KANSAS STATE UNIVERSITY

Department of Plant Pathology

Analyzing Isolates of Fusarium Head Blight in Wheat from Across Kansas

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Characterization of different samples from across Kansas provides foundational evidence of the isolate population in Kansas during recent years and enables further research regarding isolate aggressiveness and changing population structure.

Introduction

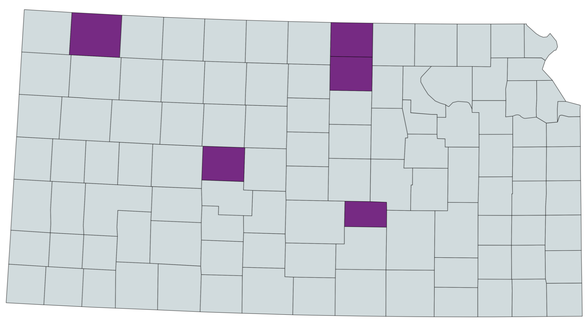
Why study Fusarium Head Blight (FHB)?

- USDA ranks FHB as the worst plant disease to hit the US causing loss of over $3 billion dollars.
- FHB releases toxin that causes sickness in humans and animals rendering infected harvested wheat impossible to sell
- FHB can survive in infested host residues and spread the infection after getting favorable moisture and temperature making it difficult to get rid of.

Fig1:I Head of wheat infected with Fusarium

Objectives

- To identify different Fusarium isolates collected in Kansas 2019-2021



Map of counties where samples originated

Results

- Multiple Samples were sent for DNA Sequencing
- All of the samples had the morphology of *Fusarium graminearum* and it is expected for all of the samples to be the same species but different strains

Fig 5. Macroconidia of Fusarium

Materials and Methods

- Physical and morphological characteristics were studied in the Applied Wheat Pathology Lab by examination of 12 samples.
- Sample isolates were obtained from a statewide survey and the contribution of Extension professionals and producers during the years 2019-2021.
- Collected wheat heads were stored in the -20C freezer until culture.
- The sorted samples were sterilized in 20 percent bleach and ddH_2O and cultured in Spezieller Nahrstoffarmer Agar (SNA) media.
- X subcultures were performed.
- The mycelium was scraped from the sub-cultured plate and was cultured in the Mung Bean Broth (MBB) for the production of macroconidia.
- Macroconidia were diluted after counting in hemocytometer and cultured in water agar to produce single spore.
- DNA was extracted from the single spore cultures using the CTAB extraction protocol and sequenced using ITS primers (White et al., 1990).

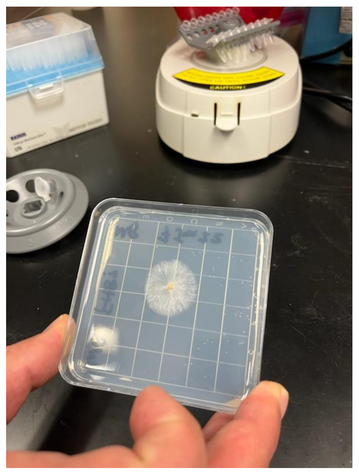


Fig 2. First Culture or Fusarium for this project

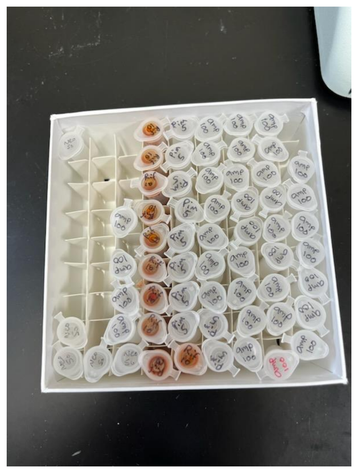


Fig 3. Antibiotics used in sterilization of media

Flowchart showing overall steps from sterilization to pathogen identification

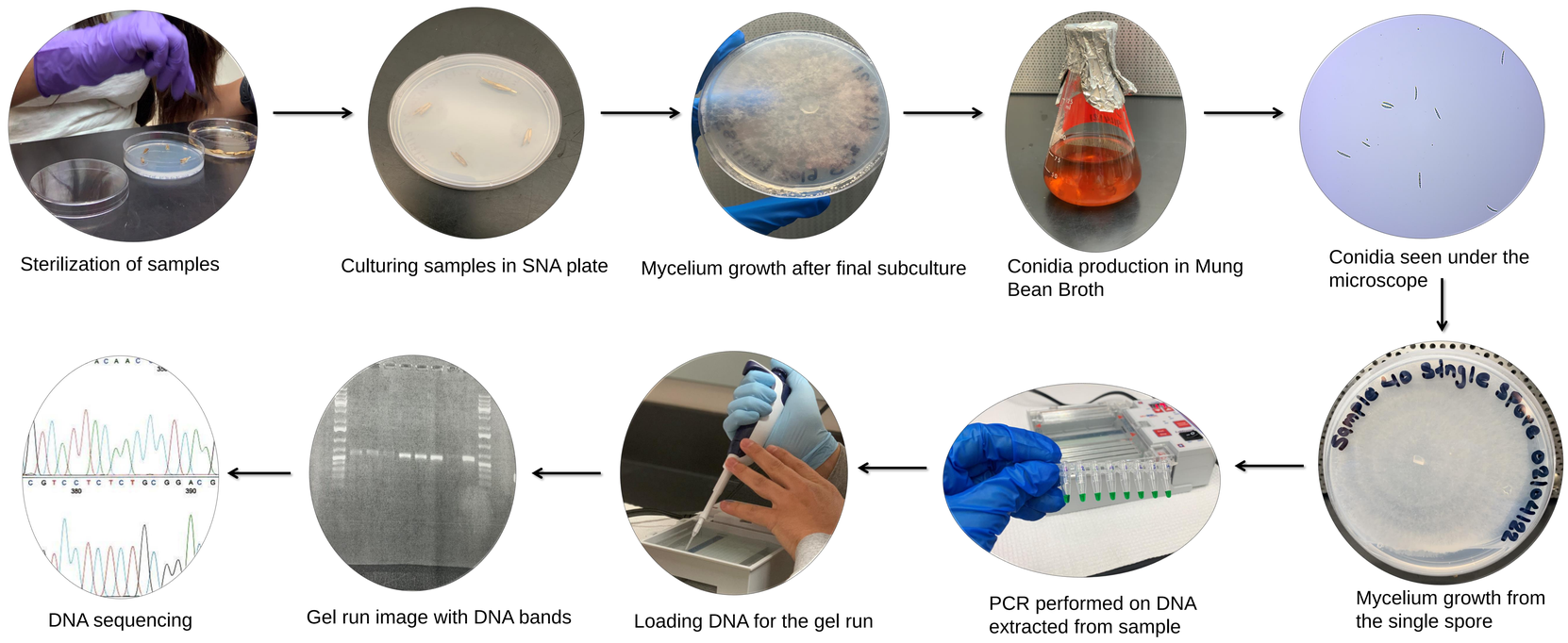


Fig 6. Flowchart for pathogen identification, Dahal, 2022

Summary and Future Works

- Fusarium confirmed samples will undergo PCR using Fusarium specific primers to identify to species level.

Acknowledgements

U.S. Wheat & Barley Scab Initiative

United States Department of Agriculture
National Institute of Food and Agriculture

An REEU Project supported by AFRI Education and Workforce Development grant no. 2019-67032-29071