Genomics - Assisted Breeding – A Significant Breakthrough for Crop Improvement

Khushbu Chittora*
PhD Scholar, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan-313001
*Corresponding Author E-mail: chittorakhushbu23@gmail.com
Received: 11.03.2020 | Revised: 16.04.2020 | Accepted: 22.04.2020

ABSTRACT
Conventional breeding methods mainly depend on breeders skills to develop new plant varieties. These methods are laborious and take several years to develop a new variety. Molecular markers, next generation sequencing, association mapping are genomics tool, developed in recent past which has increased the efficiency of conventional breeding to great extent. The combination of conventional breeding techniques with genomic tools has been used in several crops for their genetic improvement with reference to yield, fertility, stress tolerance and climatic resilience etc.

Keywords: Genomics-assisted breeding, QTL, NGS, High throughput phenotyping

INTRODUCTION
Rapidly increasing global population has increased the global demand for food and industrial raw supply worldwide. Climate changes, continuously reducing area under farming and stresses i.e. abiotic and biotic to crops are serious causes to yield losses. Plant breeding is the only way to develop new varieties with increased productivity, nutrition, quality parameters and resistance to abiotic and biotic stress. Conventional breeding methods are mainly depends on breeders skills to identify superior phenotypes. Conventional breeding techniques for cross and self pollinated crop has very low efficiency, laborious and take several years to develop a new variety. Several molecular markers are developed in recent past which has increased the efficiency of conventional breeding to great extent. The combination of conventional breeding techniques with genomic tools and approaches is leading to a new genomics-based plant breeding techniques like association mapping, marker assisted selection, gene pyramiding and genome selection (GS), which greatly accelerates the breeding. Cheaper sequencing has opened many possibilities to apply genomics tools to advance crop-breeding programs for complex traits, such as climate resilience (Kole et al. 2015) and quality traits (Migicovsky et al., 2017).
GAB enables the integration of genomic tools with high throughput phenotyping to assist breeding practices through molecular markers to facilitate the prediction of phenotype from genotype. Use of advanced DNA technologies, high throughput phenotyping protocols, knowledge from other approaches as gene expression via transcriptomics, protein function via proteomics, and metabolic pathways via metabolomics, allows the identification of molecular markers linked to complex traits, the dissection of genetic variability, identification of potential candidate genes, and their alleles for gene expression or gene function (Friedmann et al., 2018).

Molecular marker assisted selection: For a quantitatively-inherited characters, numerous QTLs or genes are usually involved. Thus, discovery of QTL or even underlying causal genes/alleles is of great importance to marker-assisted breeding. Genetic mapping via QTL analysis have accelerated identification of QTL controlling the desired traits of agronomic, quality or nutritional importance in created populations. GAB allows breeders to rapid screening of large population and select subset for more expensive phenotypic evaluation. After identifying the molecular markers associated with gene(s)/QTLs for traits of interest, the next step is to use molecular markers in back-crossing programmes to improve selection efficiency and to implement gene pyramiding especially for disease resistances.

Plant germplasm resources worldwide, comprising of wild plant species, modern cultivars, and their crop wild relatives, are the important reservoirs of natural genetic variations, originated from a number of historical genetic events as a respond to environmental stresses and selection through crop domestication (Abdurakhmonov & Abdurakhmonov (2008). The availability of high-density SNP markers has opened a way for genome wide association study (GWAS), an approach using natural populations. Association mapping could overcome several limitations of conventional linkage mapping and provide a powerful strategy for dissecting complex traits.

Next generation sequencing: Next generation sequencing (NGS) describe a DNA sequencing technology which has revolutionised genomic research. The vast amounts of data generated by NGS have broadened our understanding of structural and functional genomics. The NGS technologies are different from the classical methods of sequencing as they provide massively parallel analysis, extremely high-throughput from multiple samples at much reduced cost. Conventional phenotyping has limited ability of phenotyping of traits related to yield and stress tolerance (e.g., yield potential as well as increased drought, heat tolerance, and nutrient efficiency, etc.). NGS generates huge amounts of sequenced data in a cost-effective manner and allows profiling for nucleotide variation and large-scale discovery of functional markers. These markers will help in selection of economically-important traits in plant breeding.

High throughput phenotyping: Modern phenomics tools aim to record data on such traits on hundreds to thousands of plants in a single day, as a phenomics revolution. An International Plant Phenomics Network was set up for high throughput phenotyping via robotic, non-invasive imaging across the life cycle of small, short-lived model plants and crops (Muraya et al., 2016). Plant height, leaf length, width, and angle were measured on a phenotyping platform in the greenhouse, which was developed by the integration of LiDAR, high-resolution camera, and hyperspectral imager (Guo et al., 2017). Physiological breeding based on HTPPs and probably together with genomic selection is beneficial for the improvement of breeding methodologies, and brings out more precise breeding strategies for stress tolerance and yield (Reynolds & Langridge 2016). Laser scanning technologies (Dornbusch et al., 2012) and digital stereocameras allowing one to obtain a 3D model of a plant (Chéné et al. 2012) are used for determination of the leaf location and orientation on the stem, determination of the traits changing in the process of diurnal rhythm, and study of the plant circadian rhythms.
Use of genomics assisted breeding in crops improvement: A number of genes or QTLs associated with yield related traits and crop resistance/tolerance to abiotic and biotic stresses have been identified for crop improvement. In last few years, species-specific genomic resources are being generated and genomic resources from related cereal species are being transferred through comparative genomics studies. Several grain yield-related QTLs in rice: GW2 (Song et al., 2007), GW5 (Shomura et al., 2008) have been identified, In pearl millet during moisture stress three major QTL for grain yield (Bídinger et al., 2007) were reported. A numbers of polymorphic markers were identified associated with resistance to biotic stresses (Bohra et al., 2011; Saxena et al., 2010, fertility restoration (Bohra et al., 2011), earliness, plant height (Kumawat et al., 2012) and determinacy (Mir et al., 2013, 2014) in pigeon pea reported. Other than cereal crops genome sequencing in perennial fruit crops such as apple (Velasco et al., 2010), grape (Velasco et al., 2007), banana (D’Hont et al., 2012), cocoa (Argout et al., 2011), peach (Ahmad et al., 2011), and sweet orange (Xu et al., 2013) were also performed. Genetic region associated with abiotic stress resistance were also reported as winter hardiness (Thomas & James, 1993), vernalization response and frost tolerance (Galiba et al., 1995; Hayes et al., 1998), cold and drought-induced ABA production (Laurie et al., 1995), and osmotic stress-tolerance (Galiba et al., 1993), his includes drought-adaptive traits (Serraj et al., 2009; Tuberosa, 2012), root architecture (Wasson et al., 2012; Uga et al., 2013; Lynch et al., 2014), accumulation of water-soluble carbohydrates and their partitioning to storage organs (Salem et al., 2007; Snape et al., 2007; Rebetzke et al., 2008), abscisic acid concentration (Rebetzke et al., 2008; Rehman et al., 2011), stay-green (Yang et al., 2007; Borrell et al., 2014) also reported.

Advantages of Genomics assisted breeding:
(i) Most agronomical and economically important traits in crops are quantitative traits that are controlled by multiple QTL. Thus, discovery of QTL or even underlying causal genes/alleles is of great importance to marker-assisted breeding. So far, a huge number of QTL have been identified using this method. 
(ii) Use of genomic tools also modify the selection criteria to focus on resistance gene rather than total yield (ii) Use of GAB increase the efficiency to identify stress-tolerance genes in several crop and their exploitability in elite material and wider breeding germplasm, selection of lines with improved drought adaptation has also been successful.
(iii). Genomic assisted breeding also expand the use of minor crops, which may possess better nutritional qualities, environmental sustainability or resilience and require lower inputs than major crops.
(iv). Genomics possesses the potential to increase the diversity of alleles available to breeders through mining the gene pools of crop wild relatives (CWRs).

FUTURE THRUST: Conventional plant breeding has limited efficiency to develop new plant varieties with enhanced yield, and inbuilt stress resistance to biotic and abiotic stress. Newly developed genetic and genomics tools will enhance the efficiency of conventional breeding and evaluation processes. At present, high-throughput trait-associated markers, cost-effective genotyping approaches, and precise phenotyping platforms will help the rapid deployment of GAB and identification of candidate gene. Genomics-assisted breeding in particular is predicted to playing a significant role in the development of new and advanced varieties. Advances in DNA sequencing technologies along with advanced genomics tools will expedite the identification of novel genes and key regulatory regions of yield and stress tolerance toward the development of new cultivars.

REFERENCES
Argout, X., Salse, J., Aury, J. M., Guiltinan, M. J., Droc, G., & Gouzy, J., (2011). The genome of Theobroma cacao. Nat. Genet. 43, 101–108.
Ahmad, R., Parfitt, D. E., Fass, J., Ogundiwin, E., Dingra, A., & Gradziel, T. M. (2011). Whole genome sequencing of peach (*Prunus persica L.*) for SNP identification and selection. *BMC Genomics* 12, 569.

Bohra, A., Dubey, A., Saxena, R.K., Penmetsa, R.V., Poornima, K.N., Kumar, N., Farmer, A.D., Srivani, G., Upadhyaya, H.D., Gothalwal, R., Ramesh, R., Singh, D., Saxena, K.B., Kavi, Kishor, P.B., Singh, N.K., Town, C.D., May, G.D., Cook, D.R., & Varshney, R.K. (2011). Analysis of BAC-end sequences (BESs) and development of BES-SSR markers for genetic mapping and hybrid purity assessment in pigeonpea. *BMC Plant Biol* 11, 56.

Bohra, A., Saxena, R.K., Gnanesh, B.N., Saxena, K.B., Byregowda, M., Rathore, A., KaviKishor, P.B.Cook, D.R., & Varshney, R.K. (2012). An intra-specific consensus genetic map of pigeonpea (*Cajanus cajan* (L.) Millspaugh) derived from six mapping populations. *Theor Appl Genet* 125, 1325–1338.

Borrell, A.K., Mullet, J.E., George-Jaeggli, B., van Oosterom, E.J., Hammer, G.L., & Klein, P.E. (2014). Drought adaptation of stay-green sorghum is associated with canopy development, leaf anatomy, root growth, and water uptake. *J. Exp. Bot.* 65, 6251–6263.

Bidinger, F. R., Napolean, T., and Hash, C. T. (2007). Quantitative trait loci for grain yield in pearl millet under variable post flowering moisture conditions. *Crop Sci.* 47, 969–980.

Dornbusch, T., Lorrain, S., & Kuznetsov, D. (2012). Measuring the diurnal pattern of leaf hyponasty and growth in *Arabidopsis*—a novel phenotyping approach using laser scanning. *Funct. Plant Biol.* 39(11), 860–869.

D'Hont, A., Denoelud, F., Aury, J. M., Baurens, F. C., Carreel, F., & Garsmeur, O. (2012). The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature* 21, 217–217.

Friedmann, M., Asrat, A., Anglin, Luis, N. S., Augusto, B., Bhattacharjee, R., Brown, A., Carey, A., Ferguson, M., Gemenet, D., Lindqvist, H. K., Rabbi, I., Rouard, M., Swennen, R., & Graham, T. (2018). Genomics-Assisted breeding in the CGIAR research program on roots, tuber and Bananas (RTB). *Agriculture* 8(7), 89.

Guo, F., Wu, S. Pang, X., Zhao, L., Chen, J., Liu, B., Xue, G., Xu, L., Li, H., Jing, C., & Chu (2017). Crop 3D — A LiDAR based platform for 3D high-throughput crop phenotyping. *Science China.*

Kole, C., Muthamilarasan, M., Henry, R., Edwards, D. E., Sharma, R., Abberton, M., Batley, J., Bentley, A., Blakeney, M., & Bryant, J. (2015). Application of Genomics-Assisted Breeding for Generation of Climate Resilient Crops: Progress and Prospects. *Front. Plant Sci.* 6, 563.

Kumawat, G., Raje, R.S., Bhutani, S., Pal, J.K., Mithra, S.V.C.R., Kishor Gaikwad, K., Sharma, T.R., & Singh, N.K. (2012). Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.). *BMC Genet.* 13, 84.

Reynolds, M., & Langridge, P. (2016). Physiological breeding Current Opinion in Plant Biology, 31, 162–171.

Lynch, J. P., Chimungu, J. G., & Brown, K. M. (2014). Root anatomical phenes associated with water acquisition from drying lo soil: targets for crop improvement. *J. Exp. Bot.* 65, 6155–6166.

Migicovsky, Z. (2017). Exploiting Wild Relatives for Genomics-Assisted Breeding of Perennial Crops. *Front. Plant Sci.*, 8, 460.

Mir, R.R., Kudapa, H., Srikanth, S., Saxena, R.K., Sharma, A., Azam, S., Saxena, K.B., Penmetsa, R.V., & Varshney,
Chittora, K. (2014). Candidate gene analysis for determinacy in pigeonpea (Cajanus spp.). Theor. Appl. Genet. 127, 2663–2678.

Rebetzke, G. J., Herwaarden, A. F., Jenkins, C., Weiss, M., Lewis, D., & Ruuska, S. (2008). Quantitative trait loci for water-soluble carbohydrates and associations with agronomic traits in wheat. Aust. J. Agric. Res. 59, 891–905.

Salem, K. F. M., Roder, M. S., & Borner, A. (2007). Identification and mapping quantitative trait loci for stem reserve mobilisation in wheat (Triticum aestivum L.). Cereal Res. Commun. 35, 1367–1374.

Serraj, R., Kumar, A., McNally, K. L., Slamet-Loedin, I., Bruskiewich, R., & Mauleon, R. (2009). Improvement of drought resistance in rice. Adv. Agron. 103, 41–99.

Shomura, A., Izawa, T., Ebana, K., Ebitani, T., Kanegae, H., Konishi, S., Yano, M. (2008). Deletion in a gene associated with grain size increased yields during rice domestication. Nature Genetics, 40, 1023-1028.

Singh, V.K., Singh, A.K., Singh, S., & Singh, B. D. (2010). Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools. 563-612.

Song, X. J., Huang, W., Shi, M., Zhu, M., & Lin, H.X. (2007). A QTL for rice grain width and weight encodes a previously unknown RING-type E3 ubiquitin ligase. Nature Genetics, 39, 623-630.

Thomas, H., & James, A. R. (1993). Freezing tolerance and solute changes in contrasting genotypes of Lolium perrenne L. acclimated to cold and drought. Ann. Bot. 72, 249–254.

Tuberosa, R. (2012). Phenotyping for drought tolerance of crops in the genomics era. Front. Physiol. 3, 347.

Uga, Y., Sugimoto, K., Ogawa, S., Rane, J., Ishitani, M., & Hara, N. (2013). Control of root system architecture by deeper rooting increases rice yield under drought conditions. Nat. Genet. 45, 1097–1102.

Velasco, R., Zharkikh, A., Troagio, M., Cartwright, D. A., Cestaro, A., & Pruss, D. (2007). A high quality draft consensus sequence of the genome of a heterozygous grapevine variety.

Velasco, R., Zharkikh, A., Affourtit, J., Dhingra, A., Cestaro, A., & Kalyanaraman, A. (2010). The genome of the domesticated apple (Malus domestica Borkh.). Nat. Genet. 42, 833–839.

Wasson, A. P., Richards, R. A., Chatrath, R., Misra, S. C., Prasad, S. V., & Rebetzke, G. J. (2012). Traits and selection strategies to improve root systems and water uptake in water-limited wheat crops. J. Exp. Bot. 63, 3485–3498.

Xu, Q., Chen, L. L., Ruan, X., Chen, D., Zhu, A., & Chen, C. (2013). The draft genome of sweet orange (Citrus sinensis). Nat. Genet. 45, U59–U92.

Yang, J., Zhang, J., Liu, K., Wang, Z., & Liu, L. (2007). Abscisic acid and ethylene interact in rice spikelets in response to water stress during meiosis. Journal of Plant Growth Regulation. 26(4), 318-328. DOI: 10.1007/s00344-007-9013-8