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Discovery and utilization of trait-enhancing QTLs from wild species in rice

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Plant domestication has led to increased productivity, but at the same time it hasnarrowed the genetic basis of crop species. A major objective in plant breeding is to return to the wild ancestors of crop plants and employ some of the diversity that was lost during domestication for the improvementof agricultural yield. To enhance the rate of progress of breeding based on wild species resources, we are developing a population of rice segmental introgression lines (ILs). The ILs comprised marker-defined genomic regions taken from the wild species, Oryza rufipogon and transferred onto the genetic background of the elite inbred cultivar "Hwaseongbyeo". The ILs constitute a library of lines each carrying a single homozygous introgressed segment in the Hwaseongbyeo background. These ILs would greatly facilitate the detection of naturally occurring variation in rice. Using a series of BC3F4 nearly isogenic lines (NILs) derived from a cross between the Korean japonica cultivar Hwaseongbyeo and Oryza rufipogon (IRGC 105491), we identified a total of seven QTLs including 1,000-grain weight and spikelets per panicle across a 50 kb region on the long arm of rice chromosome 9. All seven QTLs were additive, and alleles from the low-yielding O. rufipogon parent were beneficial in the Hwaseongbyeo background. Yield trials with BC3F4 NILs showed that lines containing a homozygous O. rufipogon introgression in the target region out-yielded sibling NILs containing Hwaseongbyeo DNA, and out-yielded the Hwaseongbyeo parent. While higher yielding plants containing the O. rufipogon introgression were also taller and later than controls, the fact that all seven of the QTLs were co-localized in the same interval suggests the possibility that a single, pleiotropic gene acting as a major regulator of plant development may control this suite of agronomically important plant phenotypes. This marks the first time, to our knowledge, that a QTL cluster associated with transgressive variation for multiple yield factors has been mapped to such fine precision and delimited to a segment of cloned DNA.