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Title of Entry	: Deciphering genetics underlying high germination under anaerobic conditions in rice
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Affiliation presenting author	: Plant
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Deciphering genetics underlying high germination under anaerobic conditions in rice Sharmishtha Ghosal, Carlos Casal Jr. Fergie Ann Quilloy, Ma. Genaleen Diaz, M.S. Mendiolo, Shalabh Dixit Anaerobic condition during germination is an important abiotic stress for direct-seeded rice (DSR). Rice, in general, has low germination under anaerobic conditions which leads to poor crop stand in DSR in case of a rainfall event after seeding. The ability of rice to germinate under water reduces the risk of poor crop stands. Further, this allows the use of water as a method of weed control. Identification of genetic factors leading to high anaerobic germination (AG) is required to develop improved DSR varieties. In this study, we explored two BC1F2:3 mapping populations developed from tolerant landrace Kalaratta, and two susceptible varieties NSICRe222 and NSICRe238. Phenotyping was conducted under two types of AG conditions the first being in trays within concrete tables while the second under field like environment in the screen house. Data on germination under normal conditions was also generated. Genotyping was done through KASP SNP genotyping platform. We identified five QTLs on chromosomes 3, 5, 6, 7 and 8 for survival and four QTLs on chromosome 1, 3 and 7 for seedling height across the populations and the environments. We identified novel QTL qAGS-6-1 for survival showing a stable expression in terms of genetic background and environment. Another novel QTL qAGH-1-1 for seedling height

was identified in this study. The identified QTLs for the trait survivability explained phenotypic variation in the range of 57.6 to 73.1% while that for the trait seedling height was ranged from 13.5 to 34.3% across the two populations and different environments. The QTLs identified from this study will be subjected to QTL X environment testing and moved into the QTL deployment pipeline at IRRI for integration into IRRI's DSR breeding program. Linked markers will also be designed for most consistent QTLs for efficient marker-assisted selection.

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