Poster 19. Association analysis in a panel of eastern U.S. winter wheat lines.

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We report our results from the first year of a multi-year study to discover new disease and insect resistance genes within a diverse panel of 449 eastern U.S. winter wheat lines. The panel is comprised of both landrace and elite cultivars of current or historic importance to eastern U.S. wheat breeding programs. Lines were submitted by eastern U.S. wheat breeders for inclusion in the panel. The diseases of primary focus are *Blumeria graminis* f. sp. *tritici* (powdery mildew), *Puccinia triticina* (leaf rust), and *Stagonospora nodorum* (glume blotch). The insect of primary focus is *Mayetiola destructor* (Hessian fly). These diseases and insects can significantly decrease yields of winter wheat in the eastern U.S. While resistance genes do currently exist for each of these diseases or insects, novel genes are needed to continue to incorporate into breeding programs as current resistance begins to break down. During the 2011–12 season, this panel was grown in head rows and screened for disease resistance in three reps at three locations in North Carolina. Disease screening at each location was with *B. graminis* f. sp. *tritici*, *S. nodorum*, or *P. triticina*, with one disease per location. Disease pressure for powdery mildew and leaf rust was naturally very high at the respective sites and no inoculations were performed. Inoculation with *S. nodorum* was done by spreading wheat straw over seedlings in January, 2012. Additionally, Hessian fly screening was done in the greenhouse using biotype L. These phenotypic data were used in an association analysis with SNP data on these lines, which was obtained from the Illumina 9k wheat chip. Population structure, seedling vigor, maturity at rating, and heading date were all used as covariates in the analysis. We anticipate the use of our results in helping to characterize the genetics of resistance to these pests and pathogens and also in providing breeders with additional tools for marker assisted selection.

Poster 20. Genome-wide characterization and capture of exotic alleles for increased yield from primary synthetic bread wheat.

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To address the loss of genetic diversity due to domestication and breeding of modern wheat cultivars, exotic alleles from bread wheat progenitors, *Triticum turgidum* subsp. *dicoccum* and *Aegilops tauschii* have been captured in primary synthetic bread wheat lines developed by the CIMMYT Wide Cross Program. The primary synthetics carry resistance and tolerance to a range of biotic and abiotic stresses. We analyzed selected high-yielding lines from double haploid (DH) populations between an elite CIMMYT cultivar (Opata) and six different primary synthetics, Opata x Synthetic recombinant inbred lines (RILs), and synthetic-derived, CIMMYT semi-arid wheat yield trial (SAWYT) breeding lines. Grain yield, agronomic, and physiological measurements were collected at CIMMYT over several years in a high-yield potential, heat and drought-stressed environment. We observed several synthetic derived lines outperforming the elite parent Opata in all environments, indicating that the primary synthetics contribute alleles increasing yield. Genotyping-by-sequencing (GBS) will be used to generate whole genome profiles and identify yield promoting genomic regions inherited form the primary synthetics. We will apply specifically developed genomic selection (GS) models to rapidly introgress valuable alleles and develop high-yielding breeding lines. In a next step, allelic predictions and GS models will be validated on derivatives of these DH, RIL, and SAWYT lines. New populations derived from crosses between the highest yielding lines in the existing DH populations are under development and will be evaluated under optimal and stress conditions in yield trials at CIMMYT. Testing of multiple types of synthetic derivatives including DH lines and breeding lines will provide rigorous validation of alleles for increased yield and the predictive power of our GS models. This pioneering study takes a whole genome approach to characterize, improve, and utilize exotic germplasm to increase yield.