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GENOME-WIDE ASSOCIATION STUDY OF SALT STRESS IN RICE GERMINATION STAGE (*ORYZA SATIVA L.*)

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Background: Salt stress is one of the most influenced factors to rice yield. In order to identify genes related to salt stress, Genome-Wide Association Study (GWAS) was implemented. Seeds of 137 species in core genetic resources were grown in 250-millimeter Sodium Chloride solution. The chamber was set up to 12 of temperature and 40% of relative humidity. We measured germination rate, germination speed, germination energy, germination uniform rate, and shoot length. We conducted GWAS with re-sequencing data of rice germplasms and phenotype data. We found 11 Single-Nucleotide Polymorphism (SNP) markers related salt stress in rice germination stage. As result of GWAS analysis, we discovered two candidate gene for germination rate, two candidates for germination speed, three candidates for germination uniform rate, two candidates for germination energy, and two candidates for shoot length.

Methodology Theoretical Orientation: Seeds of 137 species in core genetic resources were sterilized by 1% sodium hypochlorite solution for 10 min and were washed three times by deionized distilled water. Theses seeds were grown in 250-millimeter Sodium Chloride. The chamber was set up to 12 of temperature and 40% of relative humidity. We measured germination rate, germination energy, germination speed and germination uniform rate for 10 days. We also measured shoot length. We grow seeds of 137 species as same condition for 10 days. We conducted GWAS with re-sequencing data and phenotype data. GWAS use Genomic Association and Prediction (GAPIT) with EMMA algorithm. Genome re-sequencing data were attained KRICE_CORE genome re-sequencing data.

Conclusion & Significance: We implemented GWAS analysis in order to identify gene related to salt stress in rice germination stage. Seeds of 137 species in core genetic resource were treated in 250-millimeter Sodium Chloride. We measured germination rate, germination speed, germination energy, germination uniform rate, and shoot length for 10 days. We conducted GWAS analysis based on re-sequencing data and phenotype data. We discovered 11 SNP marker related salt stress on chromosome 1, 3, 4, 7, 10, 11. Furthermore, we uncovered 11 candidate genes related salt stress in rice germination stage.

Biography

Joohyun Lee has been an Associate Professor in Konkuk University since 2011. He has been studied in Crop breeding and Proteomics especially in Rice through his whole life. He received a B.A from Seoul National University in 1997, and M.S from Seoul National University in 2000 and Ph.D from Louisiana State University at Baton Rouge in 2005. He also had involved in USDA-ARS as a Post Doc., and Seoul National Univ as a research fellow.

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