

Hidden diversity of planktonic *Entomoneis* species

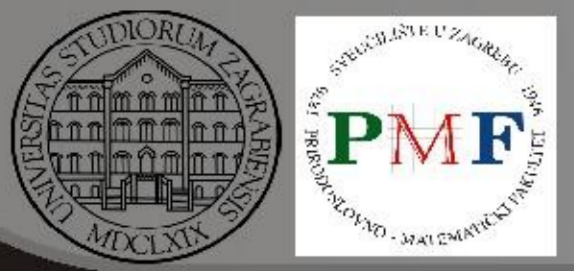
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This study reveals hidden diversity of planktonic *Entomoneis* species with combined morphological and phylogenetical approach. Previous new species descriptions based only on morphology neglected the full diversity of diatom genus *Entomoneis*, which today becomes well-known from both benthos and plankton of world's freshwater and marine ecosystems.

Samples in this study originate from BIOTA (Bio-tracing Adriatic Water Masses) cruise conducted in March 2016 in the south-eastern Adriatic Sea and middle Adriatic sampling campaigns (Telašćica Nature Park and Kornati National Park) conducted during June and October 2015. 14 monoclonal strains were established from plankton net samples and fractioned samples taken from range of different depths (30m, 100m, 250m) by manual pipette isolation.

Preliminary results are composed as LM, SEM and TEM plates of figures for each strain (Figs 1-158) and Maximum Likelihood phylogram inferred from the SSU rDNA, *psbC* and *rbcL* genes (Fig. 159). Morphometric features are indicated in plates captions as: valve length (VL), valve width (VW), frustule length (FL), frustule width at constricted part (FWC), frustule width at widest part including wings (FWW), number of striae on the valve body in 10µm (VS), number of wing striae in 10µm (WS), number of hymen perforations within stria near valve margin in 1µm (VP), number of hymen perforations within stria near keel margin in 1µm (KP), number of basal fibulae in 1µm (BF), number of interfibulae in 1µm (IF), number of raphe fibulae in 10µm (RF), number of areolae in valvocopulae in 10µm (VCA), number of areolae in copulae in 10µm (CA), total number of poroids in valvocopular advalvar areolae (ADAP), total number of poroids in valvocopular abvalvar areolae (ABAP).

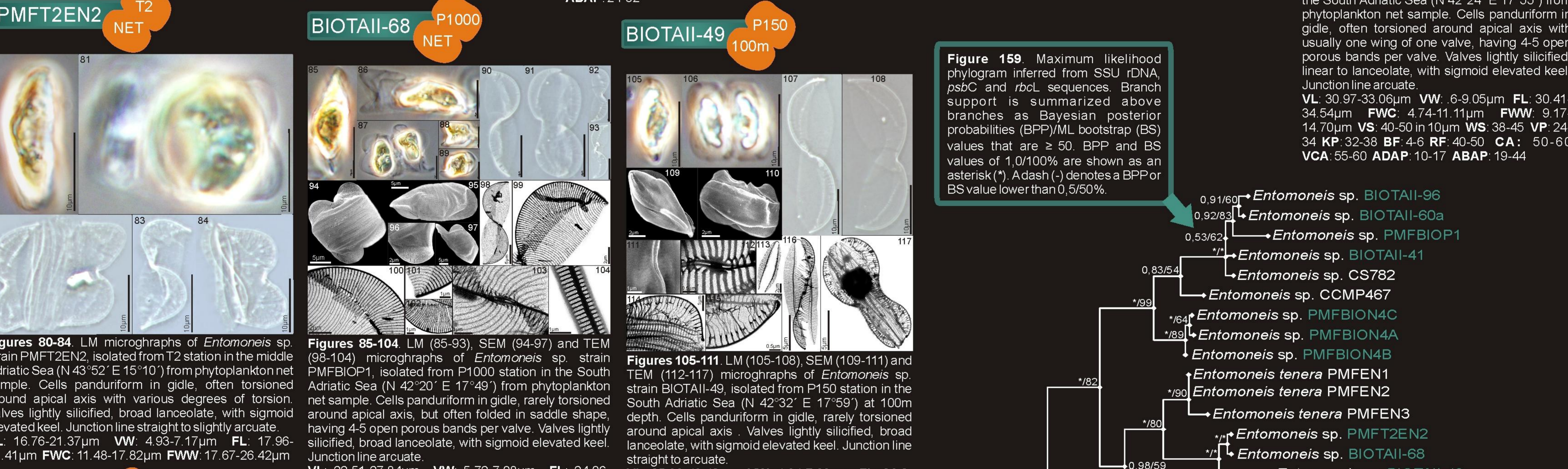
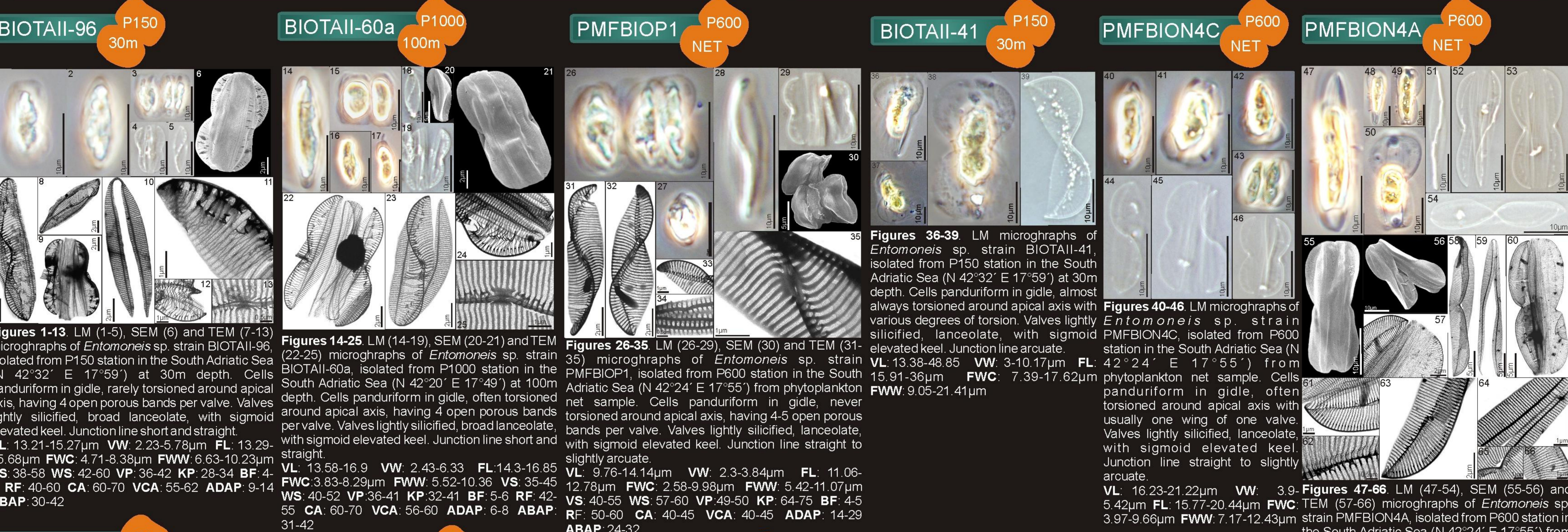
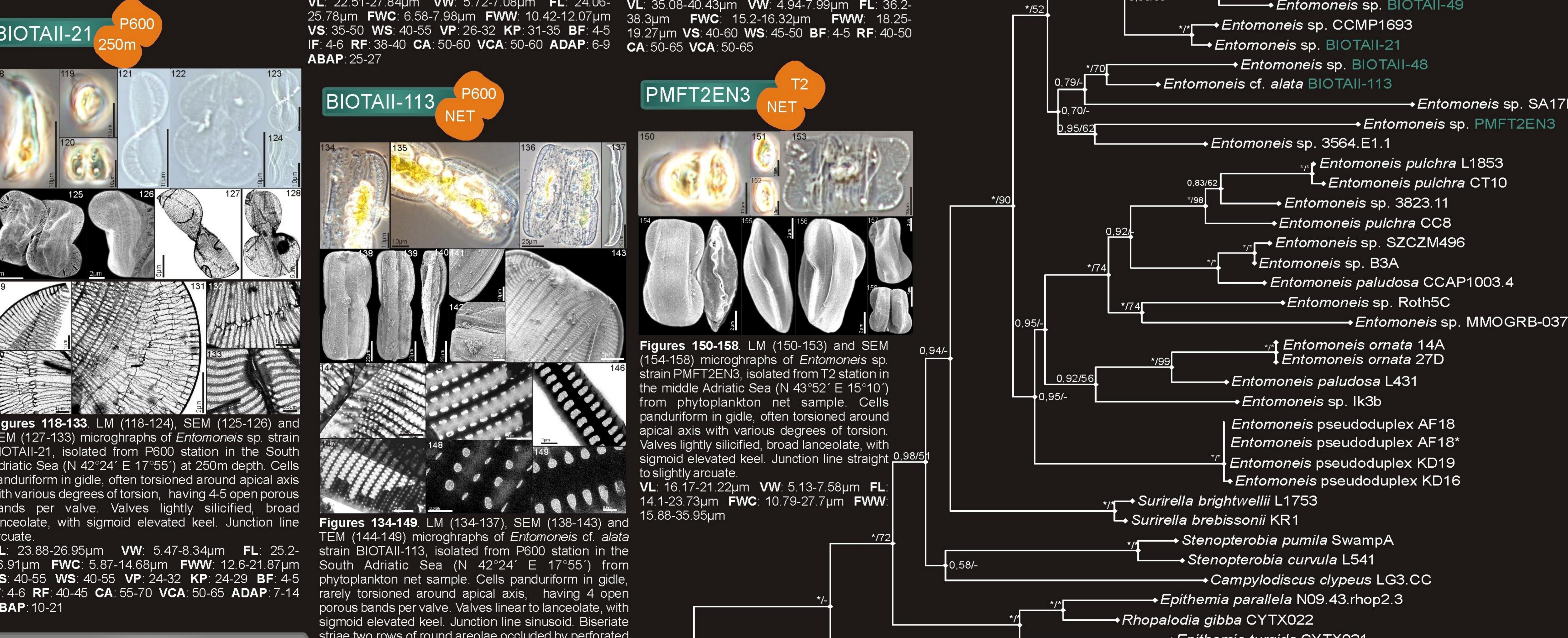
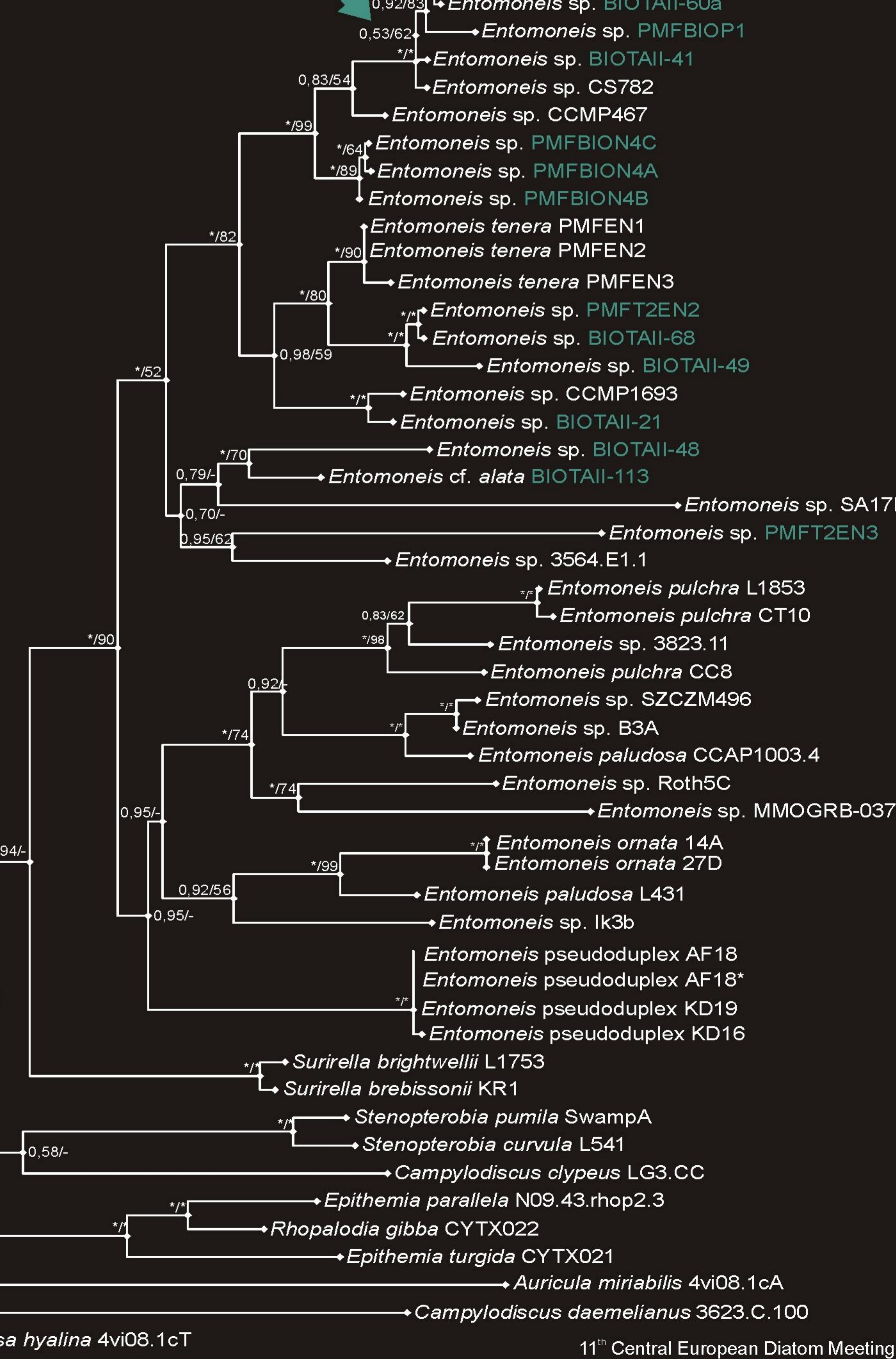


Figure 159. Maximum likelihood phylogram inferred from SSU rDNA, *psbC* and *rbcL* sequences. Branch support is summarized above branches as Bayesian posterior probabilities (BPP)/ML bootstrap (BS) values that are > 50. BPP and BS values of 1.0/100% are shown as an asterisk (*). A dash (-) denotes a BPP or BS value lower than 0.5/50%.



ACKNOWLEDGMENTS
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