramorium bicarinatum*, *Manica rubida* and *Tetraponera aethiops*.

## Composition and ecological use of venoms

- *M. rubida* and *T. aethiops* venoms less diversified than *T. bicarinatum* venom
- The U<sub>10</sub> peptide family dominates *M. rubida* and *T. aethiops* venoms : role in the defensive function ?
- More complex composition in response to a predatory function ?

### Ecological function of venom

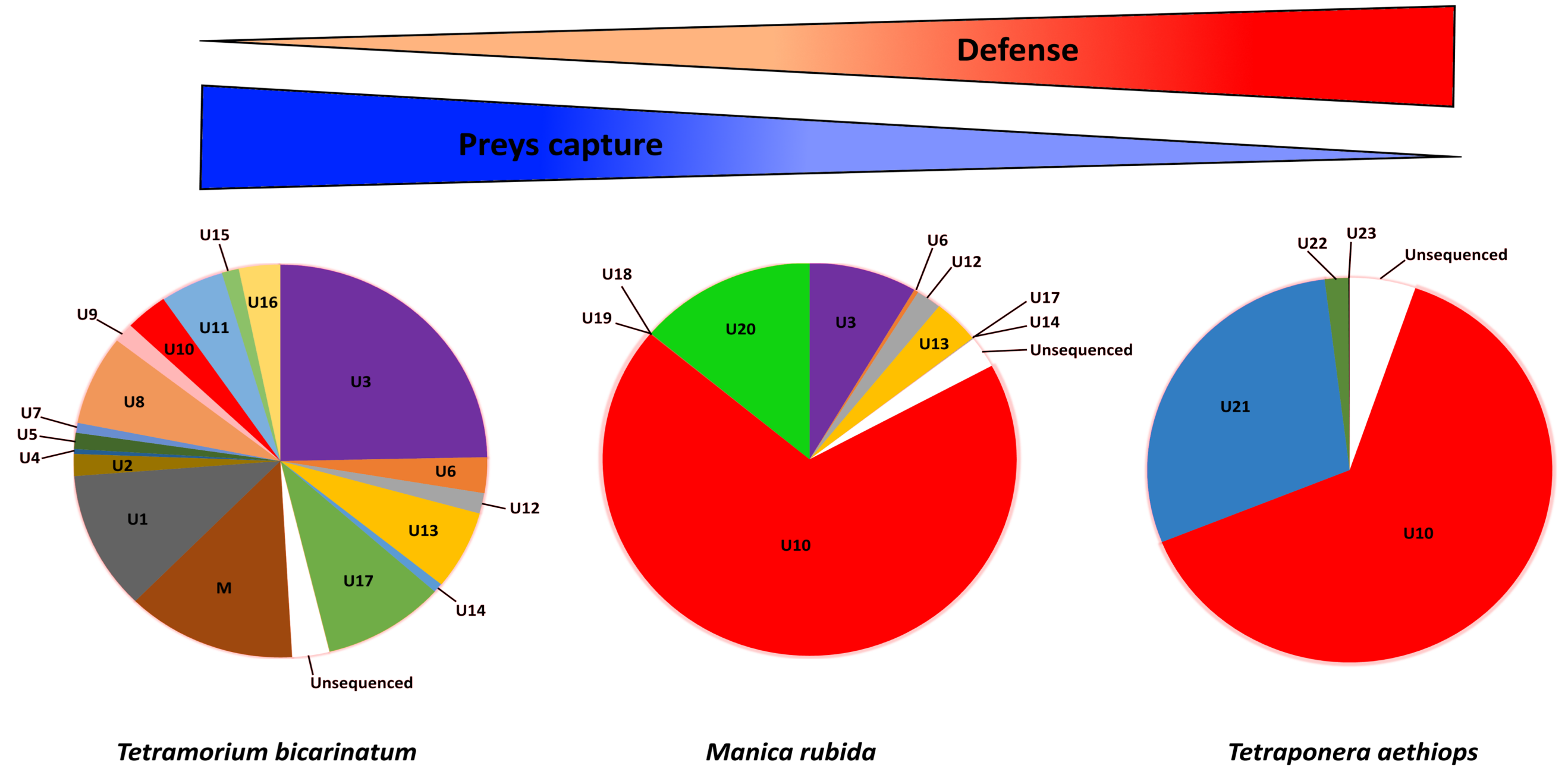


Fig. 3: Venom peptide compositions of *Tetramorium bicarinatum*, *Manica rubida* and *Tetraponera aethiops* venoms. The ecological function of venom (defense or predation) is represented by the gradient above pie charts.

## Conclusion

- 3 superfamilies of precursors
- Homologies of mature peptide sequences between different ant species.
- Venom used for preys capture might be more complex than venom used exclusively as defense.

## Prospects

- Extension of this study to other ants species
- Functional screening of mature venom peptides in a pharmaceutical context

## References:

1. Robinson, S. D. *et al.* A comprehensive portrait of the venom of the giant red bull ant, *Myrmecia gulosa*, reveals a hyperdiverse hymenopteran toxin gene family. *Sci. Adv.* (2018).
2. Tani, N. *et al.* Mass Spectrometry Analysis and Biological Characterization of the Predatory Ant *Odontomachus monticola* Venom and Venom Sac Components. *Toxins (Basel)*, 11, 50 (2019).
3. Touchard, A. *et al.* Deciphering the molecular diversity of an ant venom peptidome through a venomics approach. *J. Proteome Res.* acs.jpoteome.8b00452 (2018). doi:10.1021/acs.jpoteome.8b00452