



Breeding for abiotic stress tolerance in pulses using genomic tools

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Large scale genomic resources have been generated in pulse crops leading to availability of molecular markers, transcript reads, SNPs. With the draft sequencing of genome of chickpea, pigeonpea and development of a large repertoire of markers integration of genomic technologies in pulse breeding has now started in general for most of stresses. This converted most of the pulses from a genomic resource poor crops into genomic rich crop. Genetic studies and cultivar breeding in *P. vulgaris* have shown that heat and drought tolerance are under complex genetic control. Development of MAS methodology for drought adaptation has been done with the assistance of genomic resources developed through whole genome sequencing of Andean (accession: G19833) and Mesoamerican (accessions: BAT93, OAC Rex) bean genomes, and a bean breeder's genome toolbox and database (<http://phaseolusgenes.bioinformatics.ucdavis.edu/>). Since the genome sequence of mungbean has only recently been made available to the public, not much progress has been made on downstream analysis using the mungbean genome sequence. However, putative QTLs identified through *in silico* comparative analysis can be used as a guideline for fine mapping and identifying potential candidate genes related to specific traits. In faba bean identifying QTLs for abiotic stresses such as frost tolerance, yield components, and early flowering time associated with drought avoidance during the reproductive stage has been done. In chickpea, two QTLs and forty eight putative genes have been identified for salinity tolerance. Identification of putative candidate genes further strengthens the idea of using CaLG05 and CaLG07 genomic regions for marker assisted breeding (MAB). Further fine mapping of these key genomic regions may lead to novel gene identification for salinity stress tolerance in chickpea. Identification of nine transcript derived fragments during cold acclimatization in chickpea also point to the possibility of investigating and deploying cold tolerance genes into cultivated lines. In addition, it is also recommended to the use of advanced-backcross (AB-backcross) breeding and development of specialized populations such as multi-parents advanced generation intercross (MAGIC) for creating new variations that will help in developing superior lines with broadened genetic base. In summary, the use of integrated genomics and breeding approaches in pigeonpea, green gram, black gram, field pea and bean to enhance crop productivity in marginal environments ensures food security in developing countries.

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