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## Heat-sterility Resistance Effect of N22-derived Heat Tolerance QTL in the Genetic Background of *japonica* rice

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### [Introduction]

Rice is one of the staple crop in the world and also Korea's major food crop. This study focused on developing heat-tolerance *japonica* rice line to prepare irregular high temperature due to future climate change. ABL(Advanced Backcross Line) was developed by crossing Korea's elite *japonica* rice cultivar "Saeilmi" as a recurrent parent, and heat-tolerant rice cultivar "N22" as a donor parent. MAS(Marker Assisted Selection) was conducted using DNA markers around the region harboring qHTSF4.1, a heat-sterility resistance QTL located on chromosome 4 derived from N22.

### [Materials and Methods]

We sowed 12 seeds of 3 Saeilmi×N22 BC<sub>2</sub>F<sub>5</sub> lines(donor parent: N22, recurrent parent: Saeilmi) and parental lines, Saeilmi and N22 on 72-hole seed box tray in triplicate. Plants that reached flowering stage was placed in thermo-gradient tunnel covered with PVC film for heat-stress treatment. High temperature above 38°C lasted about 30 minutes per day in the tunnel. Three plant sets were treated heat stress for 0, 4, 7 days each. 45 days after flowering, fertility of 6 panicles from each ABLs and parents was investigated.

### [Results and Discussion]

The average fertility of Saeilmi was 20.7%, 13.6%, and 8.8% after 0, 4, 7 days of heat stress treatment, and fertility of N22 was 17.6%, 6.7%, 6.0% after same treatment of saeilmi. Ye et al.(2012) reported *qHTSF4.1*, the heat sterility tolerance QTL on chromosome 4 derived from N22 can be distinguished into tolerant type and susceptible type by detecting a SNP located on 17.69Mbp. By designing InDel markers on the region including the SNP, we could select heat sterility tolerant lines harboring N22-type *qHTSF4.1* in Saeilmi×N22 backcross population. SNABL3 and SNABL4 has N22-type *qHTSF4.1* and the average fertility range was 51.1~75.1%, 50.5~83.0% each, when treated heat stress for 0, 4, 7 days in flowering stage. SNABL2 has more narrowed N22-type segment on chromosome 4 harboring N22-type SNP on 17.69Mbp, and the average fertility 70.4~74.5%, after treatment of heat stress for 0, 4, 7 days. The three recombinant lines had improved heat tolerance in flowering stage even than heat stress tolerant parent N22. We suggest that the synerge effect between qHTSF4.1 from N22 and regional suitability of Saeilmi resulted increased heat sterility tolerant in progeny lines. Further study of the heat tolerance including background genotyping of the three ABLs is necessary to investigate the genetic reason and mechanism of heat tolerance induced by *qHTSF4.1*.

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