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Improvement of Yield Potential of Tong-il type Rice Varieties by Marker-assisted Selection

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[Introduction]

To meet the demand for rice to feed the increasing human population, increasing rice yield is essential. Improving the genetic yield potential of rice is one ideal solution. It is imperative to introduce the identified yield-enhancing gene(s) into modern rice cultivars for the rapid improvement of yield potential through marker-assisted breeding. So, this study was developed super high yield elite lines by the advanced backcross and MAS in rice breeding programs.

[Materials and Methods]

We used Hanareum2/Unkwang BC₂F₈ SubNILs 141 population selected elite line carrying *SPIKE(NAL1)*, *Ghd7*, *GW8(OsSPL16)* of improving yield gene. The *SPIKE(NAL1)* gene encoding an unknown function protein regulates grain number per panicle. The *Ghd7* encoding a CCT domain protein is involved in the regulation of heading date, plant height, and grain number per panicle. The *GW8(OsSPL16)*, encoding SQUAMOSA promoter binding protein-like (*SPL16*), controls grain width, and higher expression in young panicle promotes grain width. We detected yield genotype of 141 SubNILs population by using MAS. So, We selected finally 3 NILs carrying these gene observed phenotype in the field. And We measured by three replication grain width, length and grain number per panicle of 141 population in 2017 and 2018.

[Results and Discussions]

We selected 3 elite lines of the widest grain and the most numerous grain number per panicle in 141 population. The grain number per panicle of *SPIKE(NAL1)*-NIL and *Ghd7*-NIL are 135~154, whereas that of Hanareum2 is 112. The grain width of *GW8*-NIL is 2.99mm, while that of Hanareum2 is 2.55mm. We analyzed Single-locus ANOVA, F Value is 43.71** (*SPIKE*), 11.24** (*Ghd7*), 40.36** (*GW8*). This is recognized that single marker of identified gene is related to phenotype. This results support that this elite line will be useful information for developing varieties of super yield Tong-il type rice.

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