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PROJECT 2 ABSTRACT
(1 Page Limit)

Spring wheat is vulnerable to Fusarium head blight (FHB) or scab, and the most economical way of combating the disease is to grow varieties with genetic resistance. To develop these improved cultivars, we need access to additional resistance loci and a better understanding of the genes underlying these loci. This will allow for the development of new molecular markers to assist in the movement of entire resistance pathways into susceptible germplasm. This high-resolution information has been notoriously difficult to obtain, partly due to a lack of genomic resources of the resistant donors. To overcome this, we propose to sequence, and de novo assemble the genomes of three wheat lines that have been extensively used in crossing to increase FHB resistance in the US wheat community. Assembling these sequences into a pan-genome will allow for comprehensive characterization of their genomes. We will also add in medium-density genomic information for 20 additional lines that are related to the pan-genome individuals and represent variations of derived material of the original sources. With genome-wide information of 23 lines in-hand, parental alleles can be unambiguously identified throughout the genome, and identified in any progeny with high throughput genotyping. Mapping populations can be re-analyzed with new marker positions to improve resistance gene identification. Gene expression data will be collected and anchored to parent annotations to identify novel differentially expressed genes that may influence resistance. Finally, a targeted long-read genotyping technique will be developed to read-through complex regions and add to the pan-genome at specific known gene regions. These will be used to screen 200 derived germplasm to aid in tracking to accelerate the movement of new regions from resistant lines to elite cultivars. The results of this study will generate a large amount of genetic information that will be readily available to aid in FHB-resistance mapping and breeding efforts.