

## **DBT-NIPGR researchers make breeding of rice plants easier**



New Delhi, June 09: Rice is one of the main staple foods all over the world as it has very high carbohydrate content and thus provides instant energy. In Southeast Asia, where rice is consumed the most, it accounts for more than 75% of the calorie intake. More than 90% of the world's rice production is contributed by Asian countries majorly dominated by China and India.

There is a need to produce more rice to serve the growing demand. However, the possibility for increasing rice production with irrigation and fertilizers alone is at near saturation levels. There is a need to look for alternate methods. Genetic improvement of rice cultivars can be an effective way, with identification of new sources of genomic variants.

Single nucleotide polymorphisms (SNPs) present throughout the genome are one of the major causes of allelic variation leading to genetic variability in a population. Genetic variations lead to a multitude of phenotypes which form the basis for selection of improved cultivars for breeding and agricultural purpose.

Identification of quantitative trait loci (QTLs) by conventional method of linkage mapping or QTL mapping involves development of mapping population, which is a time-consuming

process. However, with the advent in NGS platform to accelerate genome exploration, large-scale phenotyping tools and GWAS to harness the genotype-phenotype association, the dependence on mapping population could be bypassed.

Recently, with the availability of resequencing dataset for 3,000 diverse rice accessions, a further deep and robust platform has been provided to elevate the marker-associated breeding efforts concerning various agronomic traits. Even though this panel of 3,000 accessions represents the core collection of global rice accessions, still it is relatively large in size that would present difficulties for management and phenotypic evaluation. So, there is a need to have a smaller subset mirroring such huge germplasm for convenient breeding efforts.

A team of researchers at the Department of Biotechnology's National Institute of Plant Genome Research have developed a mini-core collection (520 accessions) from the original collection of 3,004 (adding four diverse Indian) rice accession dataset, and utilized it as an association panel for GWAS.

While designing mini-core collection, we have considered genotypic (SNPs data), phenotypic data (18 agronomic traits), and representation from various regional gene pools (geographical diversity) to accommodate maximum possible diversity. On the utility front, the GWAS with the designed mini-core panel identified various novel marker-trait associations along with the validation of some of the earlier reported associations. The mini-core captured the associations prevalent in the original collection and so, rightly happens to be a representative subset.

In effect, they have been able to generate and validate the mini-core as a robust, diversified, non-redundant and manageable association panel, efficiently mirroring the larger collection of 3,004 diverse rice accessions. The comparatively small size of the association panel designed in the study will be useful and convenient for various phenotype-genotype relationship studies which usually remain a major limitation in different plant breeding programs.

Journal reference: <https://www.sciencedirect.com/science/article/pii/S2590346220300328>

Contact Person & Contact Details: Dr. Jitendra K. Thakur

Email: [jthakur@nipgr.ac.in](mailto:jthakur@nipgr.ac.in)

DBT-NIPGR website: <http://www.nipgr.ac.in/home/home.php>

Phone: 91-11-26735157, 26735143, 91-11-26741612, 14, 17

Institute mail: [administration@nipgr.ac.in](mailto:administration@nipgr.ac.in), [nipgr@nipgr.ac.in](mailto:nipgr@nipgr.ac.in)