

The Wheat Microbiome and *Fusarium graminearum*

Kristi Gdanetz and Frances Trail

Introduction:

Microbiomes encompass the total microorganisms living in a particular environment, including their respective genomes and interactions. Identifying the microbiome of wheat under different agricultural practices would help elucidate how communities of microbes interacting with this important food crop are structured, and how the microbiome is influenced by these practices.

Fusarium graminearum is a fungal pathogen of the cereal crops wheat, corn, and barley, and causal agent of Fusarium Head Blight (FHB) a devastating disease that contaminates the grain with several mycotoxins, including the tricothecene deoxynivalenol (DON), which render the grain unsuitable for consumption.

The shift from till agriculture, which effectively buried inoculum-containing crop residues, to no-till agriculture for soil conservation led to the emergence of severe FHB outbreaks in the 1990s and 2000s in the US. In addition, global warming is causing a geographical shift in mycotoxigenic *Fusarium* species, bringing mycotoxins to areas where they previously were not present and changing the species causing disease. An understanding of how agricultural practices influence the wheat microbiome, and how the microbiome affects a major disease organism would strengthen our ability to protect the crop in a shifting climate.

Preliminary Data:

Research in the Trail lab has focused on understanding the life cycle of *F. graminearum* on wheat for the last 16 years. However, our studies have been limited by a lack of information on the influence of other microbes in the interaction. We have recently demonstrated strong interactions between *F. graminearum* and wheat associated field microbes (Figure 1). These findings have led to our interest in investigating the wheat microbiome and its influence on FHB disease.

KBS has an established cropping site that can provide information on the effects of different land management practices on microbial populations of wheat, and how these microbes affect the life cycle of *F. graminearum* (Figure 2).

Objectives for this project:

Objective 1:

Characterize the microbiome of wheat under four different cultural practices: conventional till, no-till, reduced-input, and organic.

Objective 2:

Isolate culturable microbes from samples in Objective 1 and characterize possible interaction outcomes of these microbes with *F. graminearum* (Figure 3). Ultimately, we would like to identify those interactions that affect the ability of *F. graminearum* to complete its life cycle and develop screens for microbes with these effects. We hope to identify microbes that stimulate production of secondary metabolites in *F. graminearum* and how this is critical or inhibitory to the success of this pathogen.

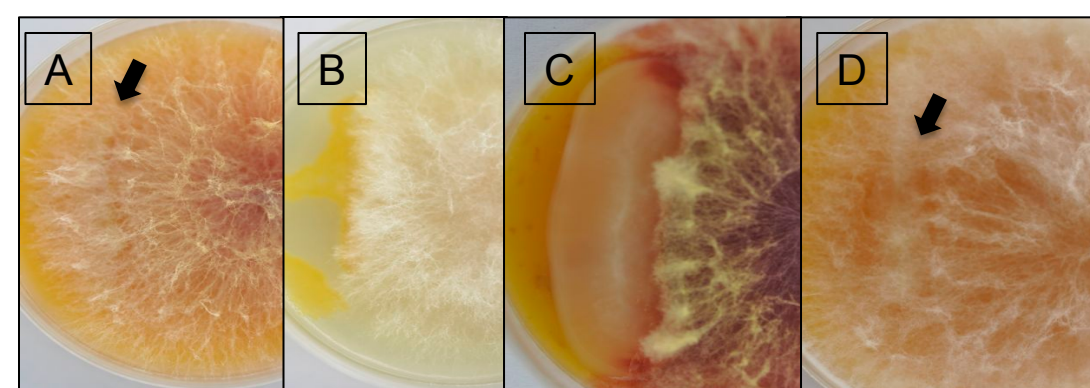


Figure 1. Interactions between *F. graminearum* and field bacteria involve secondary metabolites produced by the fungus. **A.** No phenotypic changes in bacterial or fungal growth. **B.** Hyphae are arrested in growth upon encountering bacteria. **C.** Hyphae increase secretion of antimicrobial aurofusarin (red color) and arrest growth. **D.** Aurofusarin mutant no longer interacts with bacteria (same strain as in C). Arrow indicates location of streak of bacteria.

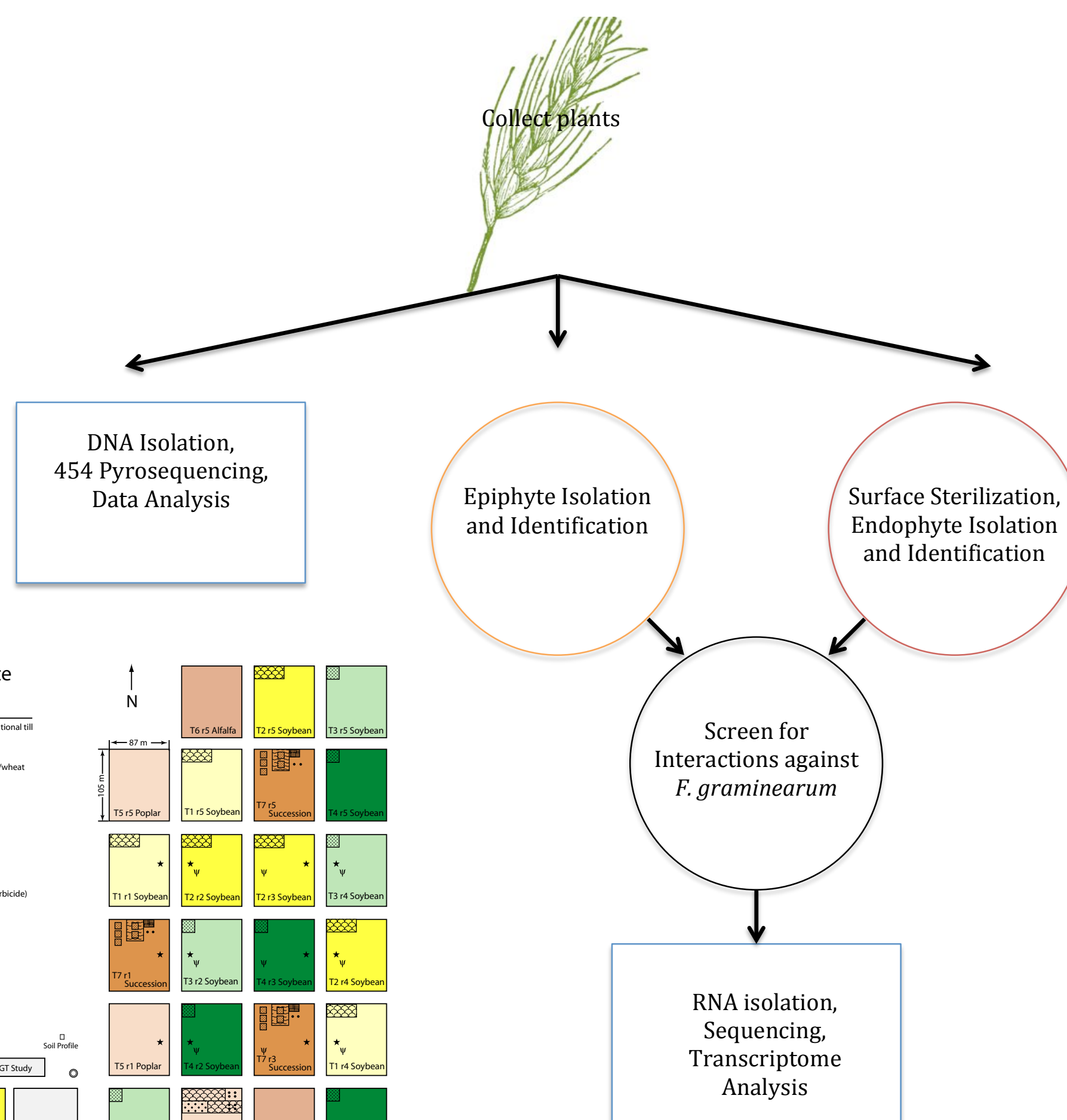


Figure 3. Overview of experimental plan.



Figure 2. Map of KBS LTER Site. Map shows planting during 2012 season. All plots labeled with soybean are now planted with winter wheat.