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# Enhancing genetic diversity and climate resilience in *Brassica juncea* using crop wild relatives and progenitor species through integrative pre-breeding

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**Abstract**

In India, *Brassica juncea* is the major oilseed crop, securing the first position among all oilseed crops. Despite its dominance, domestic production remains insufficient, leading to substantial imports to meet national demand. Among various constraints, climate change has emerged as a critical factor, intensifying heat, drought, and disease pressures, thereby threatening productivity. *B. juncea*, which contributes over 90 % of rapeseed–mustard production, is amphidiploid with a narrow genetic base, which limits the development of high-yielding varieties with more heterotic potential. In this context, crop wild relatives (CWRs), landraces, and diploid progenitors serve as invaluable reservoirs of adaptive alleles for climate resilience. At ICAR–National Institute for Plant Biotechnology (NIPB), New Delhi, a comprehensive pre-breeding framework integrating wide hybridisation, cytogenomics, and mutation breeding has been implemented to harness genetic diversity from CWRs and parental diploid species. A diverse panel comprising *B. rapa, B. nigra*, and multiple wild species was systematically evaluated using phenotypic, molecular, and cytogenetic approaches under variable environmental conditions. Resynthesized *B. juncea* (RBJ) lines and alien introgression lines derived from Diplotaxis erucoides (ERJ) were developed to broaden the genetic base and enhance tolerance to both abiotic and biotic stresses. To overcome reproductive barriers in wide hybridisation, a novel genotype, "NRCPB rapa 8," facilitated efficient *in vivo* hybrid seed development, significantly improving introgression from wild taxa. Furthermore, mutation breeding using gamma irradiation generated additional variability, particularly when amphihaploid seeds derived from *B. rapa* × *B. nigra* crosses were treated prior to chromosome doubling using colchicine. Data-driven evaluation of these populations revealed substantial genetic and phenotypic variation, including improved tolerance to heat and drought stress at early growth stages, as well as resistance to *Alternaria* blight, supported by physiological and biochemical indicators. The integration of phenomics, genomics, and cytogenetic analyses enabled the identification of stable, climate-resilient lines. Overall, this study demonstrates that CWR-assisted pre-breeding, coupled with integrative approaches, is an effective strategy for genetic diversification, trait-specific improvement, and climate change adaptation and mitigation. The developed genetic resources provide a strong foundation for breeding resilient *B. juncea* cultivars, contributing to sustainable productivity, enhanced agro-ecosystem stability, and reduced dependence on edible oil imports.

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