

ASA, CSSA, and SSSA 2010 International Annual Meetings

Oct. 31-Nov. 4 | Long Beach, CA

Green Revolution 2.0: Food+Energy and Environmental Security

[Start](#) | [View At a Glance](#) | [Author Index](#)

207-4 Assessment of Genetic Variation In Spring and Winter Wheat Populations Using Illumina High-Throughput SNP Genotyping Assay.

See more from this Division: [C07 Genomics, Molecular Genetics & Biotechnology](#)

See more from this Session: [Symposium--Technological Advances Driving the Next Green Revolution: High Throughput Genotyping](#)

Tuesday, November 2, 2010: 10:00 AM

Long Beach Convention Center, Room 102C, First Floor

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(13)Wheat Genetics, Quality, Physiology & Disease Research Unit, USDA-ARS, Pullman, WA

(14)Montana State University, Bozeman, MT

(15)Texas Agrilife Research-Amarillo, Amarillo, TX

(16)Colorado State University, Ft Collins, CO

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Advances in sequencing technologies combined with the development of highly multiplexed SNP genotyping assays hold a great promise to accelerate the analysis of genetic variation in crops. Such applications as association mapping, high-resolution genetic mapping and genomic selection that play important role in crop breeding and genetics can greatly benefit from the availability of a dense set of SNP markers. A set of genome-wide distributed SNPs located within genic regions was used to develop the 1536-plex Illumina Oligo Pool Assay (OPA). The wheat OPA was tested in a large panel of spring and winter wheat cultivars represented by historic and modern varieties used in national breeding programs. The SNP genotyping data was used to infer the population structure and genome-wide patterns of genetic diversity and linkage disequilibrium (LD). A significant proportion of SNPs segregating in both spring and winter wheat populations indicate the usefulness of the wheat OPA for genotyping diverse sets of lines. A total of 83% of polymorphisms were shared between spring and winter wheat suggesting significant amount of historic gene flow between these populations. A high proportion of polymorphic SNPs (70% - 85%) was also found within populations of different origin reflecting a high level of genetic diversity within the breeding programs. The patterns of genetic variation and LD suggest that breeding and selection had a different impact on homoeologous genomes in different populations. The extent of LD within the assembled panel of diverse lines indicates that this genetic resource will be useful for studying the genetics of complex traits using the association mapping approach.

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[<< Previous Abstract](#) | [Next Abstract >>](#)