

PB-41

Detection of QTLs for Dry-heat Tolerance of Rice Seed Using Recombinant Inbred Lines Derived from a Cross between ‘Chamdongjin’ and ‘Younghojinmi’

Hyun-Su Park^{1*}, Chang-Min Lee¹, Jeonghwan Seo¹, Jae-Ryoung Park¹, Songhee Park¹, Man-Kee Baek¹, O-Young Jeong¹

¹National Institute of Crop Science, RDA, Wanju 55365, Republic of Korea

[Introduction]

Dry-heat tolerance (DHT) of rice seed is closely related to dormancy. Since dormant seeds show strong resistance to high temperature and drying, dry-heat treatment is sometimes used to break seed dormancy and control seed-borne pests. It was reported that DHT had a positive correlation with seed longevity and negative correlation with pre-harvest sprouting (PHS). This study was conducted to investigate the relationship between DHT and PHS and identify the quantitative trait loci (QTLs) for these traits using recombinant inbred lines (RILs) derived from a cross between ‘Chamdongjin’, PHS susceptible cultivar and ‘Younghojinmi’, PHS tolerant cultivar.

[Materials and Methods]

Parents and 91 RILs were used in this study. PHS rates were evaluated after incubation for 7 days at 25°C, 100% humidity using three panicles per each lines harvested at 40 days after heading. DHT were investigated by measuring the germination rates of harvested seeds after 90°C dry-heat treatment for control, 12, 24, 36 hours. Genotyping was analyzed using 285 markers showing polymorphism between parents out of 771 KASP markers. QTL analysis was conducted using QTL IciMapping program.

[Results and Discussion]

‘Chamdongjin’ showed higher PHS rate (28.6%) than ‘Younghojinmi’ (3.1%). At all dry-heat treatment times, ‘Chamdongjin’ had lower DHT than those of ‘Younghojinmi’, and the germination rates after 36 hours treatment were 8.0% for ‘Chamdongjin’ and 57.5% for ‘Younghojinmi’. The average PHS rate of RILs was 23.2% and the range exhibited from 0.3% to 73.6%. The average DHT rates of RILs by dry-heat treatments were 91.5% without treatment (DHT_0hr), 61.6% at 12 hours (DHT_12hr), 27.4% at 24 hours (DHT_24hr), and 21.9% at 36 hours (DHT_36hr), which fell down sharply as the treatment time increased. As a result of the correlation analysis, unlike the previously reported results, it was found that there was no relationship between PHS and DHT. On the other hand, there were very high positive correlation between DHT_12hr, 24hr, and 36hr. Through the QTL analysis, no QTL was detected for PHS, but QTLs for DHT were found on chromosome 3 (*qDHT3*) and 8 (*qDHT8*). *qDHT8* was detected in all dry-heat treatments and could explain 19.4% (12hr), 14.7% (24hr), and 18.9% (36hr) of phenotypic variation. RILs carrying ‘Younghojinmi’ allele on *qDHT8* showed higher DHT than those carrying ‘Chamdongjin’ allele. Further analysis of phenotype and genotype on RILs has being performed for precise QTL identification.

[Acknowledgement]

This work was supported by the “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01606702)” of the Rural Development Administration, Republic of Korea.

*Corresponding author: E-mail, mayoe@korea.kr Tel. +82-63-238-5214