

Abundant and diverse *Tetrahymena* species living in the bladder traps of aquatic carnivorous *Utricularia* plants

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Supplementary Figure 1. Classification of *Tetrahymena* ciliates isolated from the artificial trapping method. Phylogenetic analysis to classify and group species of *Tetrahymena* ciliate isolated from artificial trapping. The analysis involved 32 *COX1* sequences, including 30 from samples collected from the wild. *Ichthyophthirius multifiliis* was used as an outgroup and *Glaucoma chattoni* was used as a closely-related species. All ambiguous positions were removed for each sequence pair, resulting in a dataset of 996 nucleotide positions. The Neighbor-Joining tree is drawn to scale, with branch lengths (shown on branches) in the same units as evolutionary distances based on *COX1* sequences. Numbers of *Tetrahymena* isolates for each lineage are shown in brackets. Scale bar: the number of base substitutions per site.

Supplementary Figure 2. Phylogenetic analysis of *Tetrahymena* species isolated from artificial trapping and named *Tetrahymena* species. Phylogenetic analysis of 77 *Tetrahymena* isolates based on *COX1* gene sequences, including 30 wild isolates grouped into 13 lineages (AT1~13), 43 named *Tetrahymena* species, three closely-related species (*Glaucoma chattoni*, *Dexiostoma campyla* and *Colpidium colpoda*), and *Ichthyophthirius multifiliis* as an outgroup. The *COX1* sequences are listed in Supplementary Table 2. The three

main clades of *Tetrahymena* are shown on the right. All ambiguous positions were removed for each sequence pair, resulting in a dataset of 810 nucleotide positions. The Neighbor-Joining tree is drawn to scale, with branch lengths (shown on branches) in the same units as evolutionary distances based on *COX1* sequences. Scale bar: the number of base substitutions per site.

Supplementary Figure 3. Phylogenetic analysis of *Tetrahymena* species isolated from three types of natural habitats in and around one pond in Taipei, Taiwan (25°07'41.1"N 121°38'09.8"E). Phylogenetic analysis of different types of natural inhabiting *Tetrahymena* lineages based on *COX1* gene sequences, including that red labels show two *COX1* haplotypes from *Utricularia* bladder traps, pale blue labels show five by artificial trapping from the open water, and green labels show two from a small pool of water in tree holes. All ambiguous positions were removed for each sequence pair, resulting in a dataset of 997 nucleotide positions. The Neighbor-Joining tree is drawn to scale, with branch lengths (shown on branches) in the same units as evolutionary distances based on *COX1* sequences. Scale bar: the number of base substitutions per site.

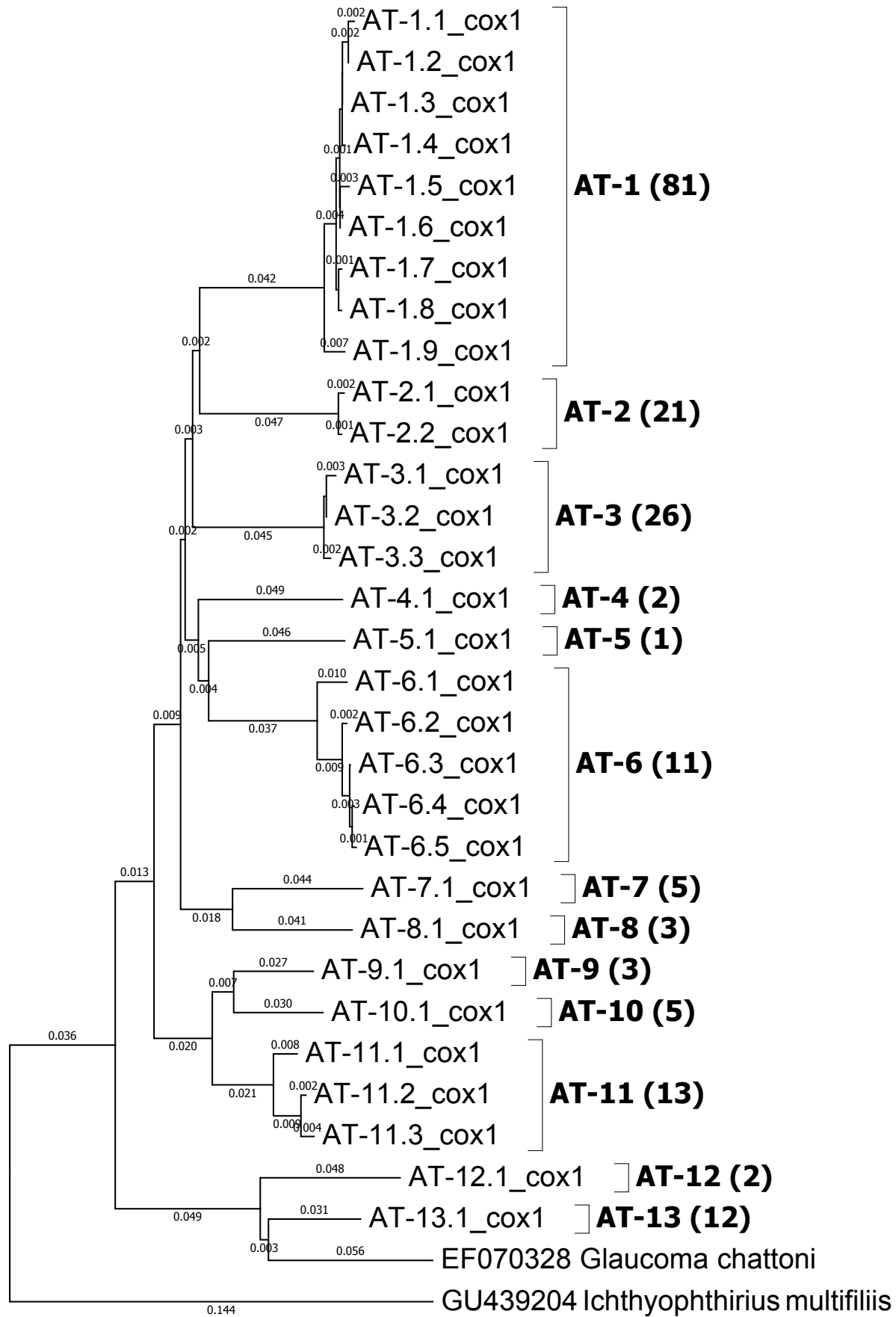
Supplementary Table 1. The list of collecting *Tetrahymena* isolated from *Utricularia* bladder traps. Table showing the information of the field survey of isolating *Tetrahymena* isolates including the isolate number, the collection date, collection site (GPS coordinate) and the species of *Utricularia* plants, etc.

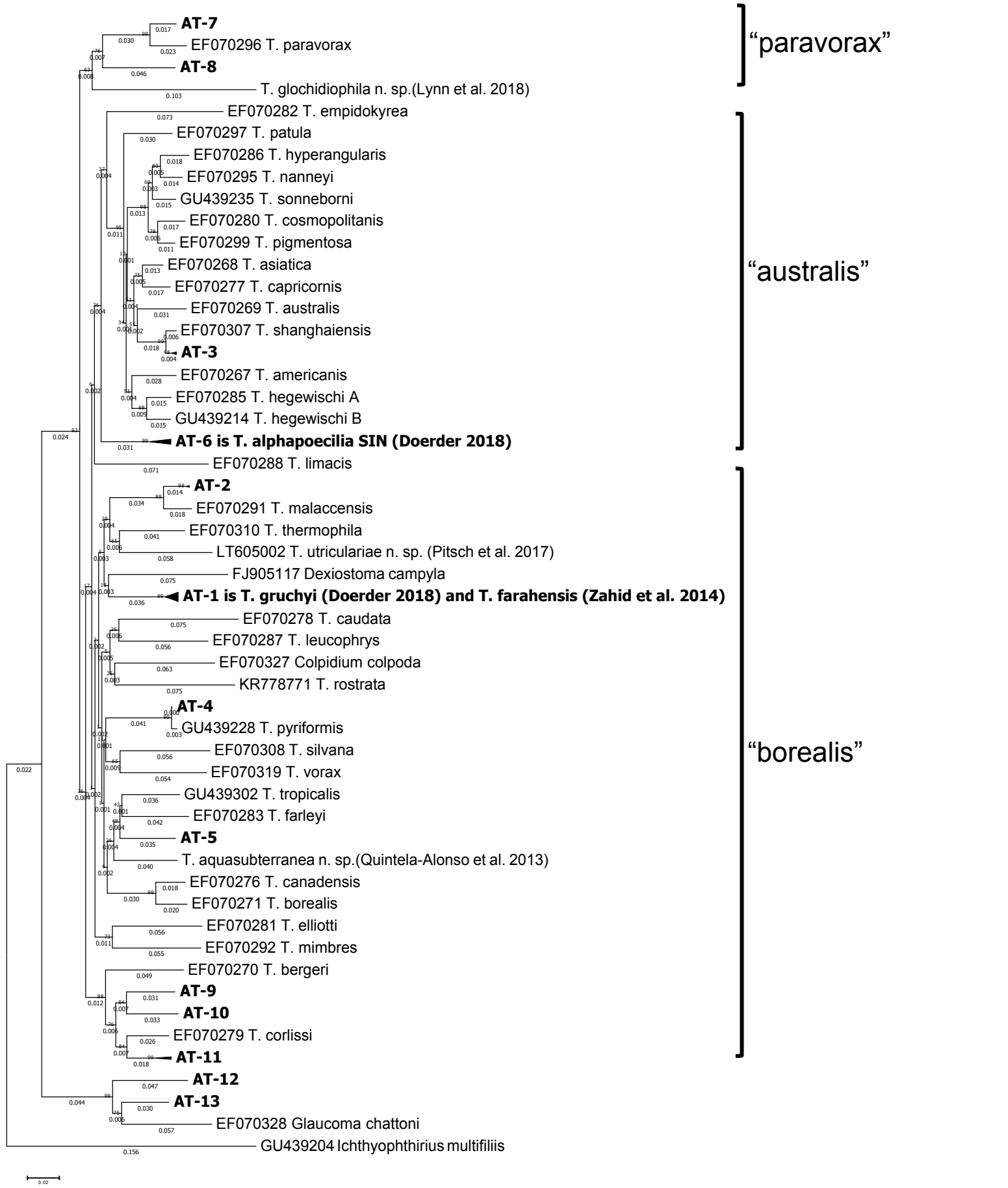
Supplementary Table 2. The list of the COX1 sequences used in the phylogenetic analysis. Table showing the COX1 accession number in the GenBank database and the COX1 sequences that were obtained in this study.

Supplementary Movie 1. *Tetrahymena*-like ciliates swim inside the bladder trap of *Utricularia aurea*.

Supplementary Movie 2 and 3. *Tetrahymena*-like ciliates associate with the decaying animal prey trapped by carnivorous *Utricularia* plants.

Supplementary Movie 4. Feeding behavior of *Tetrahymena* present in the culture medium containing animal tissue fibers.





Supplementary Fig. 3

