



Spring 2016

MOLECULAR PLANT SCIENCES GRADUATE PROGRAM
Student-Organized Seminar Series

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*"Population-scale functional
and structural diversity of the
wheat genome"*

Wednesday, February 3rd at 12:10pm

Webster 17

Washington State University

Genomic diversity underlies functional and phenotypic diversity in populations and provides the basis for adaptation to changing environment. Recent analyses of the wheat reference genome suggest that the two rounds of polyploidization and expansion of repetitive DNA space could have facilitated the generation of novel structural and functional variation at a high rate. However, due to the complexity and size of the wheat genome information about the scope of its diversity at the population level remains limited. By characterizing exomes and transcriptomes of the geographically diverse lines we investigated the nature and scale of functional and structural variation in wheat. The analysis of 1,000 wheat exomes is allowing us to create a detailed catalog of SNP and PAV variation and describe its possible effect on gene function. The high-density haplotype map was created and tested as a platform for cross-linking genetic mapping and breeding efforts. Eco-geographic patterns of genomic variation are investigated to identify alleles contributing to adaptation and assess their role in breeding. Transcriptome sequencing revealed a significant level of homoeolog-specific expression bias and silencing variation among the accessions of distinct geographic origin. Structural and functional divergence among the wheat genomes was reflected in the distribution of selective sweeps among the homoeologous chromosomes. Analyses of population-scale genomic data suggest that the wheat genome has the potential to generate limitless possibilities for the origin of novel variants that could broaden the adaptive potential of wheat. Our current efforts are directed towards building a genome-wide catalog of these adaptive genomic features.