Mother of FT and TFL1 represses wheat germination and has potential breeding applications to improve seed dormancy.

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Pre-harvest sprouting is a major problem for stable production of wheat in Japan, where the rainy season coincides with the harvest season. To solve this problem, we need to develop wheat cultivars with strong seed dormancy; identifying genes that regulate the level of dormancy will inform breeding strategies for this purpose.

To identify regulators of dormancy, we focused on the wheat seed dormancy response to temperature during seed development, in which cooler temperatures increase seed dormancy. Since temperature-dependent transcriptional regulation may control this response, we analyzed this phenomenon using a transcriptomic approach. We found that *Mother of FT and TFL1* (*MFT*) was expressed at much higher levels in embryos of dormant seeds grown at a cooler temperature. *MFT* belongs to the phosphatidyl ethanolamine-binding protein family, which also includes the flowering inducer *Flowering locus T* (*FT*) and the flowering repressor *Terminal Flower 1* (*TFL1*). In this presentation, we report our analysis of *MFT* expression, mapping of the *MFT* locus, and transformation and transient assay analysis of *MFT* function. Our results suggest that *MFT* represses germination. Moreover, *MFT* on chromosome 3A is a promising candidate for a seed dormancy QTL, and a single nucleotide polymorphism in the *MFT* promoter seems to be the causal polymorphism for the QTL. We have developed a DNA marker for this SNP to select the allele that produces strong seed dormancy. Genotyping of various wheat cultivars suggests that breeders can use this marker to improve pre-harvest sprouting tolerance in wheat.

Barley's triple spikelet meristem is controlled by Vrs4 (six-rowed spike 4).

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The appearance of the triple spikelet meristem within the genus *Hordeum* is one of the important developmental and genus-specific features. Classically, barley (*Hordeum vulgare* L.) is subdivided into two- and six-rowed barleys depending upon lateral spikelet fertility. Until today, five different loci have been identified, which can convert two-rowed barley to six-rowed barley; they include *vrs1* (2HL), *vrs2* (5HL), *vrs3* (1HL), *vrs4* (3HS), and *int-c* (4HS). Komatsuda et al. identified the *Vrs1* gene as being an HD ZIP transcription factor and, recently, Ramsay et al. found *int-c* as the barley orthologue of maize *Teosinte Branched*. Among other vrs loci (*vrs2*, *vrs3*, and *vrs4*), *vrs4* is known to produce a prominent six-rowed phenotype with many fully fertile, long awned lateral spikelets. In the present study, we mapped the *vrs4* locus in two bi-parental mapping populations, (Barke × *vrs4.k* and *vrs4.k* × Golden Promise-96 individuals in each) using SNP-based CAPS markers and VeraCode technology. *vrs4* showed linkage to markers derived from chromosome 3HS. The corresponding marker-phenotype interval comprised 27 genes in *Brachypodium*, annotations of which revealed an important transcription factor involved in inflorescence development. Resequencing of the transcription factor in *vrs4.k* and its wild type MFB 104 showed a unique deletion in the *vrs4.k* mutant, resulting in a truncated protein product. Hence, we resequenced the gene in 18 *vrs4* mutant alleles available from NordGen, Sweden and USDA, USA; most of them showed nucleotide changes in the coding region, but also in upstream or downstream regions of the gene. High-resolution mapping in around 2,000 gametes and BAC library screening have established a 274-Kb physical contig containing a single gene (*vrs4* locus). Tissue localization of the vrs4 gene expression through *in situ* hybridizations, its genetic networks by microarray analysis, and a working model for the six-rowed spike pathway, involving *vrs4*, shall be presented at the meeting.

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