

**Appendix S7.** Statistics on the data set A alignments for southern African *Trebouxia* after the removal of ambiguously aligned regions. n = number of terminal branches; PI = parsimony-informative sites. The *rbcL* alignment was 789 bases long for all clades and had no excluded positions. nrITS regions and codon positions with the same number in the Model/Partition columns were fused into a single partition (Kalyaanamoorthy et al., 2017). Model/Partition is given as ITS1:5.8S:ITS2 for nrITS and first:second:third codon positions for *rbcL*. Substitution models were as follows: 1 = SYM+G4 (Zharkikh, 1994); 2 = K2P+I (Kimura, 1980); 3 = GTR+F+R3 (Tavaré, 1986); 4 = SYM+R3; 5 = TNe+R2 (Tamura and Nei, 1993); 6 = TIM2+F+G4; 7 = K2P+R2; 8 = TIM2+F+I; 9 = TVM+F+G4; 10 = TIM3+F+I+R2.

Clade	n	nrITS			<i>rbcL</i>	
		Length	PI (%)	Model/Partition	PI (%)	Model/Partition
A	365	636	278 (44)	1:2:1	110 (14)	2:2:3
C	221	522	170 (33)	4:5:4	141 (18)	5:5:6
I	197	520	133 (26)	4:7:4	97 (12)	7:7:8
S	150	572	147 (26)	9:2:9	44 (6)	2:2:10

## References

- Kalyaanamoorthy, S., B. Q. Minh, T. K. Wong, A. Von Haeseler, and L. S. Jermiin. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587–589.
- Kimura, M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16: 111–120.
- Tamura, K., and M. Nei. 1993. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* 10: 512–526.
- Tavaré S. 1986. Some probabilistic and statistical problems in the analysis of DNA sequences, pp. 57–86, *DNA Sequence Analysis*, Lectures on mathematics in the life sciences 17. American Mathematical Society, Providence, RI, USA.
- Zharkikh, A. 1994. Estimation of evolutionary distances between nucleotide sequences. *Journal of Molecular Evolution* 39: 315–329.