Poster Session | Crop Genetics and Physiology | P4: Poster Session

[P4] Crop Genetics and Physiology

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 4 (Poster) (Crop Genetics and Physiology)

12:15 PM - 1:00 PM

[P4-17]Meta-QTLs and Candidate Genes Associated with Grain Zinc Content in Rice

*Nominated for Presentation Awards

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Zinc and Iron deficiencies affect more than half of the global population. Rice is the major source of calories but a poor source of nutrition in its milled form. Biofortification of major staple crops with essential micronutrients has emerged as one of the prominent tools to address malnutrition. However, grain yield and micronutrient traits are genetically complex and significantly influenced by the environmental factors. So, identification of stable QTLs and their use in marker assisted breeding fast track the development of biofortified rice varieties. Recently there has been significant progress in mapping QTLs for grain Zn and to breed Zn biofortified rice. We carried out a comprehensive genome-wide meta-analysis of Zn QTLs reported from 25 different studies in rice. Results revealed 51 meta-QTLs (MQTLs) distributed across the 12 rice chromosomes. A total of 415 transcripts/genes related to Iron and Zinc homeostasis were shortlisted, which were found to be involved in oxidation reduction process, trans-membrane transport, cell redox homeostasis, cation/metal ion binding etc. Haplotype analysis of 20 well characterized genes related to Zinc and Iron metabolism were further studied using the 3K rice genome panel. Results showed that 19 out of 20 genes had haplotypes ranging from 2 to 7. The results will be useful for designing markers for the precise and faster development of Zn biofortified rice varieties.