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Perspective

Genomics: A Way Forward to Tackle Climatic Challenges

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The survival and wellbeing of human population is significantly dependant on supply of food, feed and fiber of important crops. Due to abrupt changes in climatic patterns and harmful effects on environment of current agricultural practices (insecticides and synthetic fertilizers) a continuous supply of new and improved crop varieties is required. So far conventional plant breeding strategies have served the purpose very well but its limited potential to explore the currently available genetic resources is making it harder to accomplish this task day by day. However, among climatic challenges, a substantial limitation to crop production is contributed by salinity; a major environmental stress leading to 50 % land loss till the midst of 21st century a devastating global effect. Plants are ruined due to hyperionic as well as hyper osmotic stress as a result of high salt stress. Most of economically important crops including soybean (*Glycine max*), wheat (*Triticum aestivum*) rice (*Oryza sativa*), beans (*Phaseolus vulgaris*) and maize (*Zea mays*) are highly sensitive to salt stress, thus leading to massive loss in productivity. Identification of key genes and signal transduction pathways underlying plant response to salt stress are crucial in devising strategies in order to address this challenge. Hence, it is dire need to fully exploit latest developments in scientific discipline that integrate high-throughput genomic technologies to devise efficient breeding methods utilizing natural and induced genetic variations in germplasm so that resilient varieties can be released in a lesser time. NGS in combination with genome wide association study has facilitated identification of potential molecular markers, like single nucleotide polymorphisms, copy number variations and insertions and deletions, having association with growth and development and/or stress responses¹. In several plant systems, Kompetitive allele-specific polymerase chain reaction (KASPar) assay has been considered a cost-effective marker assay for the detection of SNP's and also gained a particular attention in molecular breeding applications.

Recently, Patil *et al.*² identified SNPs associated with salt tolerance trait and screened soybean genotypes successfully to detect salt tolerant lines in germplasm accessions using these SNPs based detection system. They clustered 104 soybean lines into sensitive and tolerant group phenotypically using Leaf Scorch Score (LSS) and leaf chlorophyll content (SPAD ratio). To gain insight at genomic level about genes governing salt tolerance, genome wide association study and whole genome resequencing data identified 412 and 337 SNPs having association with LSS and SPAD ratio significantly. Among these SNPs, the most significant SNP having phenotypic variance of 63% was found within fourth intron

of *GmCHX1* gene. Previous study has also shown involvement of this locus in salt tolerance³. The study of natural variations in germplasm coupled with characterization of candidate genes (having association with trait of interest) is important for harnessing genomic information to improve trait of interest. Furthermore, using SoySNP50K and WGRS data, they also identified same major loci on chromosome 3, with higher number of SNPs, thus benefiting in terms of conversion of these SNPs into functional markers. In Soybean as compared to other abiotic stresses, salt tolerance has less complex genetic base, primarily due to availability of a single dominant locus as detected by Patil *et al.*². The detected SNP genotypes were found to be in complete agreement with three structural variants groups. In addition to diverse sequencing lines, using a biparental population of Recombinant Inbred Lines (RILs), a strong association was observed between SNP genotype and reaction to salt tolerance in RIL pop at a success rate >94.5%. This study showed that gene based molecular markers coupled with genotyping assay serve as efficient tools in selection of tolerant genotype in diverse germplasm or true heterozygote in an early generation (F₂) for genetic studies or breeding purposes. Similarly, in another study by using SNP based KASPar assay, Cubizolles *et al.*⁴ determined extent of genetic diversity in elite wheat cultivars and detected genomic regions involved in agronomically important traits. Gao *et al.*⁵ investigated SNP-based barcode comprising 43 SNPs revealing 429 wheat accessions against various agronomic traits (salinity, drought and resistance against diseases), thus facilitating its effective use in wheat breeding programs.

Such assays can be applied for characterization of germplasm, allele mining and foreground as well as background selection for major and minor crops as well. Phenotyping of soybean in response to salinity is an expensive, time consuming and laborious process, so the detection of molecular markers linked to salinity would be a useful tool in order to develop resilient varieties. Furthermore, in field due to graded concentration of salt in vertical or horizontal directions, conventional breeding alone cannot accomplish the criteria for evaluation of salt-tolerance. It is concluded that conventional approaches such as monitoring of trait with robust devised phenotyping methods coupled with adoption of high through put genomic approaches would help in sustaining crop production by designing future crosses, allele mining, trait introgression and evaluation of diverse germplasm against abiotic as well as biotic stresses. Long time commitment and tireless efforts are involved in breeding cycles, thus these genomic tools have gained significant importance in plant genetics and molecular breeding due to their suitability for genetic diversity analysis,

abundance in genomes, evolutionary relationships and association with complex phenotypic traits^{6,7}. Additionally, due to their flexibility towards automation these processes are useful for high throughput genotyping and increase the selective breeding for a number of traits with correct identification and quality assurance. With rapid decline in DNA sequencing cost, there would be greater potential to deploy genomics based breeding technology for the development of diverse climate resilient crops.

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