

Interspecific hybridization to introduce useful genetic variability for pigeonpea improvement

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Abstract

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is an important grain legume grown in tropical and subtropical regions of the world. Narrow genetic base coupled with low levels of resistance against important biotic/abiotic stresses in cultivated pigeonpea is the major constraint affecting its production and productivity globally. Wild *Cajanus* species are the reservoir of many important genes including resistance/tolerance to diseases, insect-pests and drought, and good agronomic traits and can be utilized to improve the crop cultivars, enrich variability, and broaden the genetic base. Utilization of wild *Cajanus* species has contributed for the development of cytoplasmic male sterility (CMS) systems for pigeonpea improvement. Prebreeding populations involving promising wild *Cajanus* accessions belonging to secondary and tertiary gene pools as donors and popular pigeonpea cultivars as recipients were developed for enriching variability for pigeonpea improvement. Considerable variability was observed in these populations for morpho-agronomic traits and for biotic stresses. Two advanced backcross populations derived from wild *Cajanus* species are being genotyped to identify QTLs associated with agronomic traits for further deployment in pigeonpea improvement programs. Agronomically desirable and disease resistant introgression lines have been identified and shared with breeding programs for developing new high-yielding and climateresilient pigeonpea cultivars with a broad genetic base.

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