Towards cloning the powdery mildew resistance gene QPm.tut-4A introgressed to bread wheat from T. militinae.

Monika Kladivová [1], Barbora Klocová [1], Diana Posti [2], Irena Jakobson [2], Hilma Peusha [2], Kadri Järve [2], Ljudmilla Timofejeva [2], Yuqin Hu [3], Yong Zhang [3], Frank M. You [3], Ming-Cheng Luo [3], Ajay Kumar [4], Shahryar F. Kianian [4], Hana Šimková [1], Jan Šafář [1], Jaroslav Doležel [1], and **Miroslav Valárik** [1].

[1] Centre of the Region Haná for Biotechnological and Agricultural Research, Institute of Experimental Botany, Sokolovská 6, CZ-77200 Olomouc, Czech Republic; [2] Department of Gene Technology, Tallinn University of Technology, Akadeemia tee 15, Tallinn 19086, Estonia; [3] Department of Plant Sciences, University of California, Davis, CA 95616, USA; and [4] Department of Plant Sciences, North Dakota State University, Fargo, Loftsgard Hall 470G, Fargo, ND 58108, USA.

Introgression of agronomically important genes from wild relatives is one of the most effective means to improve wheat gene pool. However, introgressions often introduce collinearity and recombination aberrations. Recently, resistance to powdery mildew from the tetraploid wheat *Triticum militinae* was introgressed to hexaploid wheat cultivar Tähti. The locus with the major contribution in both seedling and adult stage was mapped on distal end of 4AL chromosome arm to the region delimited by wmc232 and wmc313 markers (~10 cM) and denominated as *QPm-tut-4A*. In the original mapping population from a cross of Tähti by resistant introgressive line 8.1, the region includes 12 markers. However, their order could not be resolved using 1,200 haplotypes. To resolve this obstruction, a combination of traditional approaches and recent advances in wheat genomics were used. For marker ordering, a 4AL-specific radiation hybrid panel and three additional recombination based mapping populations were employed. For efficient marker development, 4AL chromosome-specific BAC library was constructed, fingerprinted, and ordered into contigs. The region was anchored to the rice, *Brachypodium*, and *Sorghum* chromosome 6, 1, and 10, respectively. All genes from the collinear regions were mapped to our mapping populations. Marker development was enhanced using MDA amplified DNA from the 4AL chromosome arm of Chinese Spring, and the same arm carrying the translocation in combination with survey sequences of chromosomes 7A and 7D. Using these resources, the *QPm-tut-4A* gene was delimited in 0.2 cM region flanked with the gpw356 and gpw3079 markers. The remaining three SSR markers (barc70, gwm832, and gpw3556) completely linked to the *QPm-tut-4A* locus were used to identify three BAC contigs that comprise 158 BAC clones and cover about a 2 Mb region. From the contigs, 114 BAC ends were sequenced and used for marker development. The physical map, radiation hybrid lines, markers, and the remaining BAC-end sequences will be used to saturate the *QPm-tut-4A* map and, finally, clone the gene. This work has been supported by the MEYS of Czech Republic (Operational Programme Research and Development for Innovations No. ED0007/01/01), Internal Grant Agency PrF-2012-001, and by Estonian Ministry of Agriculture.

Cleistogamy in the Triticeae: genetic variation and its regulation.

Ning Wang, Shunzong Ning, and Takao Komatsuda. National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, Japan.

Cereals are requested for human energy and protein needs. Efforts in particular brought attention to concerns of seed-borne disease contamination as well as enhance seed production. In the typical grass flower, the florets gape as a result of the swelling of the lodicules (non-cleistogamous), but non-gaping (cleistogamous) variants are known in many species. The possibility of manipulating flower type is of particular relevance for the prevention of pollen flow from transgenic types and for the control of Fusarium head blight, a disease to which non-cleistogamous barley and wheat cultivars are especially vulnerable. In barley, the development of lodicule is genetically determined by allelic variation at the *cly1* (syn. *HvAP2*) locus. In the non-cleistogamous type flower (*Cly1.a*), *HvAP2* activity is suppressed by miR172-directed cleavage. A single nucleotide substitution at the microRNA target site generates the recessive allele *cly1.b*, in which no cleavage occurs, converting the flower into a cleistogamous type. *HvAP2* homologues among various diploid and polyploid wheats are regulated in the same fashion as in barley; in non-cleistogamous wheats, miR172-directed cleavage can be detected at each AP2 homoeologue. As the cleistogamous type is produced by a recessive *AP2* allele, to convert hexaploid wheat into a cleistogamous type, we would need to identify the recessive allele at each of the A, B, and D homoeoloci and then combine them into a single individual.