

Genome-wide analysis of polymorphisms identified domestication-associated long low diversity region carrying important rice grain size/weight QTL

A research carried out at Department of Biotechnology's institute, the National Institute of Plant Genome Research (NIPGR), New Delhi sequenced four Indian rice genotypes (LGR, PB 1121, Sonasal & Bindli) with contrasting seed size/weight trait and found that all genotypes have much more unique DNA variations than previously predicted with 3000 global rice panel pointing towards unexplored potential of Indian germplasm diversity.



Further, by comparing genomic sequences from 3004 rice samples accessions including 4 sequenced in current study, one long (~6 Mb) genomic region with unconventional low nucleotide diversity spanning the centromere of chromosome 5, named as low diversity region (LDR) was identified. The study further observed varying degree of LDR adoption and stabilization across the different rice groups. The *japonica* and *indica* populations were identified as preferred host with 97 and 83% of their accessions had this LDR footprint, respectively.

In contrast, another major rice population *aus*, an abundantly grown subspecies in East India and Bangladesh region was not tamed enough for LDR adoption. It was found that there was varying degree of selection pressure for multiple domestication-related agronomic traits including grain size and weight that might have created this intolerant polymorphic zone in frequently cultivated rice cultivars. One QTL for seed size was also identified within LDR.

Further, by comparing other 446 samples of wild rice (*O. rufipogon*) taken from all over southern Asia, LDR's historical status and its dissemination was traced across the different

rice types. The investigators also found elated proximity of *aus* genome with wild rice than *indica* and *japonica*. This observation of biased selection bottleneck across the three major rice group strengthens the hypothesis of three separate rice domestication events.

Overall, in addition to the genome-wide exploration of 4 Indian rice accessions for allele richness, the current study highlights an important and long domestication-associated genomic region, which seems to be evolutionary crafted to associate with multiple traits. Moreover, this LDR could be utilized for improving rice production by targeting various traits associated with it including the seed size.

Rice is the one of the staple food all over the world. In Southeast Asia, rice accounts for more than 75% of the calorie intake. According to FAOSTAT reports, despite having largest area under rice crop cultivation, India is the second largest after China in total yield due to low productivity. In order to meet the growing demand of India and world, production of rice must be increased significantly. Yield in rice is mainly determined by the traits like number of grains per plant and grain weight. Thus, main aim of researchers and breeders is to develop superior rice varieties with heavier grains.

Link: <https://www.biorxiv.org/content/10.1101/725242v1.full>