

**Friday, September 26, 9:30-10:00 a.m.**

*“Leveraging genomic tools to fight wheat pathogens”*

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Tetraploid wheat species *Triticum turgidum* provides us with pasta and couscous and serves as an important model for basic wheat research. To enhance genomic toolkit of wheat researchers, we designed wheat exome capture and applied it to re-sequence gene space of mutant wheat populations. In the past two years, we sequenced 1,000 mutant wheat lines, identified the mutations in the protein-coding sequences and computationally predicted mutation effect on protein function. This information is being catalogued in a reverse genetics database that will be publicly available to scientists and wheat breeders. Using simple search tools, anyone can identify induced alleles of interest and requesting corresponding wheat lines. In parallel, we conducted a forward genetics screen by exposing our mutagenized wheat population to natural disease pressure in the field and identified mutants with either enhanced resistance or increased disease susceptibility to stripe rust and other wheat pathogens. We are following up candidate mutations and employing mapping-by-sequencing to identify genetic basis for these phenotypes. In this presentation, I will describe the development of functional genomic tools for wheat and its application to dissect plant innate immunity.