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The degree of pathogenically-significant phenotypic and genotypic variation that exists in the North American population of *F. graminearum* has important implications for the durability of FHB resistance breeding efforts. The fungus is homothallic, and a high degree of genetic polymorphism has been reported in the population. However, there appears to be only limited variation among regional subpopulations in relative allelic frequencies. Thus, it is generally believed that resistant wheat varieties bred using local isolates for screening will remain effective even if strains from other regions of North America are introduced, or if novel strains are produced by sexual recombination. However, we don't really know whether members of other regional 15-ADON subpopulations may be more fit, more toxigenic, or more aggressive in the field on wheat bred for resistance against indigenous pathogen subpopulations (e.g. in Kentucky). We do know that there is quantitative variation among 15-ADON isolates in many pathogenically significant traits. As yet we do not have associated markers for these traits and thus we cannot track them in the population. The ability to follow particularly relevant alleles in the population would be very helpful for management of resistance and for improved understanding and prediction of disease and mycotoxin epidemics. Markers would also be very useful to help identify the most representative strains for resistance breeding screening. We have analyzed the results of a cross between two well-characterized and closely related lineage 7 isolates (strains PH-1 and Gz3639), both of which have sequenced genomes, and we have identified transgressive segregants that are significantly more or less aggressive and toxigenic than the parental isolates. We have established that these differences are heritable. **Our hypothesis** is that there are polymorphic loci in these two closely related members of the dominant lineage 7 that have large quantitative effects on mycotoxigenicity, aggressiveness, fertility, and fecundity. **We further hypothesize** that genetic reassortment via sexual recombination has produced the observed transgressive progeny strains, which can now be used to map the relevant loci. Identification of molecular markers linked to these QTLs could provide a useful new tool for analysis of the current and future population structure of the pathogen in North America and for selection and characterization of strains for breeding programs. Our objectives in the current proposal are: **1)** to use RNA-Seq to compare and contrast the transcriptomes of disease interactions involving highly aggressive versus non-aggressive transgressive sibling progeny strains in planta; and **2)** to use Illumina sequencing to identify SNPs linked to QTLs with pathogenicity-related effects.