

Poster 4. RNAi-mediated viral resistance in transgenic wheat.

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Wheat streak mosaic virus (WSMV) and *Triticum* mosaic virus (TriMV), are two of the major viruses in the Great Plains of the United States. Cultural practices, mite vector control, and deployment of resistant varieties are the primary methods of disease management; however, they are not fully effective. We evaluated the use of interference RNA, recognized as a natural defense mechanism, as a biotech approach to generate resistance to these wheat viruses. RNAi expression vectors were independently created from the sequences of the coat proteins (CP) of both WSMV and TriMV. Immature embryos of the wheat cultivar Bobwhite were independently co-transformed by biolistic particle-delivery system with these RNAi expression vectors and pAHC20, which contains the bar gene for glufosinate selection. After tissue culture, putative transformed plants were analyzed through PCR for the presence of the appropriate RNAi CP gene. Transgenic T₁ seeds were collected and each line was tested for transgene expression via RT-PCR. To determine viral resistance, T₁ progeny were mechanically inoculated with the corresponding virus. Viral presence was established by ELISA. In the T₁ generation, resistance was seen in up to 60% of the plants evaluated for both constructs, although some events that showed transgene presence did not exhibited resistant phenotype. Analyses of transgene presence and expression in the T₂ generation evidenced events of transgene silencing and deletion. Regardless of these phenomena, consistent resistance response in two lines of WSMV CP construct and one TriMV CP transgenic line was found.

Poster 5. QTL detection and factor analysis of yield and adaptive traits in winter wheat.

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The relationships between yield components, adaptive traits, and molecular markers were investigated in two populations of recombinant inbred lines (RILs) using QTL analysis and factor analysis. The RIL populations were derived from single crosses with Tubbs, an Oregon soft white winter wheat variety, with two western European hard red winter wheat varieties. The populations were grown in two replications at two locations in Oregon. Each plot was evaluated for total grain yield, yield components, measures of maturity, and other important traits. The values of all traits were broadly distributed and transgressive segregates were observed in both populations. The yield components most highly correlated with yield were fertile spikelets/spike and seeds/spike in both populations. In one population, these correlations ranged from 0.4 to 0.47. They ranged from 0.21 to 0.25 in the other population. Flowering time was inversely correlated with yield in both populations, ranging from -0.17 to -0.32. Heritabilities were determined for each population across locations. The heritabilities for yield components ranged from 0.44 to 0.84. Heritability for grain-fill duration varied the most between populations, ranging from 0.33 to 0.54. The interrelatedness of the traits was examined by factor analysis of each population at each location using the principle-component method. Five factors, accounting for 69.7% to 73.4% of the total variance, were selected. Important factors were observed for head fertility, tillering, and maturity. Genetic linkage maps composed of DArT and SSR markers were used to detect putative QTL, and their locations are presented. The extension of QTL analysis to factor scores was investigated.