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Select Theme	: Pathways to health and nutrition
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Keyword 1	: Biofortification
Keyword 2	: Nutrient-dense rice
Keyword 3	: Nutrition security
Title of Entry	: QTL Mapping in Six Bi-parental Rice Populations Identified Multiple QTLs for Zn
Presenting author	: Gwen Iris L. Descalsota
Presenting author email	: gidescalsota@gmail.com
Co author 1	: B.P. Mallikarjuna Swamy
Co author 2	: Mary Ann Inabangan-Asilo
Affiliation presenting author	: International Rice Research Institute, Los Baños, Laguna 4031 / University of Southern Mindanao, Kabacan, North Cotabato 9407
Affiliation 1	: International Rice Research Institute, Los Baños, Laguna 4031
Affiliation 2	: International Rice Research Institute, Los Baños, Laguna 4031
Select only one type of presentation	: 15 minute oral presentation
Abstract	: Zinc (Zn) deficiency is one of the major nutritional disorders affecting more than two billion people worldwide. Rice is the major stale food for majority of the populations in developing countries of Asia but milled rice is a poor source o grain Zn. Development of Zn dense rice varieties is one of the sustainable and cost-effective approaches for reducing Zn malnutrition. However, grain Zn is a complex trait and is significantly influenced by environmental factors. Identifying major QTLs and genes for high Zn and development of makers will be useful for faster and more precise development of high-Zn rice varieties. We carried out QTL mapping for grain Zn using five Doubled Haploid (DH) populations and one Recombinant Inbred Population (RILs) at International Rice Research Institute (IRRI). These populations were derived from IR64 x IR69428, PSB Rc82 x IR69428, IR05F102 x IR69428, PSB Rc82 x Joryeongbyeo, BR29 x IR75862, and IR95040 x JAMIR crosses, respectively. Each population was phenotyped for grain Zn in at least two seasons at IRRI. The DH and the RILs populations were genotyped with 7K SNP Chip. The linkage map constructed for each population consisted of 296 to 578 SNP markers. QTL analyses were carried out using Inclusive Composite Interval Mapping implemented in QTL IciMapping v4.1 software. We detected a total of 20 QTLs for grain Zn that explained 7.5%-37.1% of the phenotypic variance. Seven QTLs (qZn2.3, qZn3.2, qZn5.1, qZn5.2, qZn6.2, qZn8.2, and qZn12.1) on chromosomes 2, 3, 5, 6, 8, and 12 were consistent across seasons. Five QTLs (qZn2.3, qZn5.1, qZn5.2, qZn7.2, and qZn11) were detected in at least two populations. Moreover, metal homeostasis genes such as OsZIPs, OsNAS3, OsTOMs, OsMTPs, and OsNRAMP7 were found to be co-locating with these major QTLs. Consistent large-effect QTLs detected in this study will be useful for marker-assisted breeding, while multiple QTLs can be pooled by genomic selection for a rapid, resource-efficient, and advanced development of biofortified high-Zn rice varieties.

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