



identifying QTLs associated with heat tolerance in chickpea using 292 F₈-F₉ recombinant inbred lines (RILs) of the cross ICC 4567 (heat sensitive) × ICC 15614 (heat tolerant). Phenotyping of RILs was done for two heat stress (late sown) and one no-stress (normal sown) environments. Genotyping was performed with genotyping-by-sequencing (GBS) based 271 single nucleotide polymorphisms (SNPs) covering the whole genome of chickpea. Using composite interval mapping (CIM) analysis, two consistent genomic regions harbouring eight QTLs on CaLG05 and CaLG06 were identified. Several other QTLs for different traits were also found on different other linkage groups. Four major QTLs for number of filled pods, number of seeds, grain yield and % pod set, located in the CaLG05 genomic region, were found to have cumulative phenotypic variation of above 50%. Nineteen pairs of epistatic QTLs were found with significant epistatic effects, but there was no QTL × environment interaction effect except for harvest index and biomass. The candidate gene mining from the chickpea whole draft genome sequence revealed 25 putative candidate genes for heat stress lying in the two genomic regions CaLG05 and CaLG06. This is the first report on QTLs for heat stress response in chickpea. The markers linked to four major QTLs can facilitate marker-assisted breeding for heat tolerance in chickpea.

PP13: Choice of breeding method for improving yield and yield stability in faba bean

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Faba bean (*Vicia faba* L.) is partially allogamous crop with outcrossing rate varied from 0.3 to 0.83 with an average of 0.5. Breeding methods applied to this crop depends on the levels of outcrossing and the genetic basis of the varieties, and varied from location to location depending on pollinator activities. Different breeding methods were applied to improve productivity such as pedigree method, recurrent selection and development of synthetics. The purpose of this research is to evaluate the efficiency of different breeding methods. These methods were applied to six different crosses to develop 24 F₇ lines by pedigree, 30 F₇ lines by recurrent selection during five successive seasons and nine Syn1 lines using top cross from 2013 to 2015. The lines were evaluated in two cropping seasons (2014/2015 winter and 2015 summer) in alpha lattice design with two replications. Days to flowering (DFLR), days to maturity (DMAT), number of branches per plant (BRPT), pods per plant (PPNT), number of seeds per pod (SPO), number of seeds per plant (SPL), hundred Seed Weight (SW100), single-plant yield (SPY), grain yield per ha (GY) were recorded. Analysis of variance showed that genotypes, breeding methods (BM) and G X BM were found significant for DFLR, DMAT, SPP and GY. Average grain yield developed by recurrent method in both seasons were superior than the average yield of lines developed by pedigree methods and by synthetics Syn1. Stability analysis indicated that the lines developed by recurrent and synthetic methods were higher yielding and high stable than those developed by pedigree methods.

PP14: Cool Season Food Legume genome database: enabling genetics, genomics and breeding research in pea, lentil, faba bean and chickpea

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The Cool Season Food Legume Genome Database (CSFL, www.coolseasonfoodlegume.org) is an integrated and up-to-date genomics, genetics, and breeding database which facilitates basic, translational and applied research in cool season food legumes. Currently, it contains over 100 genetic maps; 90,500