

Diversity and aggressiveness of *Fusarium graminearum* in Illinois A The

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Precision management of FHB

- Site, host, and <u>pathogen</u> specific
- Requirements:
 - Pathogen surveillance
 - Population dynamics
 - Mechanisms of pathogenesis



Are wheat varieties affecting the population of *F. graminearum*?

- 5 locations across Illinois
- 1. Traditional isolation: 197
- 2. Field pathogenomics: RNA



10% of FHB cases are not caused by F. graminearum



F. armeniacum also causes FHB

- White mycelia and prominently curved conidia
- Molecular identification
- Koch's postulates
- Infects soybean, maize, others

Krone et al. Plant Disease First Look



FHB in 2016 in IL caused by NA1 population

- Field pathogenomics
- In the field:

No distinct population on lines with different levels of resistance

Fall et al. Mycologia 111(4): 563-573



Differential gene expression in *F. graminearum* between samples collected from wheat with different levels of resistance

Gene ID	Predicted Function	FDR	R vs S	R vs I	l vs S
			Log2 fold change		
G13239	oxidation-reduction process	0.01	-3.04	-4.97	1.93
G01905	arginyl-tRNA synthetase	0.02	-3.39	-5.49	2.09
G20203	tpr domain	0.02	5.00	4.00	0.35
G09227	kinesin light chain	0.04	-3.33	-0.71	-2.62

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F. graminearum differential gene expression between wheat and pure culture

Conc ID Dradicted Eurotian		R vs AX	I vs AX	S vs AX	
Gene id	Predicted Function	Log2 fold change			
G14115	antigen 1 📀	4.68	5.85	7.95	
G25079	carbonydrate metabolic process	6.50	6.32	5.57	
G16997	3-phytase precursor	3.22	4.04	5.86	
G16533	cellobiose dehydrogenase 🛛 🔊	8.56	7.60	7.95	
G12227	family inorganic phosphate transporter	-0.80	2.55	3.89	
G12833	choline monooxygenase	8.01	7.25	7.23	



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Does the isolate wheat source modulate its aggressiveness?

• Isolates from the most susceptible wheat line are consistently the most aggressive.



significantly different from each other

Overall goal: Identify determinants of aggressiveness in *F. graminearum*

Aggressiveness assays

- 60 isolates
- Does wheat line source affect isolate aggressiveness?

Whole genome resequencing

- Sequence variation
- Are candidate aggressiveness genes under selection?

Outcomes:

- Improved management strategies for FHB
- Prediction of durability of resistance

Summary

- 10% of FHB cases are not caused by *F. graminearum*
 - Are we testing resistant lines against multiple species?
- Field pathogenomics rapidly evaluated the diversity of the isolates causing the FHB epidemic of 2016
- Resistance to *F. graminearum* on wheat might not lead to increased aggressiveness of strains



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