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Preservation and application of genetic and genomic resources in barley

Ca. 15,000 accessions of wild and cultivated barleys and a wide range of experimental strains are preserved with a support from the National Bioresrouce Project. Genomic libraries and extensive cDNA resources have been developed for genomic analysis of barley which contributed to estimate gene regions on the draft barley genome sequence published in 2012. These genetic and genomic resources are used to identify agriculturally important genes on barley genome. We also found that barley and diploid wheat shared the same genomic structure and barley can be used as a diploid model of the Triticeae species, including wheat, barley and rye.



Gene isolation in barley



The study focuses on isolation and characterization of genes controlling industrially important traits using the genome diversity of barley. A recent example is a gene corresponding for barley seed dormancy (*Qsd1*), which is associated with pre-harvest sprouting and malting for brewing beer. Our analysis using a wild barley accession harboring a strong grain dormancy revealed novel insight into the genetic mechanism regulation grain dormancy in barley (Sato et al. 2016 Nat. Commun.).

The orthologous genes are also existed in wheat genomes which will be important to control seed dormancy in wheat.