

An intron of the *hsp90* gene as a new promising phylogenetic marker for the genus *Carex* L.

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Key words: *Carex*, sedges, DNA barcoding, phylogeny

Motivation and Aim: *Carex* L. (family Cyperaceae) is one of the most species-rich genera of higher plants. It contains over 2000 species. Many aspects of *Carex* taxonomy are yet unclear, so DNA sequence data is promising as a supplement to traditional morphological comparison. Traditional DNA barcoding markers, i.e. various plastid genes and intergenic spacers and the nuclear ribosomal gene cluster are often insufficiently informative, which makes the development of new gene markers an important task.

Methods and Algorithms: We tested a set of universal primers from [1] on sedges belonging to sections *Vesicariae* Meinsh., *Paludosae* Fries ex Kük., and *Carex*.

Results: Most amplifications were either unsuccessful or yielded conservative sequences with very few substitutions. However, in the case of the *hsp90* gene we obtained an intron approximately 450 bp long flanked by highly conservative exons. We designed a set of universal primers for this intron and checked amplification consistency on a set of *Carex* species. Amplification was successful in ~80% of specimens. The *hsp90* intron was found to harbor more characteristic sequence substitutions than conventional plastid and nuclear ribosomal markers. For the section *Vesicariae*, a portion of the *hsp90* intron 314–366 bp long (size difference due to indels) contained 11 parsimony-informative substitutions and 5 taxon-specific indels, while a part of the *matk* gene 591 bp long had only three parsimony-informative substitutions, and the ITS2 spacer 438 bp long had five. We should note that sequencing was impeded by the presence of two poly-T tracts, both 7–9 bp long. However, high sequence divergence of the *hsp90* intron compensates for its comparatively low reliability, and its short length makes it very convenient for the study of herbarium specimens that often have degraded DNA.

Conclusion: The *hsp90* intron is a promising marker for DNA barcoding and phylogenetic studies of sedges.

Acknowledgements: Supported by the State Assignment No. 0324-2018-0017.

References

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