possess a six-rowed genetic background. The resequencing results of *Vrs1* revealed 13 accessions with two novel *vrs1.a1* haplotypes. Following the current nomenclature of *vrs1* haplotypes, the new haplotypes were named as haplotypes 66 and 67. Resequencing at the *int-c* locus showed that 118 of the *labile*-barleys possessed the previously described *Int-c.a* allele, but only one accession was found having a novel *Int-c.a* haplotype in the homozygous state (termed *Int-c.a haplotype1*; *Hap_1*). Interestingly, 101 *labile*-barleys carried the *Int-c.a* allele and *Int-c.a haplotype1* simultaneously, suggesting maintained heterozygosity or recent gene duplication at this locus. Only one accession had a two-rowed haplotype (*Vrs1.b3*, *int-c.b1*), and one accession possessed the *Vrs1.t* (*deficiens*) and *Int-c.a* alleles (six-rowed). These two accessions were considered as misclassified *labile* genotypes and not included in further analysis. On the other hand, the phenotypic data obtained from the *labile* accessions and their comparison to the observed allele/haplotypes combinations showed that, in spite of the presence of *vrs1.a* and *Int-c.a* (genotypically six-rowed alleles) in the large majority of the analyzed accessions, the observed phenotypic data did not support the expected six-rowed phenotype in *labile*. The *labile*-barley spike phenotype displays a variable number of fertile lateral spikelets (from 0 to 2) at each rachis node. Thus, our analysis demonstrated that all of the 219 *labile* accessions studied in this work showed six-rowed alleles at *vrs1* and *int-c* but reduced lateral spikelet fertility. This reduction is most likely caused by the recessive *labile* (*lab*) locus which we are in the process to characterize further.

Poster 26. A large-scale, mutant panel of einkorn wheat developed by heavy-ion beam mutagenesis and its application for flowering-time mutant screening.

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Mutation analysis is a powerful tool for investigation of gene function. Heavy-ion beam mutagenesis has been recognized to be an effective method of producing mutations because of its high linear energy transfer (LET). High-LET radiation effectively induces DNA double-strand breaks than other mutagenic methods. We have been constructing a large-scale, mutant panel of diploid einkorn wheat (*Triticum monococcum*) using heavy-ion beam mutagenesis for 12 years. Seeds of the einkorn wheat strain KU104-1, KU104-2, or DV92 were treated with 50–58 Gy of N or C ion beam with LET of 30 ke/Vμm and then sown in the field. The spikes of M_1 plants were bagged and the harvested selfed seeds of each spike were used to produce the M_2 lines. Every year, we obtained about 1,000 M_2 lines, eventually developing a mutant panel with a sum of 10,000 M_2 lines. We are using this mutant panel for screening mutation of reproductive growth, especially for flowering-time mutants. We have identified several flowering-time mutants of great interest; nonflowering mutants (maintained vegetative phase), late-flowering mutants, and early-flowering mutants. In the late-flowering mutants, for example, we identified a mutation that had an abnormally large number of nodes; we termed this mutation *fushi-darake* (*fdk*), which means too many nodes in Japanese. The *fdk* mutant plants have increased numbers of nodes and leaves. WT plants show spiral phyllotaxy; however, *fdk* mutants have 1/2 alternate phyllotaxy with a shortened plastochron. Each tiller in the *fdk* plants branches at the upper part of the culm. A small spike sometime appears from the tip of culm in main tiller. The SEM analysis of developing SAMs indicated that transformation of spikelet meristems into vegetative shoot meristems in the *fdk* plants. Based on the phenotype, we concluded that the *fdk* mutant has a heterochronic nature, i.e., both reproductive and vegetative programs are simultaneously in operation during the reproductive phase, resulting in a shortened plastochron and transformation of reproductive spikelets into vegetative shoots.