

Plant Pathology Seminar Series

Developing KASP markers associated to avirulence genes in *Puccinia striiformis* f. sp. *tritici*, the wheat stripe rust pathogen

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Abstract

Wheat is one of the most important crops produced in the United States. Stripe rust, caused by fungal pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*), can cause severe losses in yield and quality or cost multimillion dollars spent on control with fungicides (Chen 2014, 2020). Because of the economic impact that stripe rust has on the production of wheat, it is important to develop techniques for monitoring the pathogen populations. In our lab, *Pst* populations have been characterized by virulence testing on 18 *Yr* single-gene differentials every year (Liu et al. 2017; Wan and Chen 2014, Wan et al. 2016; Wang et al. 2022), and by simple sequence repeat (SSR) and secreted protein gene based single-nucleotide repeat (SP-SNP) markers (Bai et al. 2021, 2022; Li et al. 2019, 2020; Liu et al. 2021; Xia et al. 2016a, 2016b, 2017, 2018, 2020). However, a more efficient technique is needed to monitor virulence changes in the pathogen.

This goal of my study is to develop Kompetitive Allele Specific PCR (KASP) markers associated to avirulence genes of *Pst* to be used in monitoring virulence changes of the pathogen populations. The specific objectives are (1) design KASP markers based on SP-SNP markers associated to avirulence genes identified in our lab and test the KASP markers with a selected panel of *Pst* isolates; and (2) validate markers selected from Objective 1 with *Pst* collections of the recent years. Currently, progress has been made on selecting isolates, increasing urediniospores for DNA extraction, and learning the techniques in designing primers and testing KASP markers.

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