Barley germplasm and malting barley breeding.

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In malting barley breeding, overall improvement of agronomic, malting and brewing traits is necessary and effective use of germplasm can greatly accelerate progress. We present two recent research works on beer foam and flavor stability using barley germplasm of Okayama University. Several proteins and enzymes have been identified as factors controlling foam and flavor stability. Although barley protein Z4 (Z4) and protein Z7 (Z7) have been suggested as factors responsible for foam stability, their effect is still under debate. To evaluate the effects of Z4 and Z7 on foam stability, we brewed beer samples from deficient mutants on each of these proteins. The cultivar Pirrka was used as a source of Z4 deficient, while a Z7 deficient mutant was unknown and screened from the Okayama University barley germplasm collection. The results of brewing trial suggested that the contribution of Z4 and Z7 on foam stability was not greater than that of other beer proteins. Secondly, we have developed lipoxigenase-1 (LOX-1) null barley to improve beer flavor stability. LOX-1 is a key enzyme for flavor stability. We screened LOX-1 deficiency in the Okayama University barley germplasm collection and found six LOX-1 null mutants. One of these was used in breeding by marker assisted backcrossing a recurrent parent CDC Kendall. We developed LOX-1 null variety, CDC PolarStar and brewing trial using CDC PolarStar and CDC Kendall clearly showed that the flavor stability of CDC PolarStar beer was superior.

Comparative sequence analysis of chromosomes isolated from two wild relatives of wheat (Aegilops umbellulata and Ae. biuncialis).

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Wild species of Triticeae were not exposed to domestication, exhibit large genetic and phenotypic diversity and provide a rich source of novel genes and alleles for breeding improved varieties of wheat. However, effective transfer of alien genes and gene variants either via interspecific hybridization or transgene technology from wild species requires solid knowledge of their genomes. Chromosome genomics proved to be elegant method to analyze the complex genomes of Triticeae. This approach simplifies the analysis by dissecting genomes to small parts by flow cytometric sorting of mitotic chromosomes. In wheat, chromosome genomics has been used to develop markers from sub-genomic regions, identify genes and establish virtual gene order for the complete set of chromosome arms, as well as to construct physical maps of chromosome arms to facilitate map-based cloning and production of a reference genome sequence. Here we report on developing chromosome genomics in *Aegilops* spp. We have isolated by flow cytometric sorting chromosomes 1U, 3U, and 6U from diploid *Ae. umbellulata* and homologous chromosome $1U^b$ from allotetraploid *Ae. biuncialis*. Chromosomal DNA was amplified and shotgun sequenced to a high coverage by Illumina technology; low-copy, and genic regions were assembled and used to generate annotated syntenic builds. This advance provided first large-scale insights into the sequence composition of the *Aegilops* genomes. A virtual gene order was constructed for the four chromosomes using the GenomeZipper approach. In total, 11,513 non-redundant gene loci were ordered: 2,666 loci on 1U, 3,155 loci on 3U, 3,212 loci on 6U, and 2,480 loci on $1U^b$. Moreover, syntenic relationship established between the four *Aegilops* chromosomes and genomes of *Brachypodium*, rice, sorghum, barley, and wheat, enabled discovery of multiple chromosomal rearrangements in *Ae. umbellulata* and *Ae. biuncialis*, providing a valuable reference to study genome evolution in *Aegilops*.