Title:	SRAPs and EST-SSRs provide useful molecular diversity for targeting drought and salinity tolerance in Indian mustard
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Abstract:	Abiotic stress tolerance is one of the target trait in crop breeding under climate change scenario. Selection of suitable gene pools among available germplasm is first requisite for any crop improvement programme. Drought and salinity traits, being polygenic, are most difficult to target. The present investigation aimed at exploring and assessment of the genetic variability in Indian mustard at molecular level. A total of twenty-five genotypes and five related species were used. Sixty-three molecular markers including sequence related amplified polymorphism (SRAP) markers along with twenty-three expressed sequence tag-simple sequence repeats (EST-SSRs) were used for diversity analysis. Thirty-seven SRAPs and 18 EST-SSRs showed amplification producing a total of 423 alleles of which 422 were polymorphic. These markers gave an overall polymorphism of 99.78%, with 99.67% polymorphism in SRAPs and 100% polymorphism in EST-SSRs. The study revealed the genetic relationships among different genotypes of B. juncea and related species which could be used for Indian mustard improvement for targeting drought and salinity tolerance in future. Four SRAP and two EST-SSRs identified unique bands which may be related to abiotic stress tolerance. EST sequence BRMS-040 (IM7) was similar to Brassica and radish sequences related to PR-5 (pathogenesis-related) protein.
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