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Meta-analysis of identified genomic regions and candidate genes underlying salinity tolerance in rice (*Oryza sativa* L.)**Ankit R. Chaudhary***Uka Tarsadia University, India*

Rice output has grown globally, yet abiotic factors are still a key cause for worry. Salinity stress seems to have the more impact on crop production out of all abiotic stresses. Currently one of the most significant challenges in paddy breeding for salinity tolerance with the help of QTLs, is to determine the QTLs having the best chance of improving salinity tolerance with the least amount of background noise from the tolerant parent. Minimizing the size of the QTL confidence interval (CI) is essential in order to primarily include the genes responsible for salinity stress tolerance. By considering that, a genome-wide meta-QTL analysis on 768 QTLs from 35 rice populations published from 2001 to 2022 was conducted to identify consensus regions and the candidate genes underlying those regions responsible for the salinity tolerance, as it reduces the confidence interval (CI) to many folds from the initial QTL studies. In the present investigation, a total of 65 MQTLs were extracted with an average CI reduced from 17.35 cM to 1.66 cM including the smallest of 0.01 cM. Identification of the MQTLs for individual traits and then classifying the target traits into correlated morphological, physiological and biochemical aspects, resulted in more efficient interpretation of the salinity tolerance, identifying the candidate genes and to understand the salinity tolerance mechanism as a whole. The results of this study have a huge potential to improve the rice genotypes for salinity tolerance with the help of MAS and MABC.

Biography

Ankitkumar Raghajibhai Chaudhary is a distinguished scholar in the field of Genetics and Plant Breeding, having completed his doctoral degree in 2023. His expertise extends to the realms of genetics, plant breeding, molecular biology, and biotechnology. In his recent work, Dr. Chaudhary has been conducting a meta-analysis of different Quantitative Trait Loci (QTLs) associated with drought tolerance in rice. The aim of this analysis is to provide a narrow region on the chromosome for scientists to focus on, thereby enhancing the efficiency of trait improvement. This groundbreaking work is expected to significantly reduce the efforts required by scientists to improve plant varieties. Importantly, it contributes to the development of climate-resilient crops, which are crucial in the face of global climate change. Dr. Ankit's contributions to the field are thus of immense value to the scientific community and society at large.