Using BSMV–VIGS for functional genomics in wheat.

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Our laboratory has gained significant experience using the barley stripe mosaic virus system for virus-induced gene silencing (BSMV-VIGS) as a tool for functional genomics in wheat. This presentation will summarize our experiences using the BSMV-VIGS system to functionally identify genes with essential roles in disease resistance pathways and, in particular, it will focus on the design considerations for successful VIGS experiments.

Development of resources for reverse-genetic analysis in Triticum monococcum.

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Reverse genetics is a powerful tool to discover gene function by identifying modifications in specific genes. Mutagenized populations are generated using either chemical, physical, or biological methods and screened for lesions for the desired gene of interest to identify its functional role. The goal of this project is to develop a mutagenized population of *Triticum monococcum* and screening systems for lesions in genes of interest using DNA pooling and PCR-based approaches as a reverse-genetic resource for the scientific community. We have generated mutagenized populations using 1,2,3,4-diepoxybutane (DEB) or trimethylpsoralen along with a UV treatment (TMP/UV) as a pilot study with chemical concentrations that lead to 20–25% survival rates. Experiments were conducted to identify the relative efficiency of these chemicals in a) creating mutations and b) detecting deletions/lesions using forward and reverse-genetic approaches.

We have generated approximately 1,000 M_2 families from each chemical treatment. Initial observations from five germinating seeds per M_1 plant indicated 2% albinos in 250 M_2 families per chemical treatment. DNA was isolated using a filter-based method from individual plants and, currently, is pooled to 1:8 and 1:16 times and used for screening using different methods. A total of 424 DEB-treated, M_2 families were advanced to the M_3 generation to observe visible mutant phenotypes and determine forward mutation frequency for this chemical treatment. Many phenotypic mutants, such as dwarf, early and late flowering, bushy, oligoculm, small spike, purple plants, and disease mimic were observed in this M_3 population. The percent of phenotypic mutants in the M_2 as observed in the M_3 families was 0.94% to 8.02 % for ten different phenotypes. The results of the screening for lesions in the mutagenized population will be presented, which will strengthen the use of this approach for developing reverse-genetic resources in wheat.

Poster 1. A detailed, comparative sequence analysis on the HMW-glutenin locus regions of eight genomes from diploid and polyploid wheats.

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Wheat is the most widely grown crop worldwide and feeds one-third of the world's population. As a result, wheat is foremost among the world's crops both in regards to its importance as a staple of mankind and its economic significance. Despite several successes in sequencing several plant genomes, the complex wheat genome might still represent challenges in genome-sequencing projects. Compared to most other cereals, bread wheat (*Triticum aestivum*) has an extremely large genome (~16,000 Mb); more than 30-fold greater than the rice genome. Furthermore, bread wheat is an allohexaploid species consisting of three related subgenomes (A, B, and D). To study the structural organization of wheat genomes, we sequenced large genomic regions harboring HMW-glutenin genes from eight Triticeae genomes including the D genome from diploid *Ae. tauschii*, the A^m genome from diploid *T. monococcum* subsp. *monococcum*, the A and B genomes from tetraploid *T. turgidum*, the A, B, and D genomes from hexaploid wheat, and the H genome from barley. The in-depth sequencing of the HMW-glutenin locus regions allowed us to compare sequence changes among the three