

## IDT9-057 | Development of the mungbean Nested Association Mapping (NAM) resource: transformation from opportunity crop into Queensland's most dynamic pulse

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Mungbean (*Vigna radiata*), is established as the key rotation in tropical Australia's cereal-based cropping systems. It has a short duration, wide sowing window, a range of rotation benefits and is established as a high-value product for discerning international markets.

New varieties released by the National Mungbean Improvement Program have doubled production to 70,000 tonnes since 2003. Further industry growth, expansion into new tropical production environments, and progress towards a new industry target of 170,000 tonnes annual production requires the adoption of new breeding technologies and an understanding of traits and the physiological processes determining yield and response to abiotic and biotic stress. This project is delivering new genetic knowledge that will directly assist the breeding of better mung-

bean varieties for Australian growers. The NAM framework will be used to introduce genetic diversity including abiotic/biotic resistance and new adaptive traits into elite mungbean germplasm using bi-parental and backcross breeding. Five hundred and sixty mung bean, black gram and wild accessions have been genotyped as part of a genetic diversity study completed on cultivated and wild Australian germplasm. Thirty crosses have been made to Crystal forming the NAM population, including four interspecific crosses to *Vigna* var. *sublobata*. For each population, sixty, F2 derived recombinant inbred were fast tracked to the F5 generation using controlled environment and field increases. This population is a global resource and will aid in the study of complex traits such as drought and heat stress at flowering as well as disease resistance.

## IDT9-058 | Genome wide analysis of sodium transporters and expression of Na<sup>+</sup>/H<sup>+</sup>-antiporter-like protein (*SbNHXLP*) gene in tomato for salt tolerance

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Salt stress is perceived by plants as ionic and osmotic stresses. Excess Na<sup>+</sup> and Cl<sup>-</sup> instigate conformational changes in protein architecture and membrane depolarization leading to the ion toxicity perception. At cellular level, sodium toxicity can be sensed by plasma ion transporters, membrane proteins, and Na<sup>+</sup> sensitive enzymes. In the present study, a full-length cDNA homologue of salt overly sensitive1 (*SbNHXLP*) gene was isolated from *Sorghum bicolor*, and its overexpression in tomato plants lead to less Na<sup>+</sup> and more K<sup>+</sup> accumulation in root and flower tissues indicating that it helps in proper ion homeostasis. Cambial activity and increased xylogenesis have been noticed under salt stress in transgenic root and stem tissues unlike that of untransformed controls. *In silico* protein-protein interaction studies of NHXLP revealed hypothetical interac-

tions with several sodium proton antiporter (NHX and SOS) and cation proton antiporter (CHX) proteins. Co-immunoprecipitation followed by MALDI-TOF analysis showed that NHXLP protein interacts *in vitro* with one of the cation proton antiporter (CPA) family members CHX2, belonging to CPA1 family. Comparative genomics helped in knowing the evolutionary history by studying the phylogenetic distance, divergence and synteny of Sodium transporters between sorghum, maize and rice. This information would be useful in selecting candidate genes for functional validation in relation to abiotic stress tolerance during various developmental phases in crop species. Thus, *SbNHXLP* gene appears to be associated with Na<sup>+</sup> exclusion at the plasma membrane and helps the tomato transgenics to ameliorate salt stress.