

PB-68

Genome-wide association analysis of salt tolerance in Korean cowpea accessions

Zin Mar Swe¹, Byeong Hee Kang^{1,2}, Chang Yeok Moon^{1,2}, Woon Ji Kim¹, Aron Park¹, Sehee Kang¹, Bo-Keun Ha^{1,2*}

¹Department of Applied Plant Science, Chonnam National University, Gwangju, 61186, Korea

²BK21 Interdisciplinary Program in IT-Bio Convergence System, Chonnam National University, Gwangju, 61186, Korea

[Introduction]

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important grain legumes crop providing protein for human consumption that can be grown in worldwide. However, cowpea is affected by salinity stress thus significantly decreasing cowpea production. Today genome-wide association study (GWAS) is a method of choice for fine mapping of QTLs involved in plant responses to abiotic stresses including salinity stress in cowpea. It is important to resolve the genetic of salinity tolerance in cowpea to enrich breeding program. The objective of this study was to identify genomic loci associated with salt tolerance in cowpea using GWAS.

[Materials and Methods]

In this study, a total of 384 cowpea accessions were planted in 50 port plastic tray in greenhouse. At the V1 stage, 150mM of sodium chloride (NaCl) solution was treated after two weeks of sowing. Leaf scorch scoring was visually scored based on the criteria of 1 as resistant and 5 as susceptible after about 8 weeks of NaCl treatment. A total of 384 cowpea accessions were genotyped with the Cowpea iSelect Consortium Array containing 51,128 single nucleotide polymorphisms (SNPs) and 49,516 SNPs markers were used to identify loci controlling salinity tolerance in cowpea by using QTL Max analysis

[Results and Discussion]

GWAS analysis identified three SNP markers, rs_2_07060, rs_2_52922, rs_2_23533 on chromosome 4 that were highly significantly associated with salt tolerance ($p < 0.00001$). Approximately eight candidate genes that are associated with salt tolerance were identified for the significant SNP markers. SNPs markers identified in this study can be used in marker assisted breeding for accurate and rapid screening of cowpea tolerant genotypes to salinity.

[Acknowledgement]

본 연구는 바이오그린연계농생명혁신기술개발사업(사업번호: PJ015680012021)의 지원에 의해 이루어진 결과로 이에 감사드립니다.

*Corresponding author: E-mail, bkha@jnu.ac.kr Tel. +062-530-2055