FY20 USWBSI Project Abstract

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Project Title: FgMutantDB Migration to USWBSI Servers and Added Functionality

PROJECT 4 ABSTRACT

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FgMutantDb was created as a community-driven and community-curated web accessible resource that offers easy to navigate records on the location of mutants and experimental data generated by researchers studying *Fusarium graminearum*. Prior to the advent of this resource, an informal spread sheet was passed around between investigators to compile information on mutants and their location within the global *F. graminearum* research community. Development of a web-based resource for access to information on mutants created and their phenotypes was identified as a desired output on the USWBSI - PBG committee as far back as 2007. This initiative started with Dr. Jin-Rong Xu by accumulating mutants on an excel sheet and we further developed it into a simple web-based accessible spreadsheet database for storing phenotypes, unpublished information, and communicating the current locations of mutants. Additionally, the FgMutantDb cross-references different *Fusarium graminearum* assemblies, links out to and shares data with *F. graminearum* genomic resources. To date, 1,248 comments were uploaded to FungiDB sharing information on mutants and publications via FgMutantDb. The database is accessed weekly and internationally from the UK, France, Germany, Australia, and other countries. FgMutantDb aids researchers by promoting the sharing of information and material for *F. graminearum* mutant strains. Unfortunately, the current Google hosted database through Google Drive™ is not accessible from places that block google, including China. There is a dire need to migrate FgMutantDB to the USWBSI website, where USWBSI can retain control of the data. Working with the USWBSI webmaster data will imported to USWBSI servers under a new framework. Added functionality will be designed so researchers have their own accounts, can easily upload and download excel files of their stock mutant collections, and can link phenotypic and genomic data for each mutant.