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Molecular Breeding

for Genetic Improvement of Pearl Millet

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Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is a climate-resilient crop that accounts for two-thirds of the global millet production. It belongs to family *Poaceae* and has chromosome number 2n-14. This cross-pollinated crop is having 1.79 GB of genome. It is rightly termed as "Nutricereal" and also called the "Powerhouse of Nutrition" as it's contains high amount of fibre, metabolizable energy, protein, essential amino acid, macro and micro nutrients, iron and zine. Though pearl millet is highly resilient to diverse agro climate conditions but its improvement was slower until recent with the development of larger number of molecular markers and mapping populations, a good pace was observed in pearl millet improvement especially for disease resistance. Grain minerals and domestication traits like flowering and plant height. Still there is need to exploit molecular biology tools to develop high yielding hybrids of pearl millet for farmers residing in semi-arid and rainfed regions of Indian and African subcontinent (Satyavathi *et al*., 2021).

What is Molecular Breeding?

Molecular breeding (MB) is defined as the use of genetic manipulation performed at DNA molecular levels to improve characters of interest in plants, including genetic engineering or gene manipulation, molecular marker-assisted selection, genomic selection, etc. to develop plant varieties with desired traits (Singh and Shekhawat, 2018).

Molecular Breeding Methods

1) Marker Assisted Selection (MAS)
2) Marker Assisted Backcrossing (MABC)
3) Genomic Selection (GS)
4) Marker Assisted Gene Pyramiding and
5) Quantitative Trait Loci (QTL) and
6) Association Mapping (Serba and Yadav, 2016).

Case Studies

Ambavat *et al*. (2016) developed a high density linkage map for pearl millet rust resistance based on DAFT and SSR markers. A total of 286 loci (229 DArT markers and 57 SSRs) were

distributed across the expected 7 linkage groups. A major QTL responsible for rust resistance was detected on LG 1, LG 4 and LG 7.

Anuradha *et al*. (2017) examined localization of genomic regions linked with enhanced grain iron and zinc content and its association with SSRS and genic markers using association mapping. Wide range of variation was observed for grain iron and zinc content. STRUCTURE analysis revealed presence of three sub-populations. For grain iron content six markers while for grain zinc content 10 markers were observed scattered on different LGs.

Kumar *et al*. (2018) reported large-effect Fe and Zn content quantitative trait loci (QTLs) using diversity array technology (DAFT) and SSRS markers in 317 recombinant inbred line (RIL). A total of 19 QTLs for Fe and Zn were detected, of which 11 were for Fe and eight were for Zn. The portion of the observed phenotypic variance explained by different QTLs for grain Fe and Zn content varied from 9.0 to 31.9% (cumulative 74%) and from 9.4 to 30.4% (cumulative 65%), respectively. QTLs for grain Fe and Zn exhibited pleiotropic effect as co-localized on LG 1 and LG 7.

Pujar *et al.* (2020) used genome-wide association study (GWAS) to identify significant marker trait associations (MTAS) for Fe, Zn, and protein content (PC) for enhanced bio fortification Breeding. A diverse panel of 281 advanced inbred lines was evaluated for Fe, Zn, and PC over two seasons. A total of 78 MTA were identified, of which 18 were associated with Fe: 43 with Zn, and 17 with PC Four SNPs identified were located on chromosomes Pg104 (1), Pgl05 (2) and Pg107 (1), respectively were co-segregated for Fe and Zn.

Jangra *et al* (2021) carried out marker-assisted selection (MAS) with an aim to develop improved version of HHB 226 by introgression of QTLs for terminal drought stress tolerance into the male parent of the hybrid. Morpho-physiological analysis of BCH generation at field-level under terminal drought stress conditions observed that the QTL introgressed lines showed higher grain yield. 1000-seed weight, relative water content (%), and lower electrolyte leakage (%) than the recurrent parent line number 63 performed the best with all the four foreground markers with, 97,20% recurrent parent genome recovery.

Priya *et al*. (2022) carried out simple sequence repeats (SSR) analysis in pearl millet in order to assess the degree of polymorphism within and among genotypes. The genotypes were evaluated using 28 SSR markers that were found to be polymorphic among the 50 SSR markers tested. The number of alleles generated by each marker per locus ranged from 4 to 7 with average of 5.37 alleles per locus. The polymorphic information content (PIC) values ranged from 0.74 to 0.93 with an average of 0.83.

Conclusion

DArT provides high-quality markers that can be used to construct medium-density genetic linkage maps for plants even when no sequence information is available. DArT array also prove useful for background genotyping in marker-assisted backcrossing programs to speed up recovery of elite recurrent parent genetic backgrounds on genomic regions outside that targeted for introgression of donor parent alleles. Developed linkage maps integrating DATT and SSR markers, to identify QTLs for pearl millet rust resistance. Association mapping using SSRs and genic markers, for identification of superior alleles for grain nutritional traits like iron and zinc content. The promising lines with favorable alleles identified and used for generating new cultivars which accumulate all or most of the favorable alleles for high grain iron and zinc content. Two co-localized QTLs were detected on LG1 and LG7. After further validation, these QTL may be used in marker-assisted breeding programs for the development of high grain Fe and Zn hybrid parental (A-/B- and R-) lines and in marker-assisted population improvement (MAPI) programs globally. Advances in high

throughput genotyping technologies such as genotyping-by-sequencing (GBS), DArT and GWAS have enabled the use of these powerful approaches in dissecting quantitative traits. Marker-assisted breeding in the introgression of desired gene/trait/QTLs into the elite cultivars/varieties/hybrids, with an ultimate aim to develop improved versions of the elite cultivars/varieties/hybrids with the desired trait.

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