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PROJECT 1 ABSTRACT
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The overall goal of our project is to identify genes recently affected by natural selection in *F. graminearum* (*Fg*) to provide additional targets for pathogen control. Recent evidence of distinct genetic clusters of US *Fg* isolates and shifts in these populations suggest natural selection is favoring some fungal variants over others, and while some have speculated that different trichothecene mycotoxin chemotypes underlie the genetic clusters and direct selection on chemotypes causes these shifts, these conclusions are premature. We posit that natural selection may be favoring a variant at some other gene, and one trichothecene chemotype has managed to hitchhike along to higher frequency. Furthermore, we stress the unique opportunity to scan for the selected gene based on patterns of DNA variation left by the selection process, as variation at this gene would be biologically and ecologically relevant and affect fungal fitness, and thus methods to target the gene could drastically reduce its fitness and help control its growth or spread. Importantly, our selective sweep mapping genome scan approach should identify the selected gene regardless of where it resides in the genome or what its function is, while other candidate-based approaches could easily miss it or may be biased in their choice of candidates. We must let the pathogen tell us which genes are the best targets for control.

Project objectives:

1. Genotype a large sample of *Fg* from the US using a newly developed genotype by sequencing (GBS) protocol that will result in an unprecedented density of polymorphic markers.

2. Analyze population structure using the GBS markers to infer clusters, compare cluster membership with collection location and trichothecene genotype, and see how differentiation varies by genomic location.

3. Scan the genome for footprints of recent selection in our population to identify the regions responsible for population shifts, and from these regions identify candidate genes that can be targeted for fungal control.

4. Measure linkage disequilibrium (LD) between GBS markers and determine how rapidly LD decreases with physical distance between markers to lay the groundwork for genome-wide association studies in *Fg*.

The GBS markers we genotype help to reduce the complexity of the genome for Illumina sequencing and allow us to study a much larger sample size than simple whole-genome resequencing would. We expect our GBS loci will represent a common set of up to 20,000 genome-mapped loci for every isolate in our sample. We will analyze sequence polymorphisms in these loci with various population genetic methods to detect patterns of variation informative of the origin and history of segregating alleles in the population, including those that drive population shifts, even if the causative allele is not among the sequenced GBS loci. Our project targets research priority 2 for the FY14 PBG program. Our investigation into the cause of population shifts and their relationship with mycotoxin chemotypes or accumulation levels will identify novel genes that are critical for fungal fitness against which we can develop strategies for toxin reduction and FHB control.