IDT6-037 | Molecular mapping of flowering time genes in chickpea (*Cicer arietinum* L.)

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Flowering time is an important trait of chickpea that influences crop adaptation to a given climate. Earliness in both flowering time and maturity are important traits for increasing and stabilizing chickpea productivity in short season environments by avoiding end of season drought. A study was conducted to identify genes/quantitative trait loci (QTLs) controlling flowering time in chickpea using four F2 populations (ICCV 96029 × CDC Frontier, ICC 5810 × CDC Frontier, BGD 132 × CDC Frontier and ICC 16641 × CDC Frontier). Genetic studies revealed monogenic control of flowering time in the crosses ICCV 96029 × CDC Frontier, BGD 132 × CDC Frontier and ICC 16641 × CDC Frontier, while in the cross ICC 5810 × CDC Frontier, it was under digenic control with complementary gene action. The genetic linkage maps developed from four crosses consisted of 75, 75, 68 and 67 markers spanning 248.8 cM, 331.4 cM, 311.1 cM, and 385.1 cM, respectively. A consensus map spanning 363.8 cM with 109 loci was developed by integrating four genetic maps. QTL mapping detected major genomic regions controlling early flowering genes *efl-1* (*Qefl1*-2) on CaLG04, *efl-2* (*Qefl2*-1, *Qefl2*-2, *Qefl2*-3, *Qefl2*-4) on CaLG01, 03, 04 and 08, *efl-3* (*Qefl3*-3) on CaLG08 and *efl-4* (*Qefl4*-1) on CaLG06. Analysis of QTL regions on CaLG04 and CaLG08 provided several important candidate genes involved in regulation of flowering time and homeotic functions. The identified genomic regions with linked molecular markers can be deployed for introgressing early flowering trait into elite chickpea cultivars through marker-assisted breeding (MAB).

IDT6-038 | Screening mungbean lines for salinity tolerance using Salinity Induction Response (SIR) technique

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Mungbean [*Vigna radiata* (L.) Wilczek] is one of the important fast maturing warm season legumes of the world. However, static productivity in last decades largely accounts for its susceptibility to various biotic and abiotic stresses at different growth stages. Among them, salinity severely limits growth and yield worldwide. Tolerance to salinity involves complex responses at cellular, molecular, physiological and whole-plant levels. Largely, intrinsic response of crop varieties/genotypes differ to adjust several physiological and biochemical processes for salt stress. Considering these, the present study was aimed at screening mungbean lines for salinity tolerance using Salinity Induction Response (SIR) technique. Forty mungbean lines procured from WorldVeg, South Asia, were screened at seedling stage for salinity response. Germination and seedling recovery response during the stress and post recovery were accounted as selection criteria. The identified nine tolerant and nine susceptible lines were further evaluated and validated for field level salinity tolerance (whole plant level with 150 and 300 mM NaCl stress). The results indicate that there is a substantial reduction in growth and yield performances of both tolerant and susceptible lines, however a few lines could maintain relatively better biomass and pod yield, which was on par with non-stressed (non-saline) plants. Based on seedling and whole plant level tolerance, a few tolerant (EC 693358, EC 693366, ML 1299, EC 693371) and susceptible lines (NM 94) were identified for further investigation, which showed consistency in their salinity response.