

Cimerman Ž., Anžlovar S. & Strgulc Krajšek S. (2025) Genus *Aneura* (*Marchantiophyta*) in Slovenia and new potential lineages for Europe. – Preslia 97: 589–612.

Supplementary Table S4. Partitions and substitution models used in maximum likelihood partition analysis.

To find the best-fitting partitioning scheme, PartitionFinder 2 (Lanfear et al. 2016) was used. The appropriate model of evolution for each partition was determined automatically with ModelFinder (Kalyaanamoorthy et al. 2017).

Partition	Substitution model
ITS1	GTR+I+G
<i>trnL</i> exon 2, <i>trnF</i> , 5.8 S rRNA	TRNEF+I+G
ITS2	GTR+G
<i>trnL</i> intron, <i>matK</i> 1 st , 2 nd codon pos.	GTR+G
<i>matK</i> 3 rd codon pos.	TVM+G
<i>psbA</i> 1 st codon pos.	TIM+G
<i>psbA</i> 2 nd codon pos.	F81+G
<i>psbA</i> 3 rd codon pos.	K81UF+G
<i>psbA-trnH</i> intergenic spacer	TVM+G
<i>trnH</i>	TRNEF+I
<i>trnL</i> exon 1	K80+I
<i>trnL-trnF</i> intergenic spacer	HKY+G

References

- Lanfear R., Frandsen P. B., Wright A. M., Senfeld T., & Calcott B. (2016) PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. – *Molecular biology and evolution* 34: 772–773.
- Kalyaanamoorthy S., Minh B. Q., Wong T. K. F., Haeseler von A. & Jermini L. S. (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. – *Nature Methods* 14: 587–589.