Integrating 3D imaging with multi-locus phylogenetic analysis to update the diversity of the aegisthid genus *Pontostratiotes* Brady, 1883 (Copepoda: Harpacticoida)

Fanny Sieler [1], **Sahar Khodami** [2], **Martin Husemann** [3], **Paul Schütz**[4], **Thomas van de Kamp**[5], **Nancy F. Mercado-Salas** [1]

1 Leibniz Institute for the Analysis of Biodiversity Change (LIB), Hamburg, 20146, Germany
2 German Centre for Marine Biodiversity Research (DZMB), Wilhelmshaven, 26382, Germany
3 State Museum of Natural History Karlsruhe (SMNK), Karlsruhe, 76133, Germany
4 INI Research, Hamburg, 22083, Germany
5 Karlsruhe Institute of Technology (KIT), Karlsruhe, 76131, Germany

Pontostratiotes is a genus within the family Aegisthidae Giesbrecht, 1893.

➤ Hyperbenthic taxa, like *Pontostratiotes*, are <u>often neglected</u> in sampling and sorting campaigns.

➤ Existing molecular records of the genus are predominantly from the <u>Pacific Ocean</u>.

➤ Many specimens were collected during cruises in the <u>North Atlantic</u> (IceAGE/IceDiVA projects).

? **Does *Pontostratiotes* remain <u>monophyletic</u> under increased taxon sampling?**
How <u>diverse</u> is the genus in the North Atlantic and Pacific Ocean?

Monophyly

- Concatenated alignment of Aegisthidae sequences:
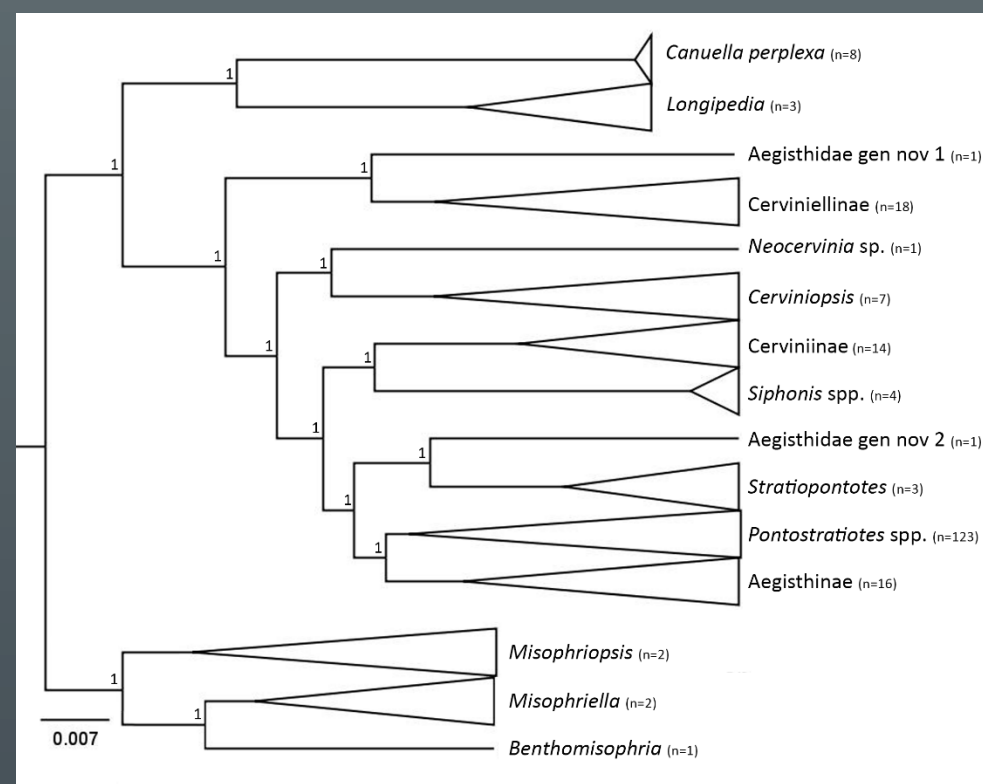- Partitions and alignment lengths: 18S (1799bp), COI (861bp), 28S (722bp)

Figure 1.
Bayesian tree of concatenated COI, 18S and 28S sequences. Values on branches are posterior probabilities. N equals the number of specimens per collapsed branch.

Take-Away

1. *Pontostratiotes* recovered as <u>monophyletic</u> lineage
2. Wide distributional ranges in North Atlantic and Pacific Ocean could enable future analysis of connectivity
3. Integrative approach revealed <u>five</u> species new to science
4. 3D high-resolution imaging opens new possibilities to obtain a better understanding of functional morphology

Biodiversity

a) Molecular approach for species delimitation

- Genetic distance-based model (Assemble Species by Automatic Partitioning/<u>ASAP</u>) + Tree based model (Generalized mixed Yule-coalescent/ <u>GMYC</u>)

b) Morphological identification (<u>M-ID</u>):

- Light and Confocal Laser Scanning Microscopy (CLSM)
- Synchrotron radiation-based microcomputed tomography (SRµCT) (→ **QR-Code below**)

Figure 2.
CLSM-Scan of *Pontostratiotes* n. sp, male. The associated species cluster in Figure 3 is indicated by a double asterisc. Scalebar = 1mm.
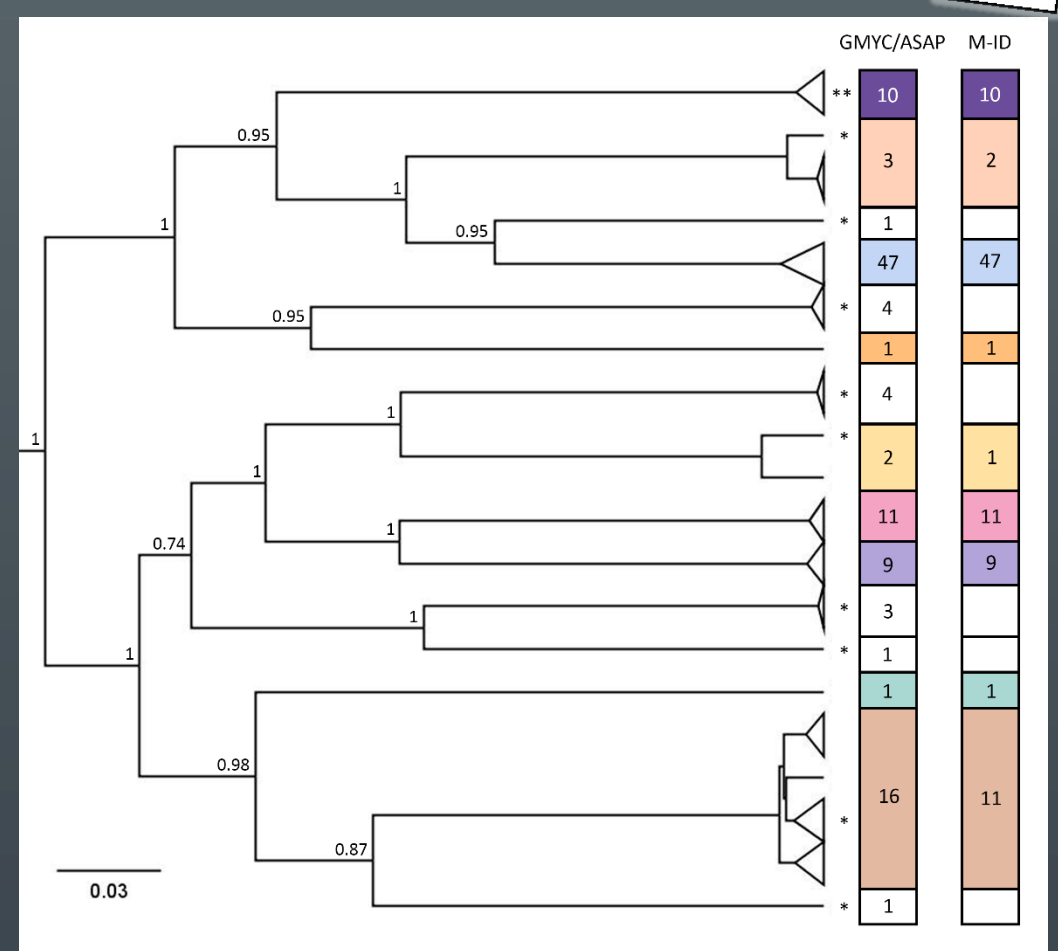

Figure 3.
Bayesian tree of COI sequences from 114 *Pontostratiotes* specimens. Results of molecular (GMYC/ASAP) and morphological species delimitation (M-ID) are shown as vertical bars. Numbers indicate specimen count. Colors refer to species clusters. Single asterisks mark sequences from Pacific specimens, downloaded from the National Center for Biotechnology Information (NCBI).

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