conferenceseries.com SciTechnol

Gi-An Lee et al., J Plant Physiol Pathol 2017, 5:3
DOI: 10.4172/2329-955X-C1-009

# Detection of new genetic loci associated with seed germinability in rice

**Gi-An Lee[1], Young-Ah Jeon[1], Do-Yun Hyun[1], Jung-Ro Lee[1], Myung-Chul Lee[1], Sok-young Lee[1], Kyung-Ho Ma[1], Ho-Sun Lee[2] and Hee-Jong Koh[3]**
[1]National Agrobiodiversity Center, RDA, Republic of Korea
[2]International Technology Cooperation Center, Republic of Korea
[3]Seoul National University, Republic of Korea

The seed germinability, one of the quantitative traits, has been crucial phenotype in unpredictable wetting causes preharvest sprouting, but the molecular mechanism of seed germinability is uncertain until now. So in this study, we tried to detect naturally occurred genetic loci associated with seed germinability to expand valuable alleles in cereal crops. After re-sequencing of representative 21 accessions and enrichment analysis, we found about 20 thousand SNPs revealing distinguished allele distribution between PHS resistant and susceptible group, and some regions presenting high number of distinguished SNPs were overlapped with previously reported QTLs. The genotypes of 144 rice germplasm using candidate 39 SNP loci were analyzed, and ten SNP loci revealed significant distribution of seed germinability according to the allele types. Based on these significant SNP loci, we constructed PHS regression equation revealing adjusted $R^2$ value of 0.401 in *japonica* rice. The validation of this regression equation in additional accessions showed R2 value of 0.430 between predicted values and actual measurements. While the relative low values of adjusted R2 and correlation impose that the additional factors associated with PHS might be in existence, newly detected SNP loci could be valuable sources for study and regulation of seed germinability in cereal crops.

## Biography

Gi-An Lee is currently working at National Agrobiodiversity Center RDA, Republic of Korea and his expertise is in evaluation and characterization of plant genetic resources. He has worked at the National Agrobiodiversity Center (NAc, RDA, Republic of Korea) for more than 11 years as a Researcher. He has analyzed the genetic diversity of conserved genetic resources using molecular marker systems and developed microsatellite markers for several crops such as safflower and *Rubus* species.

gkntl1@korea.kr

**Notes:**