Poster 30. Genotyping U.S. wheat germ plasm for the presence of stem rust resistance genes Sr2, Sr24, Sr26, Sr36, and Sr1RS-Am.

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Wheat germ plasm from throughout the U.S. was surveyed for the stem rust resistance genes *Sr2*, *Sr24*, *Sr26*, *Sr36*, and the T1AL·1RS rye translocation that have conferred resistance to race TTKS of *Puccinia graminis* f.sp. *tritici* identified in Uganda and Kenya. A collection of 804 cultivars and breeding lines of wheat and 12 lines of durum wheat from all growing regions of the United States were screened with simple sequence repeat (SSR) and sequence tag site (STS) markers linked to stem rust resistance genes to determined frequencies of these genes U.S. wheat germ plasm. None of the U.S. lines surveyed possess the *Th. ponticum*–derived gene *Sr26*. In general, the marker analysis revealed less resistance in the spring wheat germ plasm than in U.S. winter wheats. The *Sr24*/*Lr24* translocation is present in 11% of lines tested and is most frequent in hard winter wheat lines from the Great Plains. The T1AL·1RS translocation that confers resistance to TTKS was present in 7% of the winter wheat lines surveyed and was not present in any spring wheat germ plasm. Eastern soft winter wheat germ plasm has been the primary source of *Sr36*. The SSR marker *Xgwm533* was not predictive of the presence of *Sr2*, and new markers are being tested to screen for this gene. For 413 lines, phenotypic data from evaluation of seedlings with stem rust was used to validate the genotypic data. In general, the molecular marker data was consistent with phenotypic observations. Identification of the principle sources of stem rust resistance genes in U.S. germ plasm effective against the TTKS race of stem rust will aide in the development of more diverse and durable resistance profiles.

Poster 31. A simple, bead-based assay for multiplex SNP analysis in wheat.

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Single nucleotide polymorphisms (SNPs) are the most abundant form of DNA polymorphism and are highly suitable for automated analysis. These polymorphisms can be used in plants as simple genetic markers for many breeding applications and are useful for cultivar identification, genetic mapping, trait association, and marker-assisted selection. With the influx of various SNP genotyping assays in recent years, there has been a need for an assay that is robust, yet cost effective, and suited to marker-assisted selection. The Luminex system is a simple, bead-based assay that utilizes a fluorescent microsphere sorter and can be used for low to medium throughput genotyping projects capable of analyzing anywhere from one SNP in one individual up to 100 SNPs in an unlimited number of individuals. This device uses FlexMAP beads that are fluorescent microspheres comprising 100 unique color codes enabling individual beads to be identified using a Luminex 100 instrument. This instrument is capable of analyzing either single-base extension (SBE), allele-specific primer extension (ASPE) or direct hybridization (DH) assays. Here, we present preliminary data on mapping SNPs in wheat and its potential uses in developing a high-throughput system for analyzing multiple SNPs in any given assay.