Article PHYTOTAXA

Verification of taxonomic relationships within the genus *Secale* (Poaceae:Pooideae: Triticeae) based on multiple molecular methods

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Abstract

This study aimed to verify the taxonomic relationships within the genus *Secale*. The plant material included 16 wild rye accessions from four species. Two approaches were applied: 1) whole genome scanning using three molecular marker systems: diversity arrays technology sequencing, simple sequence repeats and sequence-specific amplification polymorphism; and 2) characterisation based on polymorphisms within the sequences of two genes involved in benzoxazinoid biosynthesis: *ScBx1* and *ScBx5*. Bayesian and neighbour-joining clustering and principal coordinate analysis were applied to illustrate relationships among species and accessions of *Secale* based on genetic distance (GD) matrices. Pearson's correlation analysis between GD matrices was conducted. Clustering of *Secale* accessions revealed that *S. sylvestre* samples were the most divergent. The remaining accessions formed two clusters. One of them comprised *S. strictum* accessions while the second cluster consisted of subspecies of *S. cereale*, the species *S. vavilovii* and *S. strictum* subsp. *ciliatoglume*.