

## Supplementary Material

### **Characterization of new cristamonad species from kalotermitid termites including a novel genus, *Runanympha*.**

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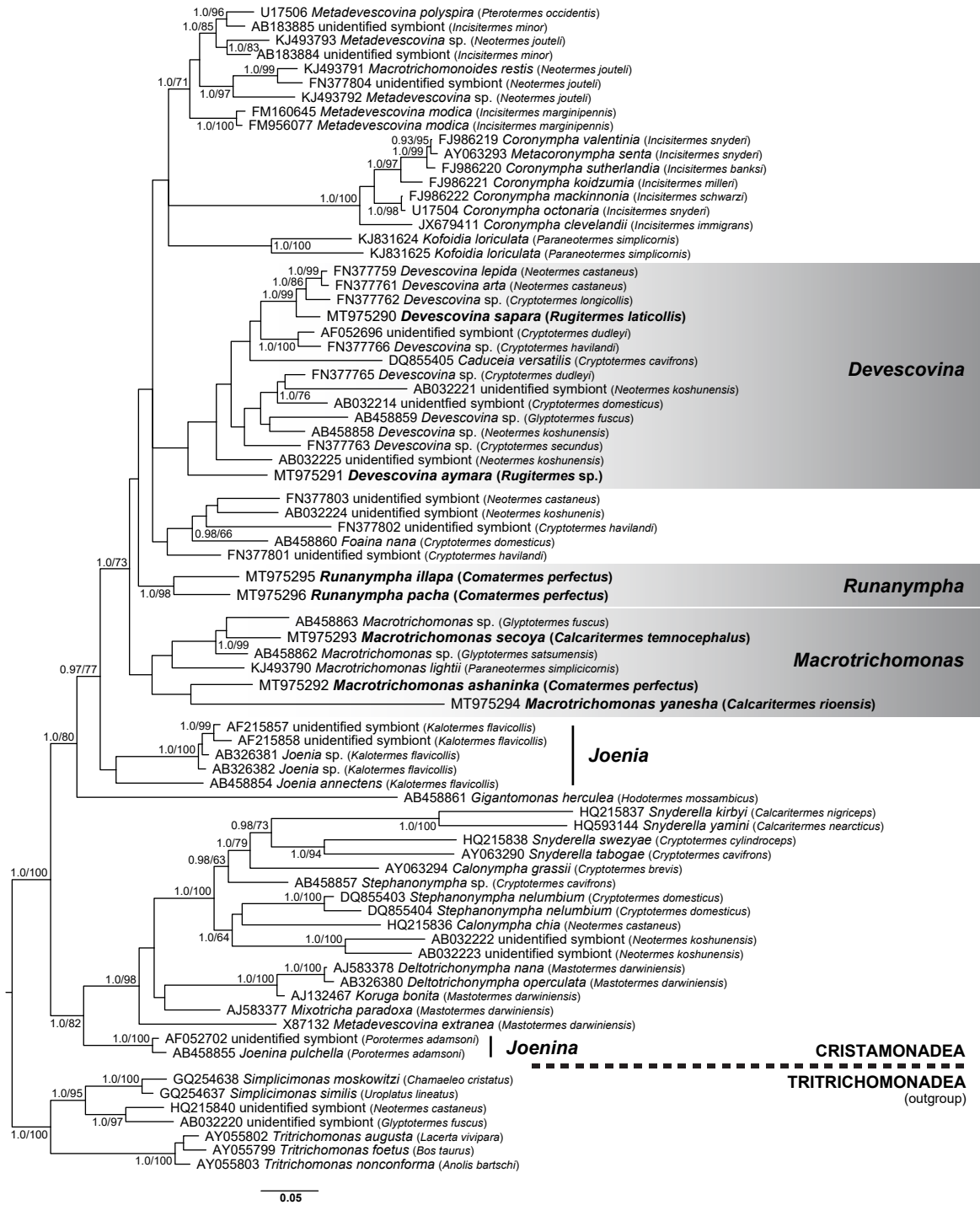
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## Supplementary Figure Legends

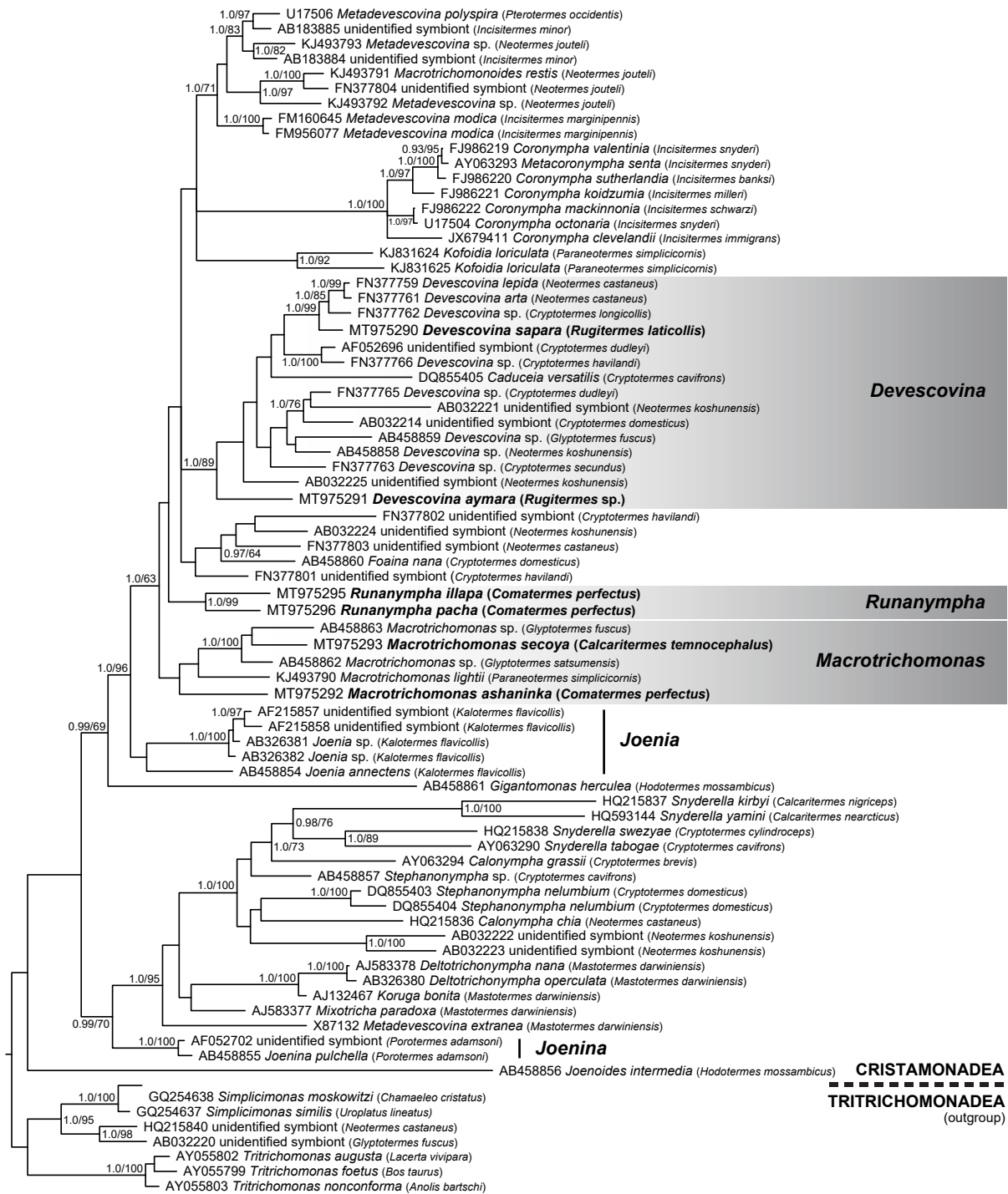
**Supplementary Figure S1.** Bayesian phylogeny of SSU rRNA sequences of the class Cristamonadea (1527 bp) including the sequence from *M. yanessa*. The tree is rooted with sequences from the closest known relatives to the Cristamonadea, members of the class Tritrichomonadea. Sequences obtained in this study are in bold type. Taxon names include GenBank accession numbers and the name of the termite host. Numerical values at nodes indicate Bayesian posterior probability (where greater than 0.90) and % ML bootstrap support (out of 1,000 replicates, where in agreement with the Bayesian topology and greater than 60%). Sequences assigned to or likely belonging to the joeniid genera *Joenia* and *Joenina* are denoted by a thick vertical bar. Tree figures were generated using the FigTree software v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>) and edited in Adobe Illustrator (<https://adobe.com/products/illustrator>).

**Supplementary Figure S2.** Bayesian phylogeny of SSU rRNA sequences of the class Cristamonadea (1526 bp) including the sequence from *Joenoides intermedia*. The tree is rooted with sequences from the closest known relatives to the Cristamonadea, members of the class Tritrichomonadea. Sequences obtained in this study are in bold type. Taxon names include GenBank accession numbers and the name of the termite host. Numerical values at nodes indicate Bayesian posterior probability (where greater than 0.90) and % ML bootstrap support (out of 1,000 replicates, where in agreement with the Bayesian topology and greater than 60%). Sequences assigned to or likely belonging to the joeniid genera *Joenia* and *Joenina* are denoted by a thick vertical bar. Tree figures were generated using the FigTree software v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>) and edited in Adobe Illustrator (<https://adobe.com/products/illustrator>).

**Supplementary Video S1.** Differential interference contrast (DIC) microscopy video clips of new *Devescovina*, *Macrotrichomonas*, and *Runanympha* specimens. Symbionts were observed with an Axioplan 2 DIC microscope (Zeiss) and multiple cells of each symbiont species were filmed with a 3CCD HD video camera XL H1S (Canon).



Supplementary Figure S1.



0.06

Supplementary Figure S2.

## Supplementary Tables

**Supplementary Table S1.** Mean pairwise identities of SSU rRNA sequences within new Cristamonadea species and across species. Mean pairwise identity values across species are calculated between each new cristamonad specimen and the sequence with which the species shares the highest mean pairwise identity (also listed in the table). Sequences that were obtained in this study are marked with an asterisk (\*) whereas sequences collected from Genbank are presented with Genbank accession numbers.

Species	Mean pairwise distance of sequences within species	Mean pairwise distance to closest sequence in the tree	Closest sequence in the tree
<i>Devescovina sapara</i>	99.21 %	97.43%	FN377761.1 – <i>Devescovina arta</i>
<i>Devescovina aymara</i>	98.51%	94.21%	FN377763.1 – <i>Devescovina</i> sp.
<i>Macrotrichomonas ashaninka</i>	97.62%	93.74%	AB458862.1 – <i>Macrotrichomonas</i> sp.
<i>Macrotrichomonas secoya</i>	98.12%	95.77%	AB458862.1 – <i>Macrotrichomonas</i> sp.
<i>Macrotrichomonas yanesha</i>	99.13%	89.96%	* <i>Macrotrichomonas ashaninka</i> sequence 14_50_38Mac17_32
<i>Runanympha illapa</i>	97.46%	95.59%	* <i>Runanympha pacha</i> sequence 19_10_43_17Placo_8
<i>Runanympha pacha</i>	96.82%	95.58%	* <i>Runanympha illapa</i> sequence 18_10_26_35Joe_37_2