

**Supplementary material**

***Fassettia*, a new North American genus of family Ceratophyllaceae:  
evidence based on cladistic analyses of current molecular data of *Ceratophyllum***

Evgeny V. Mavrodiev<sup>A,E</sup>, David M. Williams<sup>B</sup>, Malte C. Ebach<sup>C</sup> Anna E. Mavrodieva<sup>D</sup>

<sup>A</sup>Florida Museum of Natural History, University of Florida, PO Box 117800,  
Gainesville, FL 32611, USA.

<sup>B</sup>Department of Life Sciences, the Natural History Museum, Cromwell Road,  
London, SW7 5BD, UK.

<sup>C</sup>Paleontology, Geobiology and Earth Archives Research Centre, School of Biological,  
Earth and Environmental Sciences, UNSW, Kensington, NSW 2052, Australia.

<sup>D</sup>University of Florida, Gainesville, FL 32641, USA.

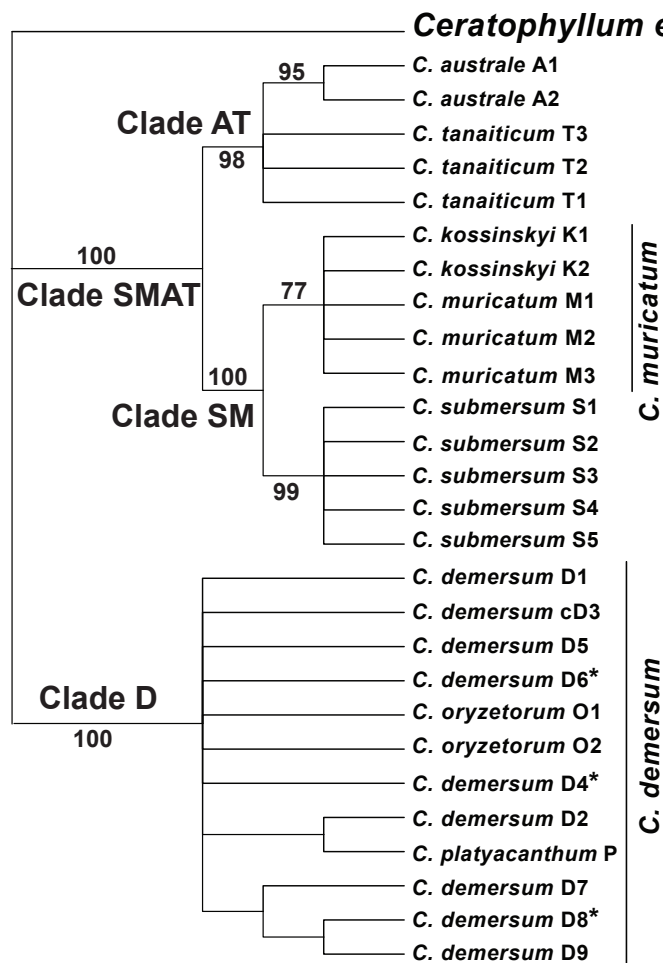
<sup>E</sup>Corresponding author. Email: [evgeny@ufl.edu](mailto:evgeny@ufl.edu)

**Table S1. Summary of the results of the standard MP, 3TA, 3TS-AC, and AC analyses of the combined molecular alignment of *Ceratophyllum L.* (Szalontai *et al.* 2018) and its binary representations**

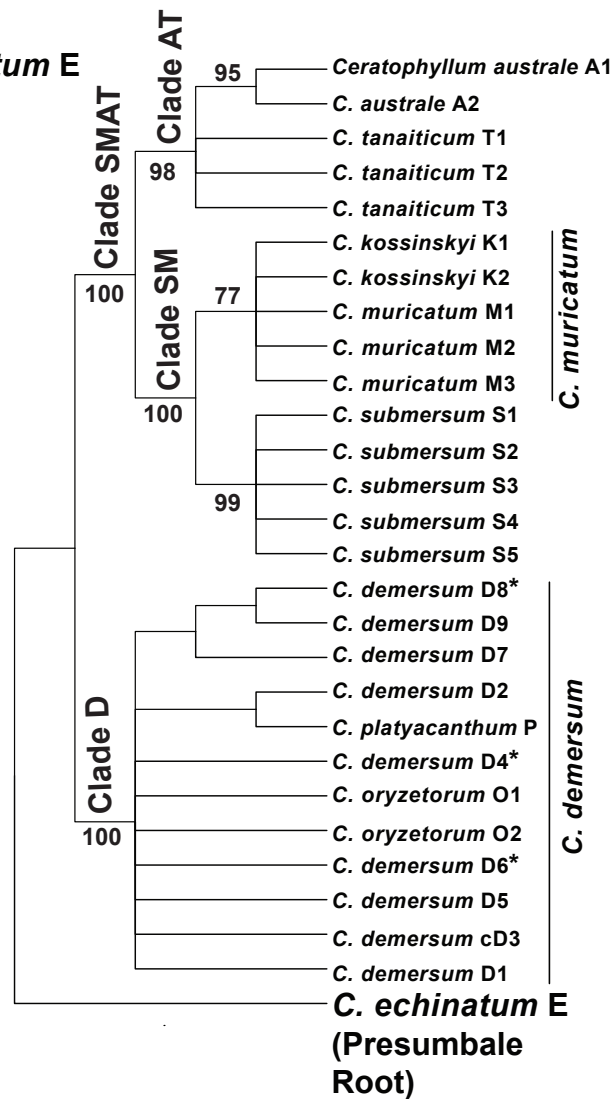
Abbreviations: AC, average consensus; A-Z, all-zeros outgroup; BM, binary matrix; CI, consistency index; FP, Fitch parsimony; FW, practional weighting; IT, input trees (for AC analyses); MaxT, ‘maximal’ trees (or relationships); MM, molecular matrix; N, Newick (Phylip) format; O, outgroup; OO, operational outgroup; OT, output trees; PIC, parsimony-informative characters; RI, retention index; UW, uniform weighting; WP, Wagner parsimony; 3TSs, three-taxon statements

Figure	Data	Analyses	O	OO	Number of PIC or IT	Number of OTs	Length of the OTs	CI	RI	AC score
S2A	BM	WP	A-Z	–	252	1	450	0.7356	0.917	–
S2B	MaxT (N)	AC	A-Z	–	252	18	–	–	–	0.02038
S2C	3TSs (N)	AC-UW	A-Z	–	144 515	18	–	–	–	0.06392
S2D	3TSs (BM)	WP-FW	A-Z	–	144 515	6	26 536.0104	–	0.823	–
S3A	MM	FP	<i>Acorus</i>	–	104	1	498	0.9317	0.947	–
S3B	3TSs (N)	AC-UW	A-Z	<i>Acorus</i>	140 872	108	–	–	–	0.07928
S3C	3TSs (BM)	WP-UW	A-Z	<i>Acorus</i>	140 872	1	148 568	–	0.9454	–
S4A	MM	FP	<i>Ranunculus</i>	–	104	1	499	0.9399	0.955	–
S4B	3TSs (N)	AC-UW	A-Z	<i>Ranunculus</i>	130 898	135	–	–	–	0.0571
S4C	3TSs (BM)	WP-UW	A-Z	<i>Ranunculus</i>	130 898	1	137 222	–	0.9517	–
S5A	MM	FP	<i>Chloranthus</i>	–	106	1	461	0.9262	0.949	–
S5B	3TSs (N)	AC-UW	A-Z	<i>Chloranthus</i>	118 708	540	–	–	–	0.10026
S5C	3TSs (BM)	WP-UW	A-Z	<i>Chloranthus</i>	118 708	2	125 185	–	0.9454	–

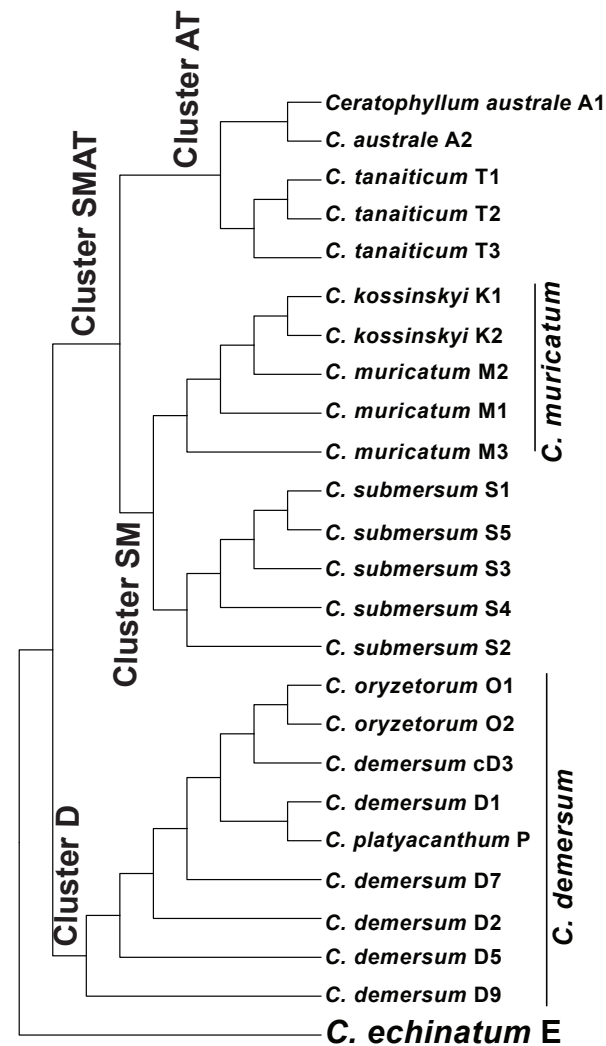
A.



B.



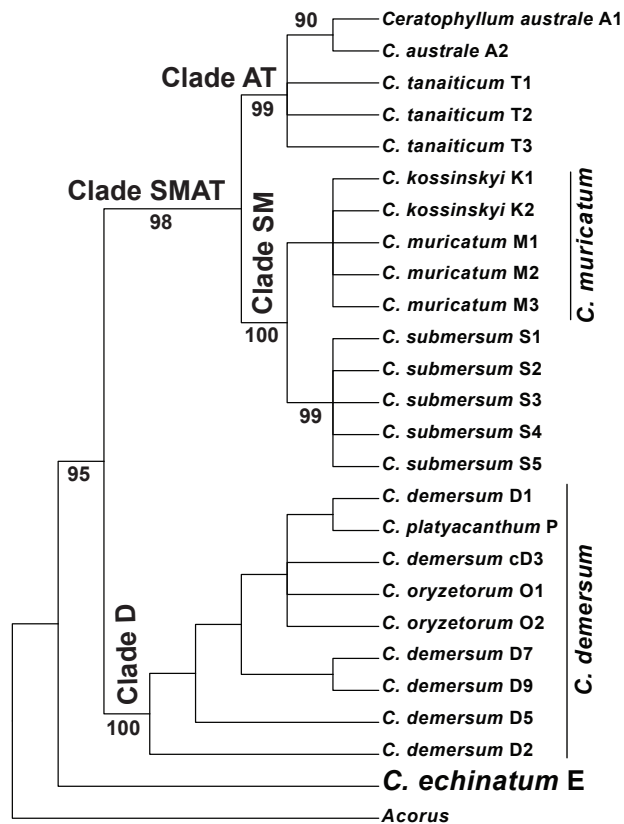
C.



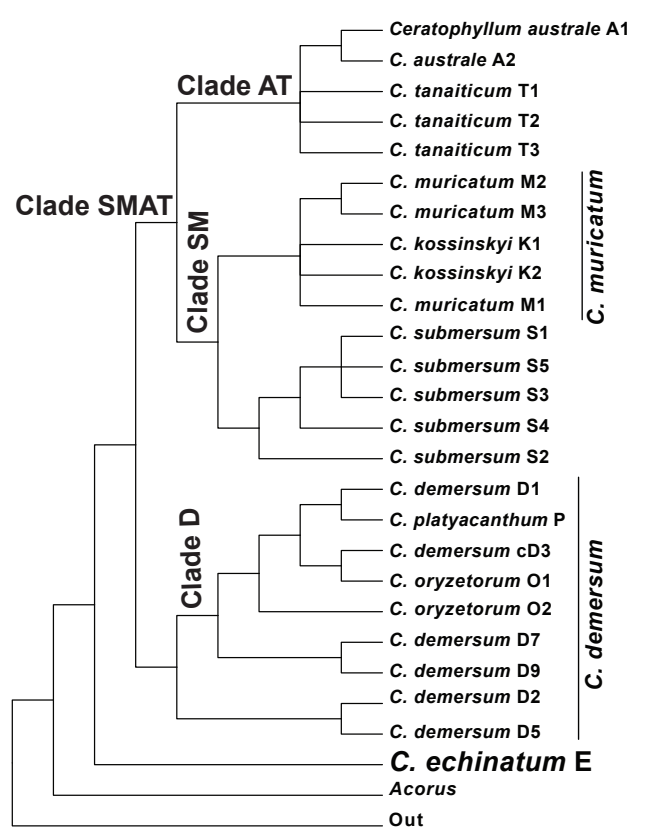
**Fig. S1.** Summary trees based on Szalontai *et al.* (2018, p. 166, their fig. 1) in comparison with the phenogram resulted the UPGMA analysis of the molecular data from the same authors. A. Unrooted tree summarising the results of the MP and BI analyses of the combined molecular alignment of *Ceratophyllum* (Szalontai *et al.* 2018, p. 166); numbers above or below the branches indicate MP bootstrap support values/posterior probabilities. B. The same tree as A, but *a posteriori* rooted relative to *Ceratophyllum echinatum*. C. Phenogram resulted the UPGMA analysis of the same combined molecular alignment (A) of *Ceratophyllum*. The names of the clades/clusters are taken from Szalontai *et al.* (2018).



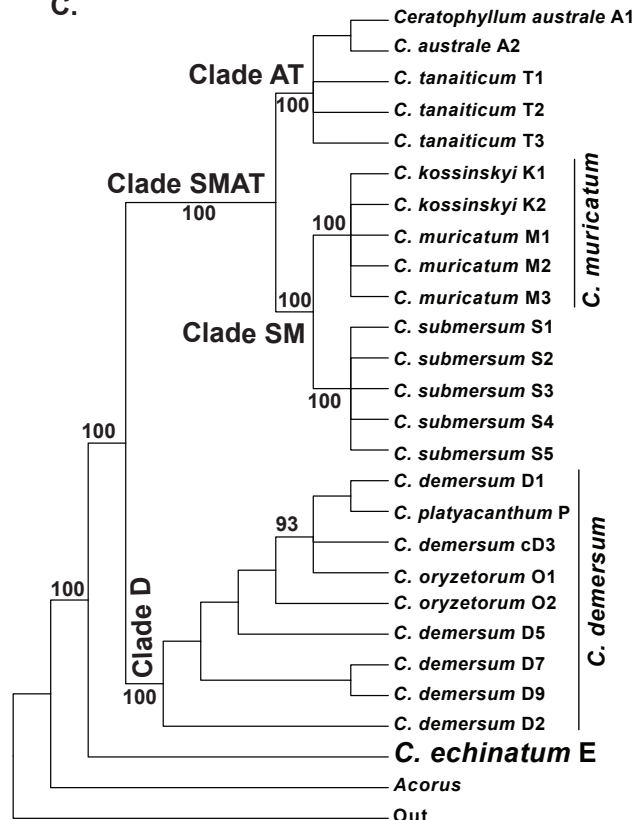
A.



B.

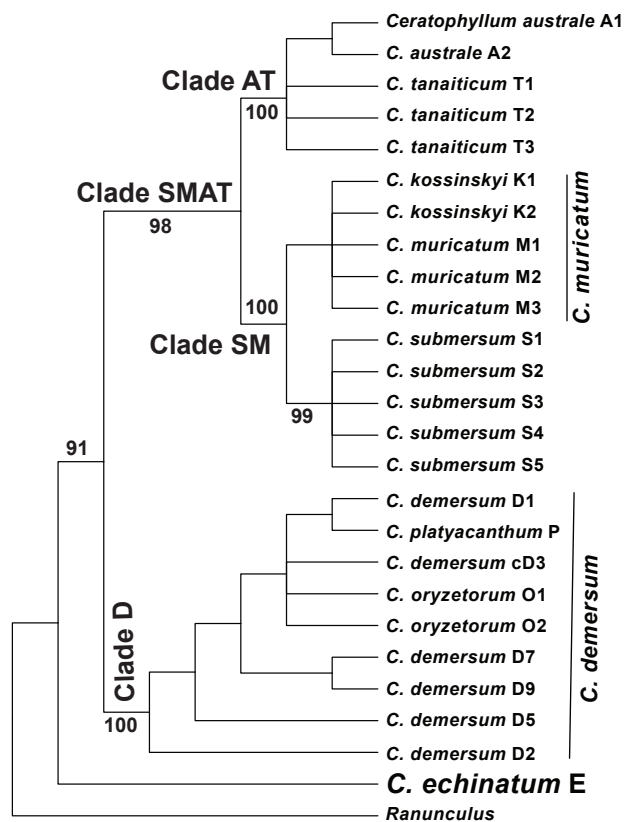


C.

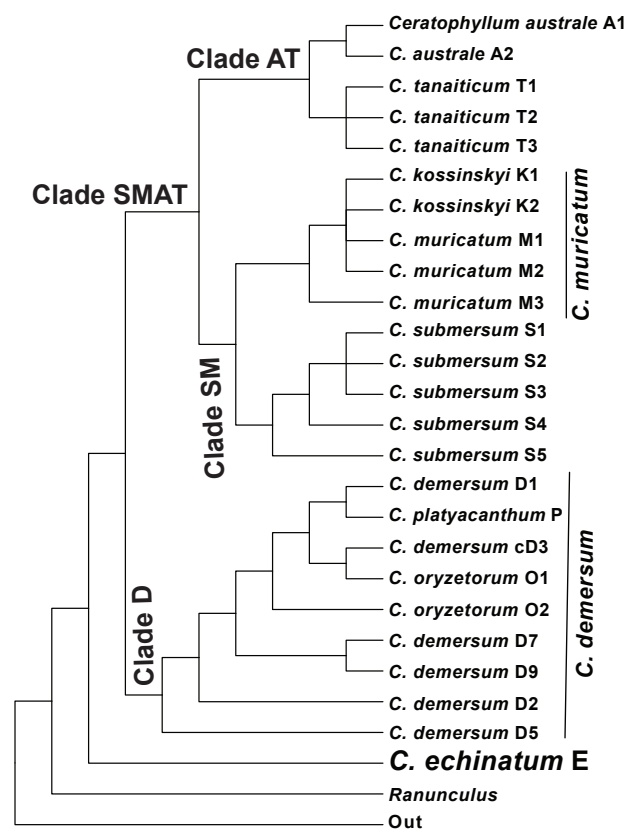


**Fig. S3.** The results of the AC and MP analyses of the combined molecular alignment of *Ceratophyllum* based on the data from Szalontai *et al.* (2018), with the addition of the sequence data of *Acorus* assumed as an outgroup of *Ceratophyllum*. A. single most parsimonious tree (standard MP). B. Strict consensus of 108 nested hierarchies of patterns (3TS2 ACA). C. Single most parsimonious nested hierarchy of patterns (3TA). For 3TS-ACA and 3TA (B and C) the value of the operational outgroup assumed as a value of *Acorus*. Numbers above or below the branches (standard MP/3TA) indicate MP bootstrap support values equals or more than 90%. See Table S1 for more detail. The names of the clades are taken from Szalontai *et al.* (2018).

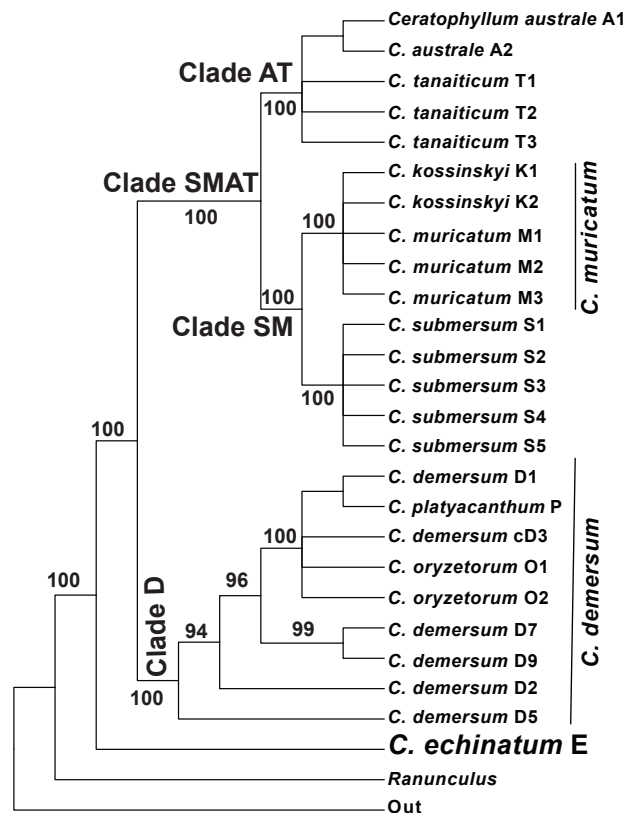
A.



B.

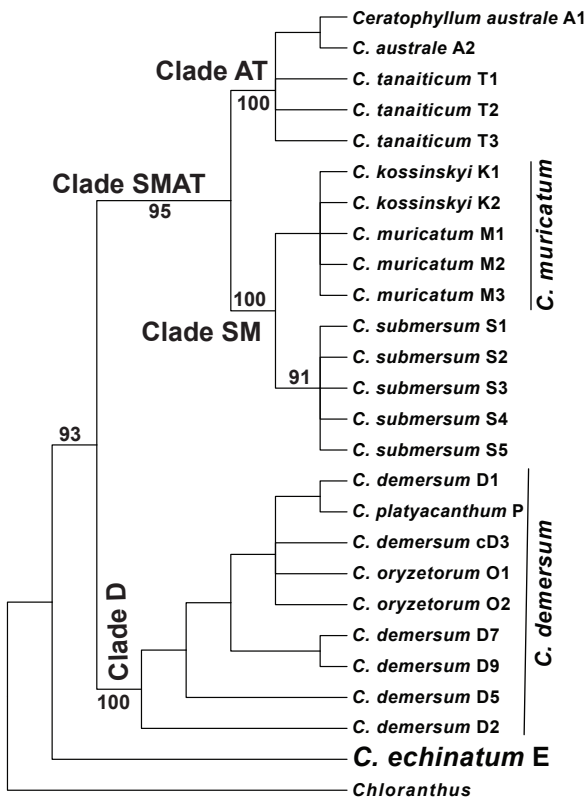


C.

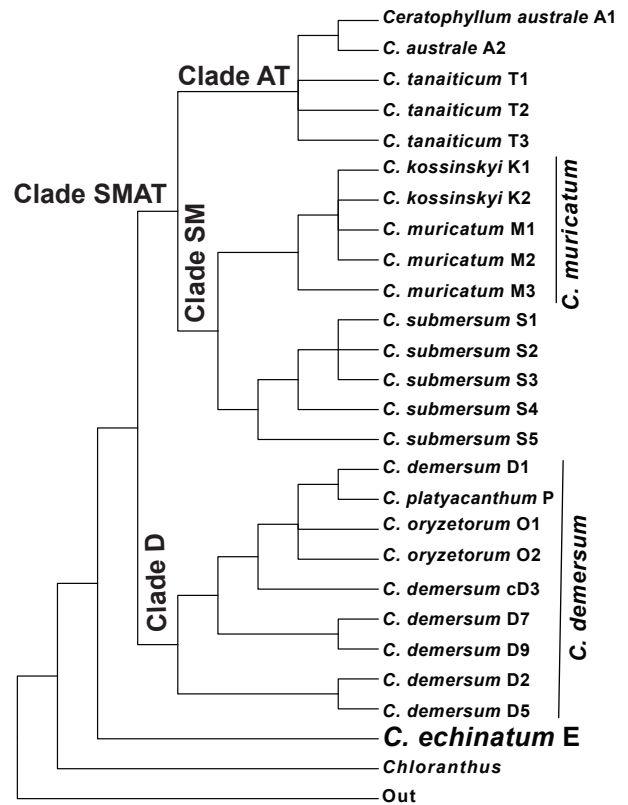


**Fig. S4.** The results of the AC and MP analyses of the combined molecular alignment of *Ceratophyllum* based on the data from Szalontai *et al.* (2018), with the addition of the sequence data of *Ranunculus* assumed as an outgroup of *Ceratophyllum*. A. single most parsimonious tree/standard MP. B. Strict consensus of 135 nested hierarchies of patterns (3TSACA). C. Single most parsimonious nested hierarchy of patterns (3TA). For 3TS-ACA and 3TA (B and C) the value of the operational outgroup assumed as a value of *Ranunculus*. Numbers above or below the branches (standard MP/3TA) indicate MP bootstrap support values equals or more than 90%. See Table S1 for more detail. The names of the clades are taken from Szalontai *et al.* (2018).

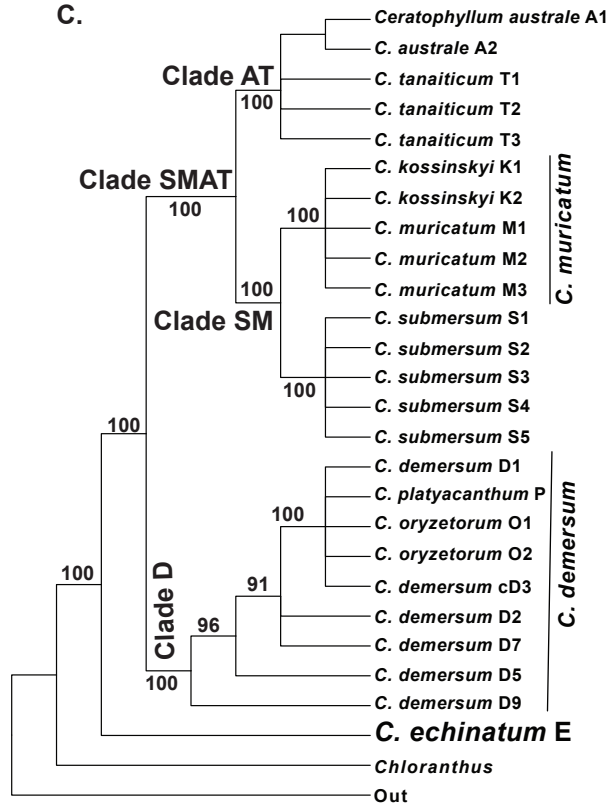
A.



B.



C.



**Fig. S5.** The results of the AC and MP analyses of the combined molecular alignment of *Ceratophyllum* based on the data from Szalontai *et al.* (2018), with the addition of the sequence data of *Chloranthus* assumed as an outgroup of *Ceratophyllum*. A: single most parsimonious tree (standard MP). B. Strict consensus of 540 nested hierarchies of patterns (3TSACA). C. Strict consensus of two nested most parsimonious hierarchies of patterns (3TA). For 3TS-ACA and 3TA (B and C) the value of the operational outgroup assumed as a value of *Chloranthus*. Numbers above or below the branches (standard MP/3TA) indicate MP bootstrap support values equals or more than 90%. See Table S1 for more detail. The names of the clades are taken from Szalontai *et al.* (2018).

## Reference

Szalontai B, Stranzinger S, Mesterhazy A, Scribailo RW, Les DH, Efremov AN, Jacono CC, Kipriyanova LM, Kaushik K, Laktionov AP, Terneus E, Csiky J (2018) Molecular phylogenetic analysis of *Ceratophyllum* L. taxa: a new perspective. *Botanical Journal of the Linnean Society* **188**, 161–172. [doi:10.1093/botlinnean/boy057](https://doi.org/10.1093/botlinnean/boy057)