Supplementary Material - file 3

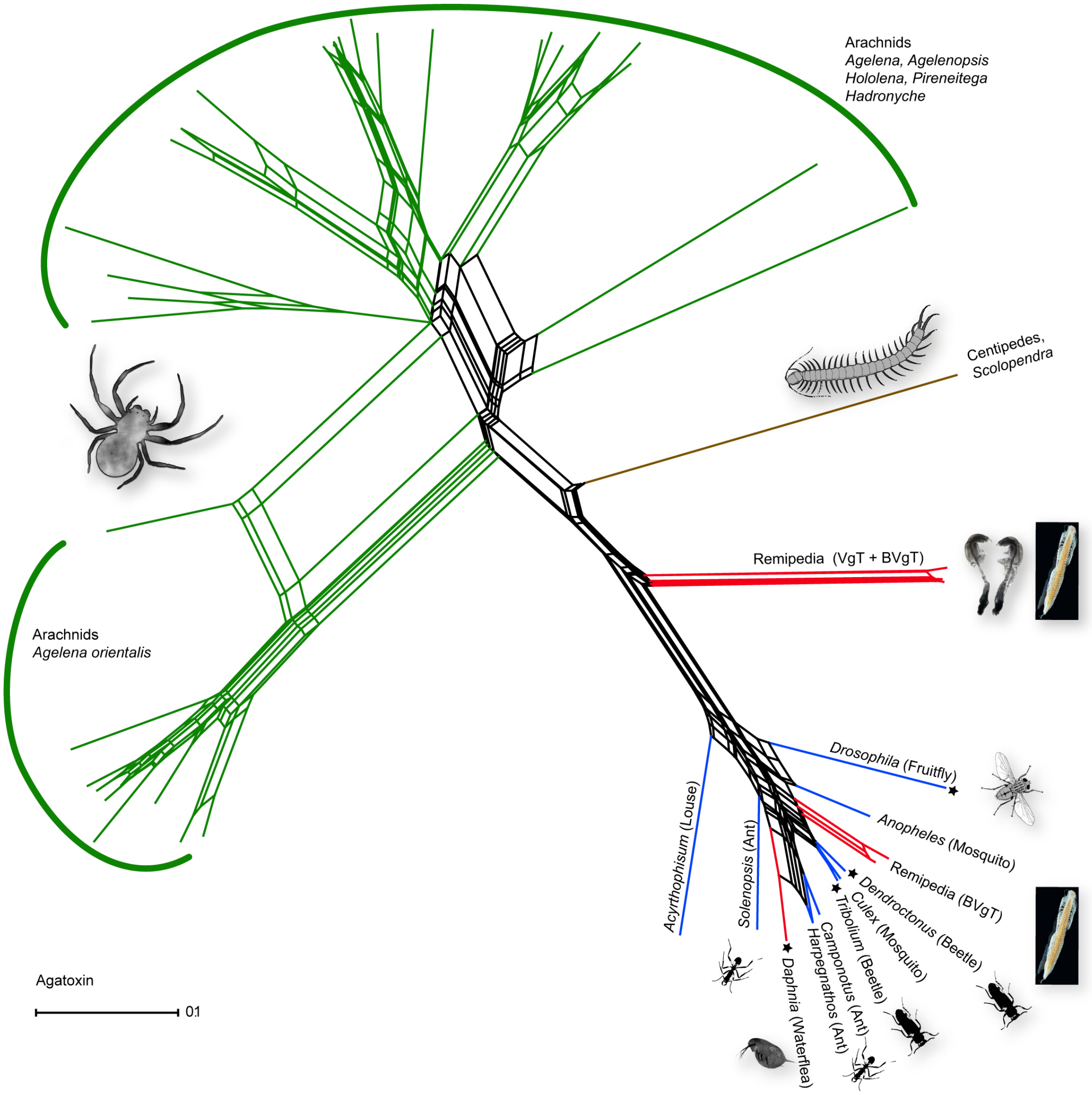
The first venomous crustacean revealed by transcriptomics and functional morphology: remipede venom glands express a unique toxin cocktail dominated by enzymes and a neurotoxin

Research Article

Björn M. von Reumont*[1], Alexander Blanke[2], Sandy Richter[3], Fernando Alvarez[4], Christoph Bleidorn[3], Ronald A Jenner*[1]

The supplementary PDF files include:

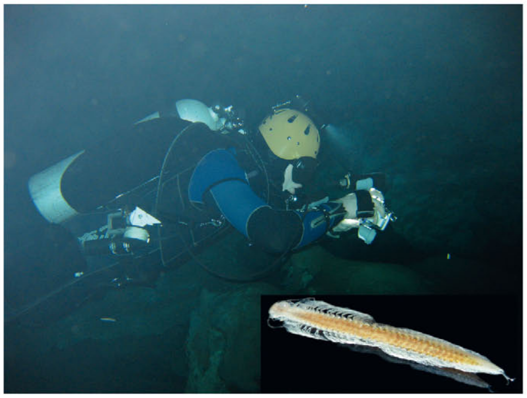
Supplementary_file1: Supplementary Text, Supplementary Figures 1-2
Supplementary_file2: Supplementary Figures 3
Supplementary_file3: Supplementary Figures 4-6
Supplementary_file4: Supplementary Figures 7-9
Supplementary_file5: Supplementary Tables 1 and 2



Supplementary Figure 4

Neighbour joining network of remipede agatoxin-like neurotoxin sequences. Network was reconstructed in Splitstree. Spiders are represented by green lines, centipedes by brown lines, hexapods by blue lines and crustaceans by red lines. Non-venomous taxa are marked by stars.

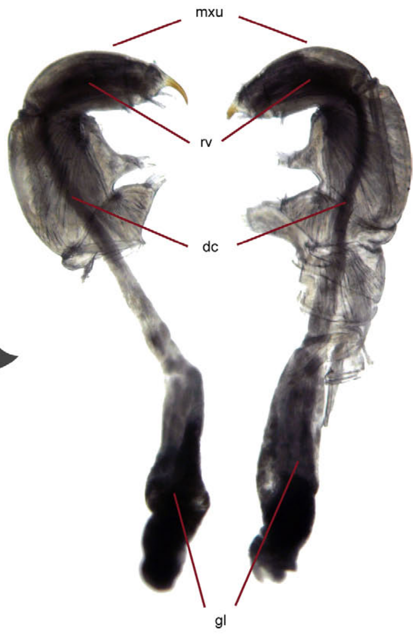
a) Collection of material in anchialine cave systems, here Yucatan, Mexico.



b.) Preparation of fresh material for direct dissection in RNAlater.

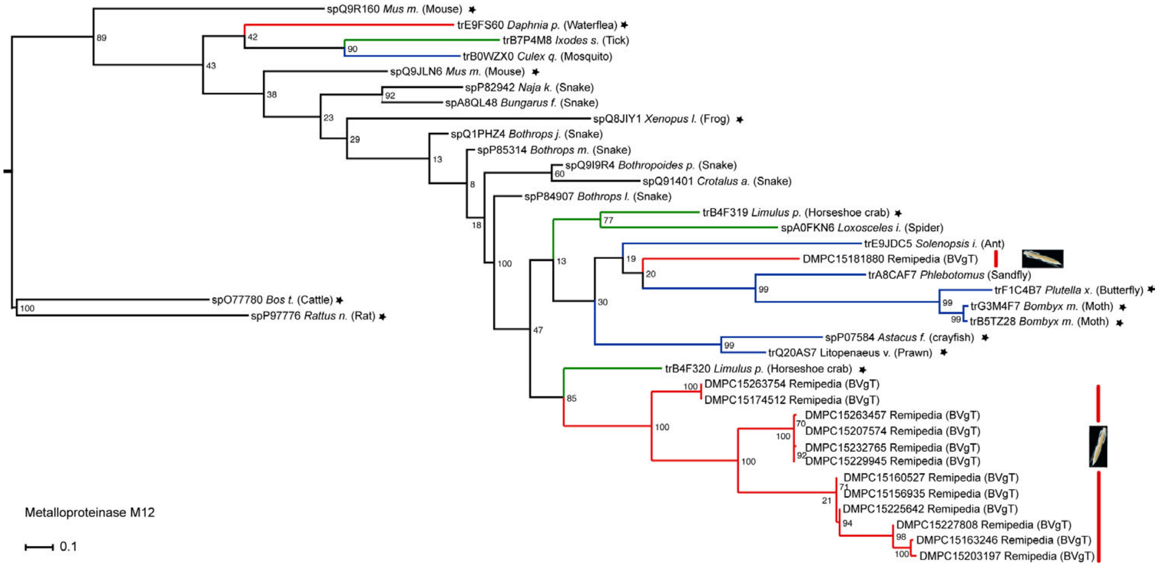
c.) Dissection of cephalothorax and first maxillula to isolate venom glands.

d.) Final dissection and isolation of the venom glands and preservation of gland tissue.



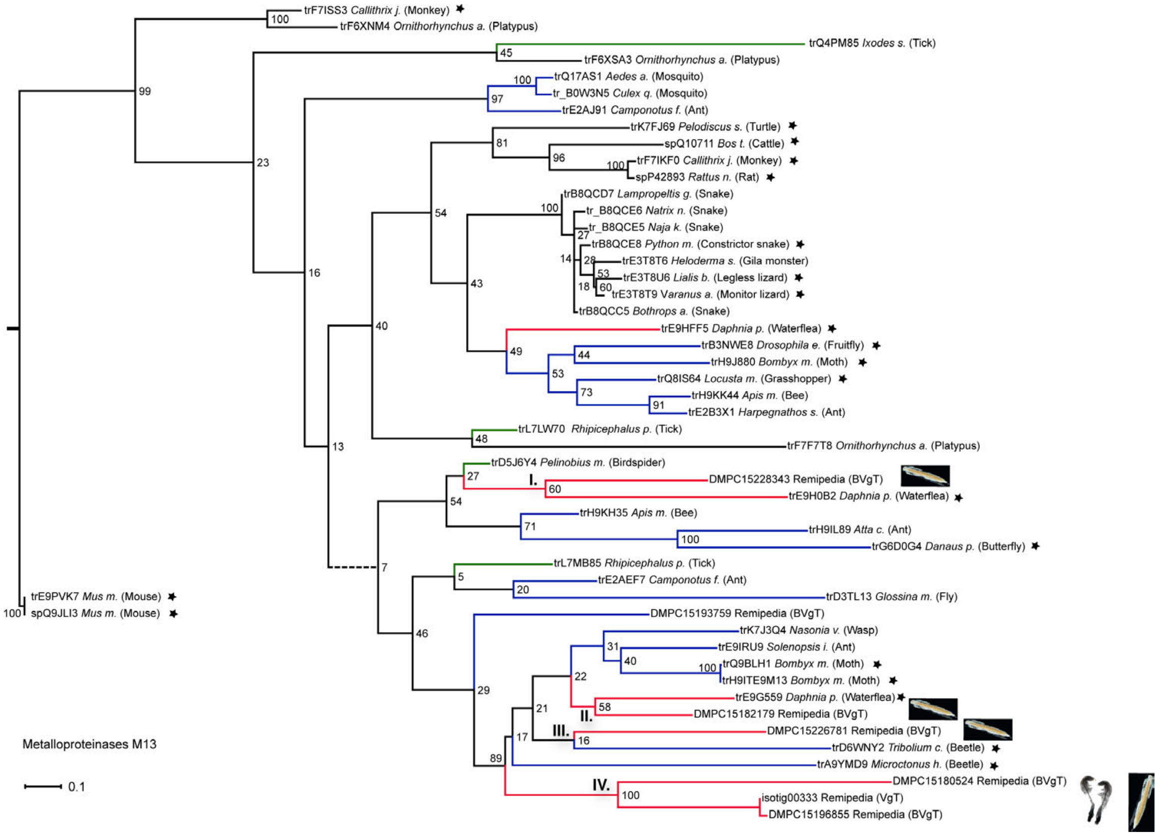
Supplementary Figure 5

Collection and dissection scheme to isolate venom gland tissue only transcripts. After the collection of the specimens by cave diving (a.), specimens are dissected in RNAlater (b.) to dissect the first segments of the cephalothorax (c.) to isolate venom glands and venom reservoir (d.). Cep= cephalothorax; mxu=Maxillula; rv=venom reservoir; dc= venom ductus; gl= venomgland.predicted to have one to three less likely (lower than 65 percent of probability) disulphide bonds (Lin and Tseng 2010), the dotted black lines indicate these less likely bonds.



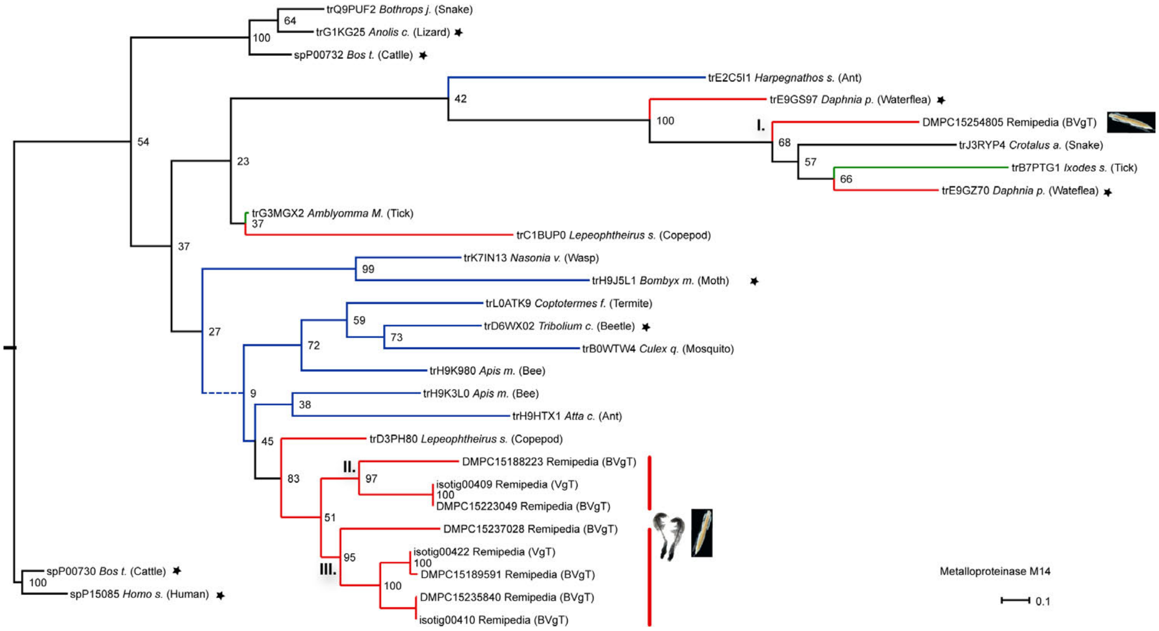
Supplementary Figure 6a

Phylogenetic tree of the Metalloproteinase M12 sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAIFWAG, 1000 bootstraps. See previous figures for description.



Supplementary Figure 6b

Phylogenetic tree of the Metalloproteinase M13 sequences. The tree was reconstructed in RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAILG, 1000 bootstraps. See previous figures for description.



Supplementary Figure 6c

Phylogenetic tree of the Metalloproteinase M14 sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAILG, 1000 bootstraps. See previous figures for description.