Genetic structure identification and assessment of interrelationships between *Brassica* and allied genera using newly developed genic-SSRs of Indian mustard (*Brassica juncea* L.)

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Highlights

- Four hundred sixty genic-SSRs were tested for cross-transferability to 21 accessions representing 19 species from eight different genera of the family *Brassicaceae*.

- A total of 200 genic-SSRs yielded single amplicons of which 150 exhibited cross-transferability.

- One hundred twenty-one genic-SSRs were found to be polymorphic.

- The cross-transferable genic-SSRs were employed to analyze population structure, Nei's genetic distance-based clustering, and principal coordinate analysis.

- The efficacy of cross-transferable genic-SSRs in delineating taxonomic status of *Brassica* and allied genera was established.

Abstract

Brassica and allied genera are valuable sources of edible oils, vegetables, condiments and other products. They also find utility for specific applications as renewable industrial or fuel oils. Wild and weedy species of these genera are precious genetic resources of agronomic and economic

traits. Scientists have developed a large number of genomic resources for cultivated species of *Brassica.* However, members of allied genera including wild and weedy species have remained mainly neglected. In this study, we tested the cross-transferability of 460 genic-SSRs, out of the 4108 genic-SSRs developed in our earlier study in *Brassica juncea*, to 21 accessions representing 19 species from eight different genera of the family *Brassicaceae*. A total of 200 genic-SSRs yielded single amplicons of which 150 exhibited cross-transferability. Cross-taxa allelic distribution analysis of the cross-transferable genic-SSRs highlighted preferential accumulation of 15 private alleles in cultivated Brassicas with distinct niche-specific roles. One hundred twenty-one genic-SSRs were found to be polymorphic with polymorphism information content values ranging from 0.09 to 0.66. The cross-transferable genic-SSRs were employed to identify population structure, Nei's genetic distance-based clustering, and principal coordinate analysis. The results convincingly demonstrated the efficacy of cross-transferable genic-SSRs in delineating taxonomic status of species of *Brassica* and allied genera and thus could be efficiently used in more extensive marker-based studies.