

Department of Plant Pathology

Exploring root rot pathogens in wheat-pea rotations in Kansas

Nathan Smith, Dylan Mangel, Nick Beyer, Nar Ranabhat, Mark Davis, Myron Bruce, and Jessica L. Rupp

¹Department of Plant Pathology, Kansas State University, Manhattan, KS Email: jrupp@ksu.edu



Introduction

In 2018, over 277,000 bushels of wheat were produced on 7.7 million acres of land in Kansas alone. Based on the price of wheat by the end of 2018, this accounted for \$1.44 million. This wheat is normally rotated with soybeans or fallow, but recent interest has arisen regarding the growth of peas in northern Kansas. As of 2019, there are both research and commercial growing operations underway.

Many plant diseases have been especially prevalent during the summer because of the high rainfall and heat. In order to assess the severity of pea disease in Kansas, as well as explore potential interconnectivity between wheat and pea pathogens, a survey was conducted, and efforts were made to isolate and culture fungal pathogens of both wheat and pea.

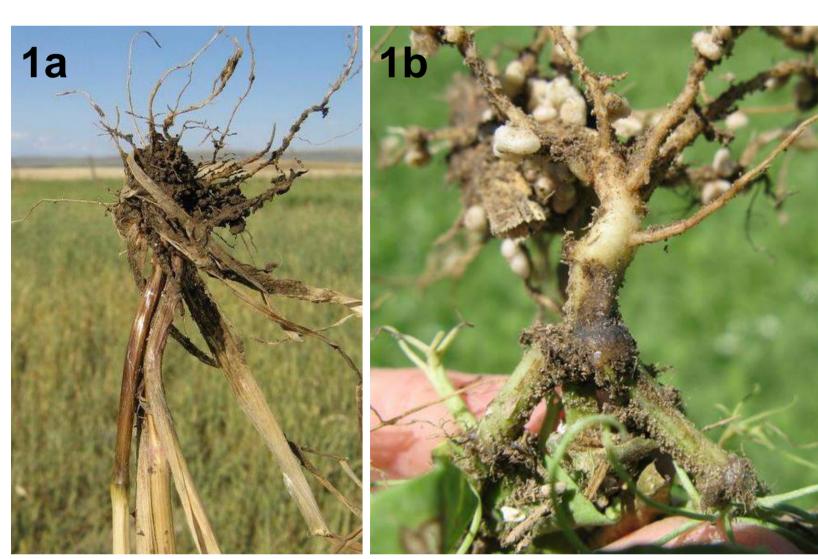


Figure 1a. (Left)
Fusarium root rot of wheat. (Ernesto Moya, Bugwood.org)

Figure 1b. (Right)
Fusarium root rot of peas. (Mary Burrows, Bugwood.org)

Materials and Methods

- Wheat samples were obtained from the diagnostic lab, cleaned, and stored in a 4°C freezer until they were cultured.
- Additional wheat samples were delivered from statewide travels by the Applied Wheat Pathology Lab and Dr. Erick DeWolf.
- Pea samples were collected during a statewide survey of multiple experimental trials and growers' fields.
- All samples received a unique ID number and were then cleaned and surface-sterilized using 10% bleach followed by 70% ethanol and two rinsing steps with ddH₂O.
- Root cuttings (< 1 cm) were plated on ¼ strength PDA containing ampicillin (100 μg/L) and neomycin (50 μg/L).
- Plates were grown in a 22°C incubator for 5-14 days with 12H dark/light.
- DNA was extracted using CTAB extraction protocol. Quality and concentration were measured using a nanodrop spectrophotometer.
- ~20 ng of DNA was added to Promega PCR MasterMix (Promega, Madison, Wisconsin) using the PCR protocol outlined in White et al. (1990). DNA sequencing was performed by McLab of San Francisco, California.



Figure 3. Counties surveyed for wheat root rot.

Wheat Root Rot Samples Collected by County

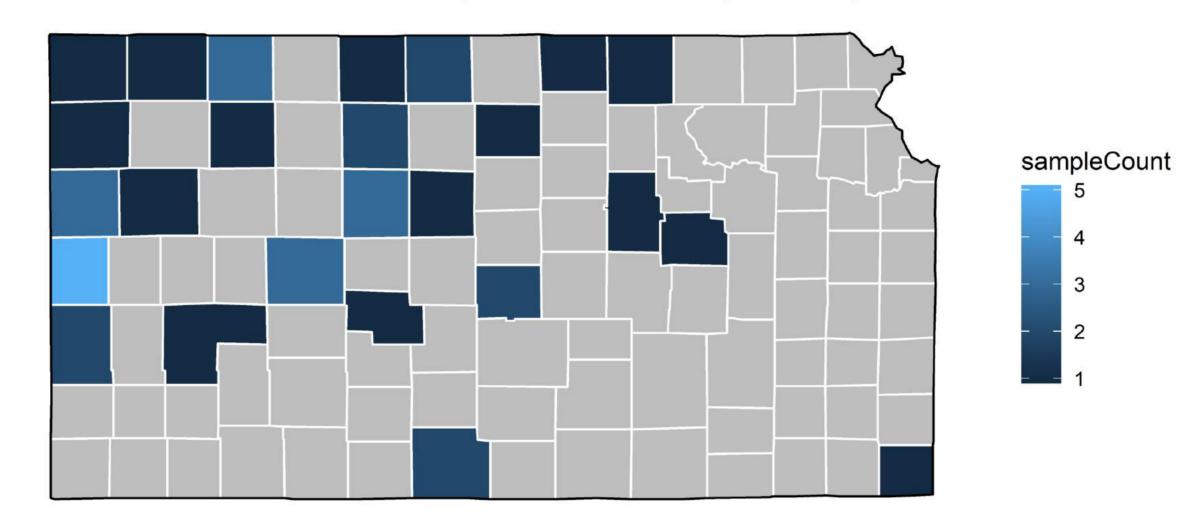
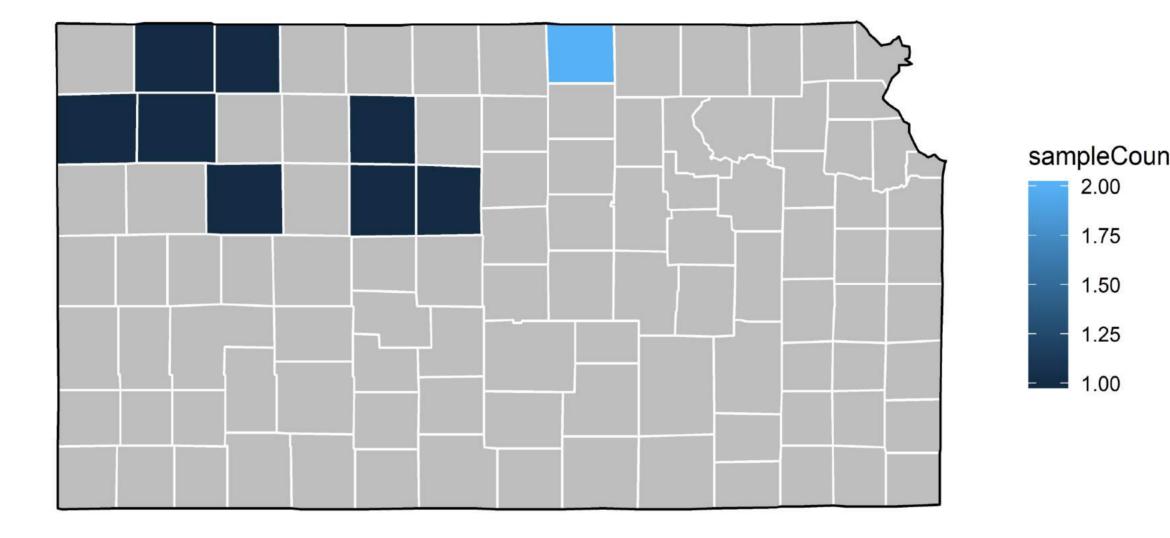


Figure 4. Counties surveyed for pea root rot.

Pea Root Rot Samples Collected by County



- Over 630 miles of statewide travel resulted in visiting 8 experimental plots and 2 growers' fields to survey for pea diseases in Kansas.
- Wheat was surveyed in 23 counties with the combined help of both the Applied Wheat Pathology Lab and Dr. Erick DeWolf.

Figure 5a. and 5b. Pea fields with symptoms of pea root rot in low lying areas of a producer's field in Ellis Co, KS.



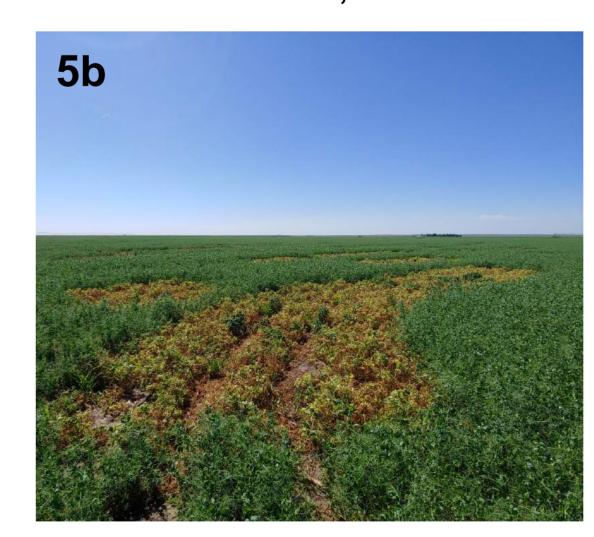
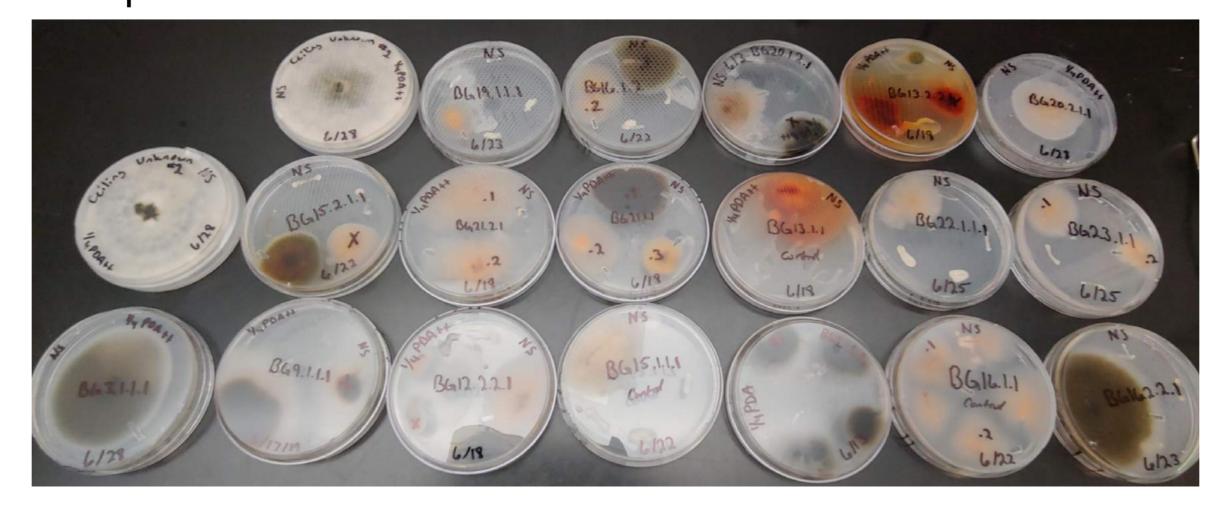


Figure 6. Diversity of fungal samples isolated from wheat and pea roots.



Results

Figure 6. Chromatograph showing DNA sequencing results of select pea roots.

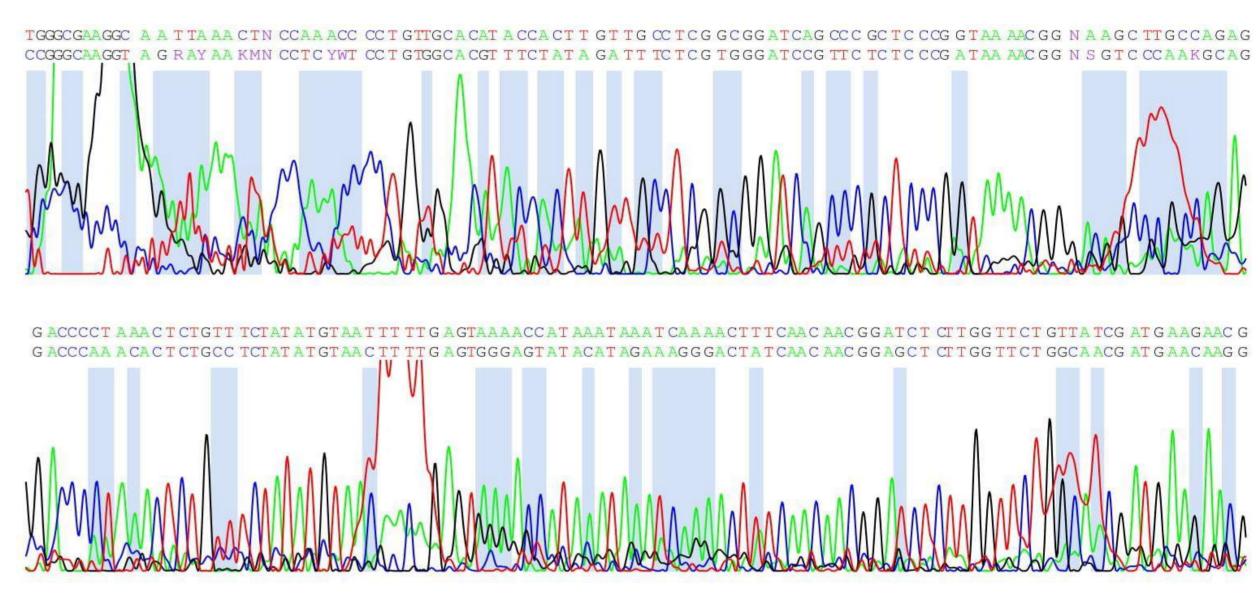


Figure 7. Sequence alignment of pea roots with *Fusarium oxysporum*. To date, 13 different fungal species have been identified from wheat and 2 from pea.

Range 1: 4 to 493 GenBank Graphics ▼ Next Match ▲ Prev					
Score 880 bi	ts(47	Expect 6) 0.0	Identities 484/490(99%)	Gaps 0/490(0%)	Strand Plus/Plus
Query	1	CGTAGGTGAACCTG	CGGAGGGATCATTACCGAGTT		TGTGAACA 60
Sbjct	4	CGTAGGTGAACCTG	CGGAGGGATCATTACCGAGTT	TACAACTCCCAAACCCC	TGTGAACA 63
Query	61		CGGCGGATCAGCCCGCTCCC		
Sbjct	64		CGGCGGATCAGCCCGCTCCC	GTAAAACGGGACGGCC	
Query	121	GACCCCTAAACTCTG	STTTCTATATGTAACTTYTGAG	STAAAACCATAAATAAA	TCAAAACT 18
Sbjct	124	GACCCCTAAACTCT	STTTCTATATGTAACTTCTGAG	STAAAACCATAAATAAA	TCAAAACT 18
Query	181	TTCAACAACGGATCT	CTTGGTTCTGGCATCGATGA	AGAACGCAGCAAAATGC	GATAAGTA 24
Sbjct	184	TTCAACAACGGATCT	CTTGGTTCTGGCATCGATGA		GATAAGTA 24
Query	241		ATTCAGTGAATCATCGAATCT		
Sbjct	244		ATTCAGTGAATCATCGAATCT		
Query	301		CCTGTTCGAGCGTCATTTCA		
Sbjct	304		CCTGTTCGAGCGTCATTTCA		
Query	361		CGCGTTCCTCAAATTGATTGG	CGGTCACGTCGAGCTTC	CATAGCGT 42
Sbjct	364	GACTCGCGTTAATTC	CGCGTTCCTCAAATTGATTGG	CGGTCACGTCGAGCTTC	CATAGCGT 42

Summary and Future Work

- Multiple fungi were identified from survey samples using morphological and molecular techniques.
- Future surveys with broader sampling will be necessary to get a better understanding of pathogens shared between wheat and peas.
- The Applied Wheat Pathology Lab will continue isolating and identifying fungal organisms present in survey samples.





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