Research Area : Plant Functional Genomics

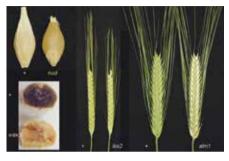


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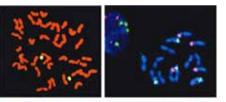
1H

Molecular dissection of beneficial genes in barley



Barley is typically characterized by grains with inseparable chaffs. A single mutation event produced a free-threshing variant, called naked barley, about 8,000 years ago somewhere in the Near East. We clarified the genes controlling naked caryopsis (*nud*), which is suitable for food rich in soluble dietary fiber (*wax.b*). We are also interested in photosynthesis of non-foliar tissues, such as awns and spikes for improved productivity and quality. Using short awn (*lks2*) mutants and white spike (*albino lemma 1*) mutants, we are clarifying their contribution to photosynthesis and grain yield in barley.

Chromosome manipulation of wheat with introduced barley segments



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Through intergeneric hybridization between wheat and barley, we aim to produce unique wheat lines with introduced tiny barley chromosome segments with useful genes. These target genes are expected to confer higher dietary fiber content in seeds and improved disease resistance.