

DNA barcoding evaluation in the genus *Bromus* (Poaceae-Bromeae) using nrDNA sequences

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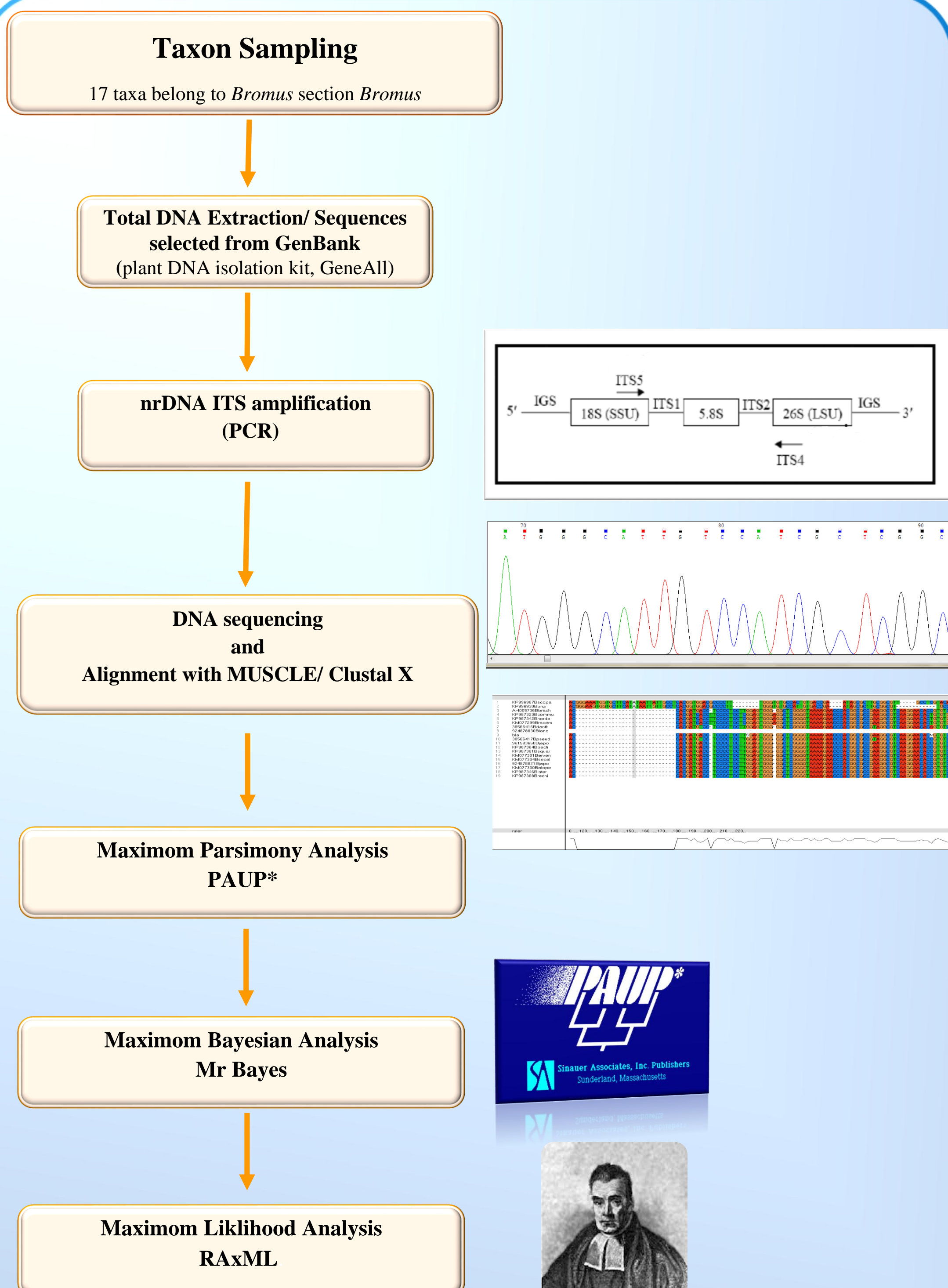
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1. Introduction

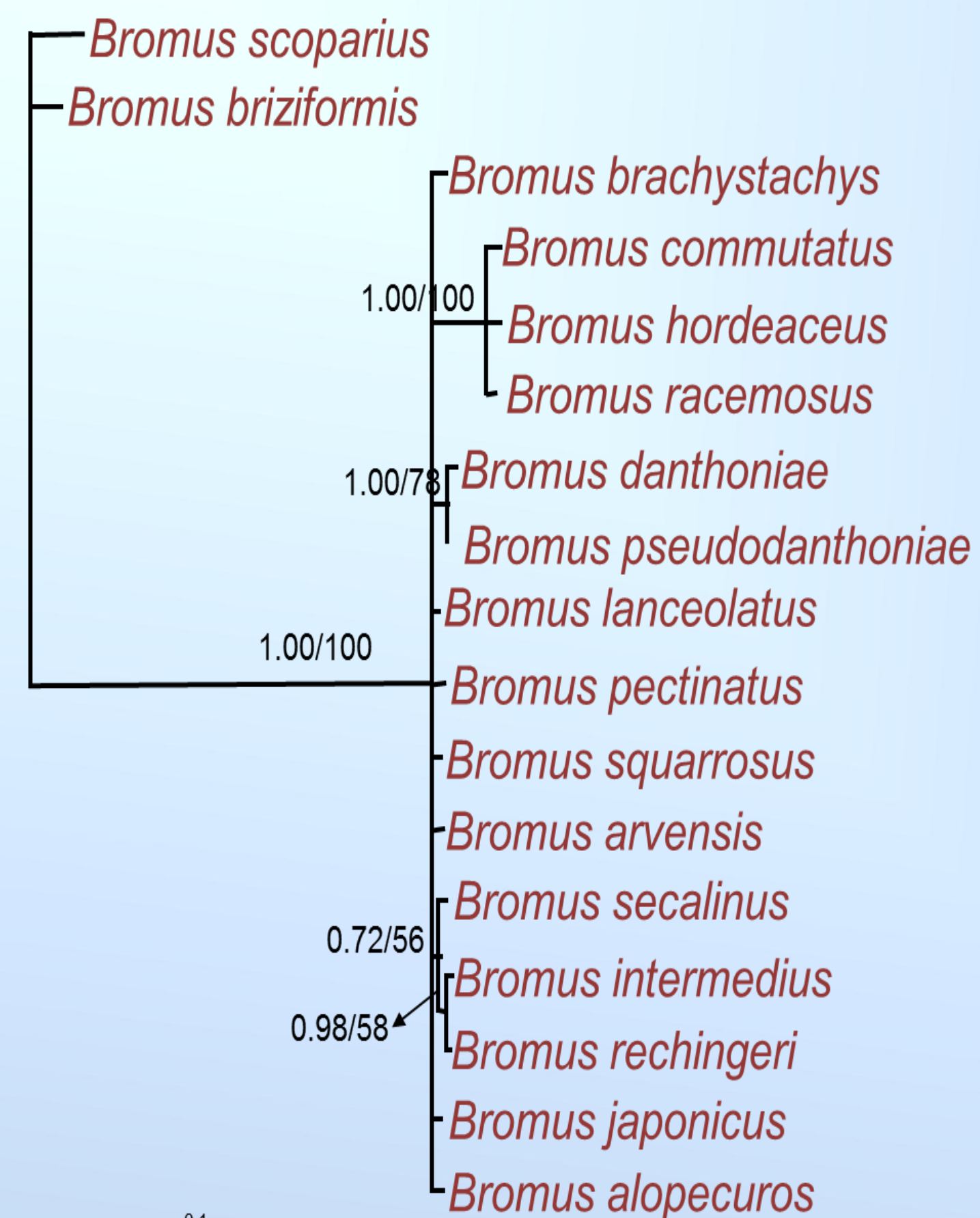
The novel technique of identifying biological specimens using short DNA sequences from either nuclear or organelle genomes is called DNA barcoding. DNA barcoding not only helps in the identification of species but can also define species boundaries, flagging of new species and species delimitation [1,2]. The Consortium for the Barcode of Life Plant Working Group (CBOL) [3] evaluated seven chloroplast genomic regions across the plant kingdom and proposed a combination of *matK* and *rbcL* as plant barcodes. In closely related species, the discriminating ability of these two markers is low [4,5]. Therefore, the China Plant BOL Group [6] proposed the addition of nuclear ITS (Internal Transcribed Spacer) to the *matK* + *rbcL* combination as plant barcode in order to achieve maximum identification rates even in closely related species. *Bromus* L. with more than 151 species in the world comprises annual to perennial species. *Bromus* taxonomically is a complex genus with difficult nomenclatural history and many species are hard to distinguish due to their high degree of morphological similarity [7].

2. Computational Method



3. Results and Discussion

- From total of characters (561), 243 were informative.
- 264 shortest tree with L= 264 steps and CI= 0.981 and RI= 0.982 were generated.
- Dataset were analyzed with GTR+I model by Bayesian inference using program MrBayes.



Fifty percent majority rule consensus tree resulting from Bayesian analysis. Numbers above branches are posterior probability and parsimony bootstrap values, respectively. Values <50 % were not shown.

4. Conclusion

- All species within the study were recognized with nrDNA ITS sequence.
- The nrDNA ITS sequence is an appropriate species marker for *Bromus* section *Bromus*.

5. References

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