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Profiling of genes related with grain yield in rice germplasms

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Abstract

Rice is a staple food for nearly half of the world's population, with more than 10,000 rice varieties providing almost one-quarter of the global per capita dietary energy supply. Grain size, panicle size and branch number, grain number in a panicle are directly associated with rice productivity. Recently several genes which increase grain yield were identified through map-based cloning. *Gn1a*, Cytokinin oxidase, is a major grain number QTL and regulates grain number per panicle. *Dep1* increases panicle branching and reduced rachis length. *SCM2* (*APO1*) was identified by a QTL for culm strength and increased spikelet number. *OsSPL16* (*GW8*) controls grain size and shape and then increases 1000-weight of seed. In here, to identify genotype of genes related to yield in 400 of rice germplasms possessed in National Institute of Crop Science, we had first chosen 4 of well-known genes related to yield; *Gn1a*, *Dep1*, *SCM2*, and *OsSPL16*. Among these germplasms, 195, 382, 165, and 353 of germplasms harbored the dominant type of *Gn1a*, *Dep1*, *SCM2*, and *OsSPL16*, respectively. We grouped these germplasms into a total of 10 groups using genotypes of *Gn1a*, *Dep1*, *SCM2* and *OsSPL16*. Most rice germplasms belong to group 1, harbored *Gn1a*, *dep1*, *gw8* and *APO1*, and group 10, harbored *gn1a*, *Dep1*, *GW8* and *apo1*. Hanareum2 is the highest productive cultivar in Korea but do not have dominant type *OsSPL16*, so belong to group 1. On the other hand, in the case of Unkwang, belongs to group 10, which has dominant type of *OsSPL16* but do not have the remaining genes. We can grasp the differences in rice germplasms through the Profiling of genes related to these grain yield, which will be useful for cross-breeding to integrate grain yield genes. We are continuously observing the genotype and phenotype of rice that possesses grain yield genes.

Keywords: rice, germplasm, genotype profiling, grain yield

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