Poster 8. Identification of seed dormancy for four populations derived from synthetic hexaploid wheat.

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Seed dormancy is a key adaptive trait for wild species and is also a major domestication-related trait for crop species. Cereal cultivars have been selected for rapid, uniform germination during domestication and breeding. Consequently, they generally have an insufficient degree of seed dormancy to resist preharvest sprouting (PHS). To seek dormancy genes from the wheat wild relative *Ae. tauschii*, we have identified four populations of doubled haploid (DH) or recombinant inbred (RI) lines derived from synthetic hexaploid wheat. The four populations, coded as DH1, DH2, DH3, and RI1, were developed from crosses between different synthetic hexaploid wheat lines and the nondormant line ND495. Plants were grown in field conditions during summer seasons of 2006 and 2007. Seeds/panicles were harvested at physiological maturity, air-dried in a greenhouse for 7 days, and then stored in the cold room (4–5°C) prior to dormancy testing. The degree of dormancy was measured by germinating threshed seeds (refer to threshed seed germination) and seeds on the intact panicles (refer to intact seed germination) at 20°C. Threshed seed germination for the DH1, DH2, DH3, and RI1 populations was 46.0 ± 23.9, 77.7 ± 16.5, 95.6 ± 7.4, and 66.7 ± 24.0 (%), respectively, after a 7-day incubation, and 55.8 ± 22.2, 82.7 ± 13.6, 97.7 ± 4.3, and 68.0 ± 23.0 (%), respectively, after a 14-day incubation. An overwhelming majority of lines from the populations displayed stronger dormancy with the threshed seeds than the nondormant parent ND495 (germination rate >93%) under the same conditions, suggesting that *Ae. tauschii*-derived, synthetic hexaploid wheat could be a novel source of seed dormancy genes imparting PHS resistance to common wheat. In a preliminary experiment, a subpopulation of 60 lines from the DH1 population harvested in 2007 displayed 39.9 ± 26.2 and 27.5 ± 27.5 (%), respectively, for threshed and intact seed germination after a 10-day incubation. The threshed and intact seed germination rates were highly correlated with $r = 0.784$ and $r^2 = 0.61$, respectively. This result implies that the seed covering tissues in the synthetic wheat-derived lines may also have germination inhibitors enhancing PHS resistance. We are using a QTL analysis strategy to identify dormancy genes from the above populations.

Poster 9. Markers linked to the adult-plant, leaf rust resistance gene Lr12 in bread wheat.

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The resistance gene *Lr12* provides adult-plant, race-specific resistance to wheat leaf rust caused by *Puccinia triticina*. A population of 115 F_3 families segregating for resistance was generated from a cross between Thatcher and the Thatcher isoline containing *Lr12*. At anthesis, flag leaves were inoculated with leaf rust isolate PRTUS25, which is avirulent on *Lr12*. Resistance segregated as a single qualitative gene. The simple sequence repeat marker *Xgwm251* was located 0.9 cM proximal to the *Lr12* locus and *Xgwm149* was 1.9 cM distal. These markers can be used in marker-assisted selection to combine leaf rust resistance genes in wheat. Using wheat deletion stocks, we located *Lr12* in the deletion bin 4BL-5 (0.84–0.89) that comprises 5% of the 4BL arm. We are developing a high-resolution mapping population for fine mapping of *Lr12*.