EuroSciCon
4th Edition of International Conference on
Plant Genomics
Plant Genomics 2018
June 20-21 2018 | Rome,Italy

Genome-wide association study of salt stress in rice germination stage (*Oryza sativa* L.)

Taegyu Kim, Mr., Konkuk University, Korea
Yoonjung Lee, MA., Konkuk University, Korea
Yeon-ju An, Mrs., Konkuk University, Korea
Chang Kwon, Mr., Konkuk University, Korea
Ill-Min Chung, PhD., Konkuk University, Korea
Seong-Hyun Kim, PhD., Konkuk University, Korea
Joohyun Lee, PhD., Konkuk University, Korea

Abstract (300-word limit)

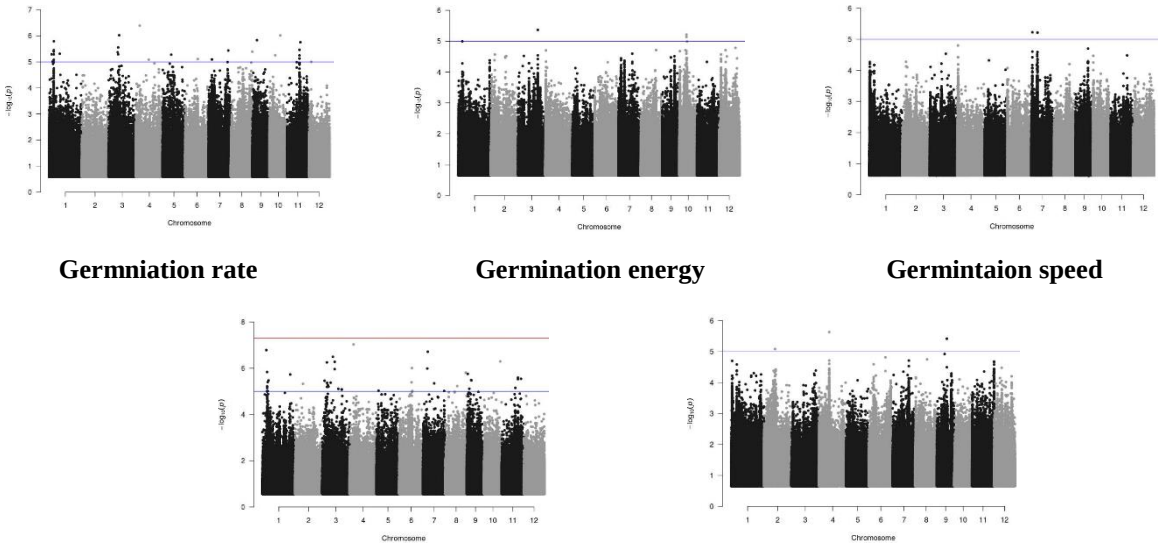
Salt stress is one of the most influenced factors to rice yield. In order to identify genes related to salt stress, genome-wide association study (GWAS) was implemented. Seeds of 137 species in core genetic resources were grown in 250mM NaCl solution. The chamber was set up to 12℃ of temperature and 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 and Theoretical Orientation: Seeds of 137 species in core genetic resources were sterilized by 1% sodium hypochlorite solution for 10 min and were washed 3 time by deionized distilled water. Theses seeds were grown in 200mM NaCl solution. 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.

Findings: as Q-Q plot and manhattan plot result, SNP markers related germination rate were found on chromosome 1, 3, 11. SNP markers related germination speed were found on chromosome 4, 7. SNP markers related germination uniform rate were found on chromosome 1, 3. SNP markers related germination energy were found on chromosome 4, 10. SNP markers related shoot length were found on chromosome 4. As result of GWAS analysis, Os01g0217800, Os11g0499600 are candidate gene for germination rate, Os04g0110700, Os07g0246600 are candidate gene for germination speed, Os01g0198100, Os03g0218300, Os03g0216733 are candidate gene for germination uniform rate, Os04g0112300, Os10g0328700 are candidate gene for germination energy, and Os04g0299500 Os04g0300100 are candidate gene for shoot length after 10 days.

Conclusion and 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 250mM NaCl solution. 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.

Image:



Germniation rate **Germination energy** **Germintaion speed**

Germination uniform rate **Shoot length**

Figure 1. Result of manhattan plots

Recent Publications

1. Proteomic and genetic approaches to identifying defence-related proteins in rice challenged with the fungal pathogen Rhizoctonia solani (2006) Molecular Plant Pathology 7, vol 5 : 405-416
2. Alternative workflows for plant proteomic analysis (2006) Molecular Biosystems, 2:621-626
3. Shotgun Proteomic Analysis for Detecting Differentially Expressed Proteins in the Reduced Culm Number (RCN) Rice (2011) Proteomics, 11(vol. 3) 455-468
4. A quantitative shotgun proteomics analysis of germinated rice embryos and coleoptiles under low-temperature conditions (2015) Proteome science, 13
5. Quantitative shotgun proteomic analysis of cold-stressed mature rice anthers (2017), 11:417-427



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.A 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.

Email : Joohyun00@gmail.com