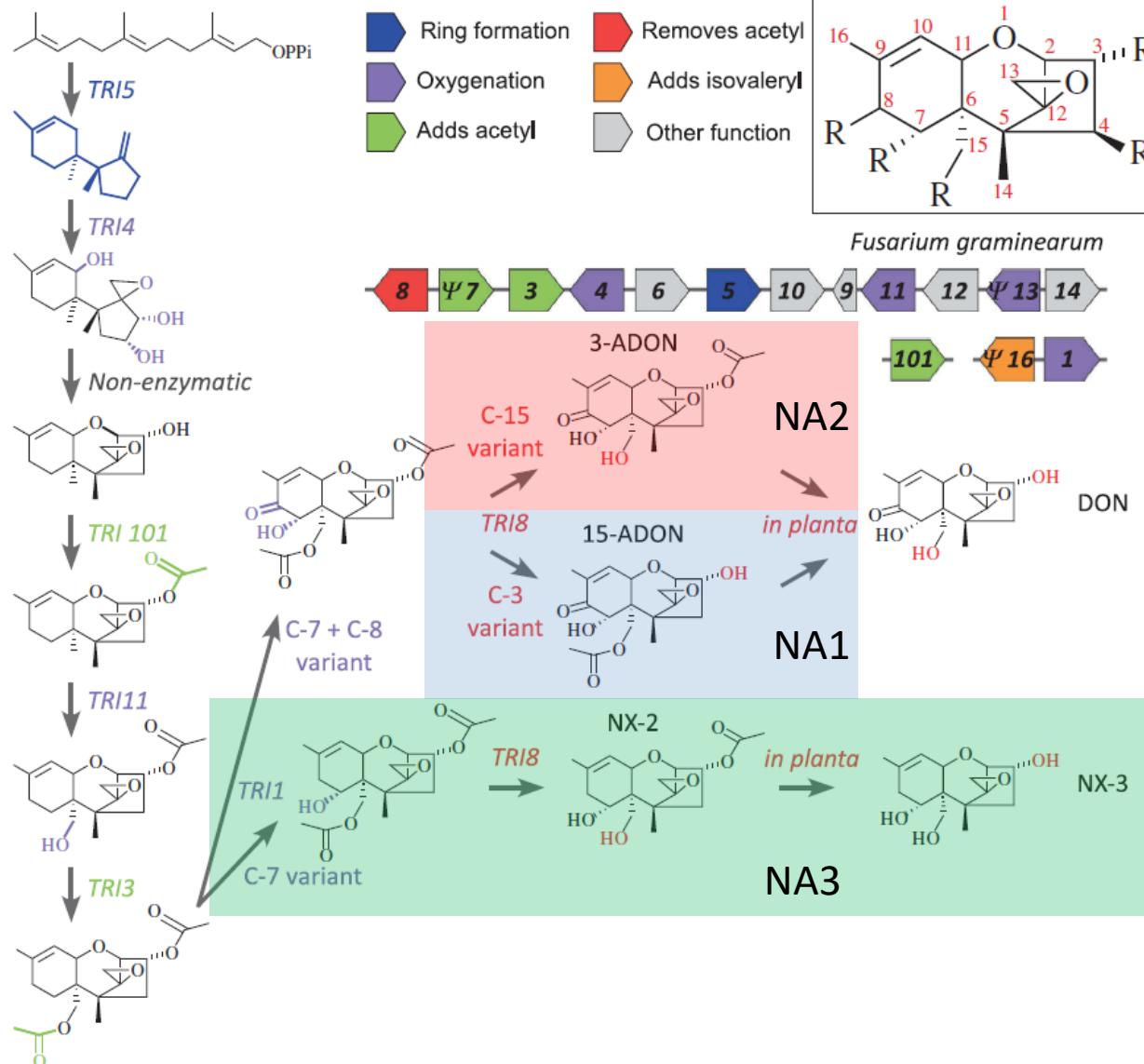


# *Fusarium graminearum* Population-Specific Differences During Wheat Infection

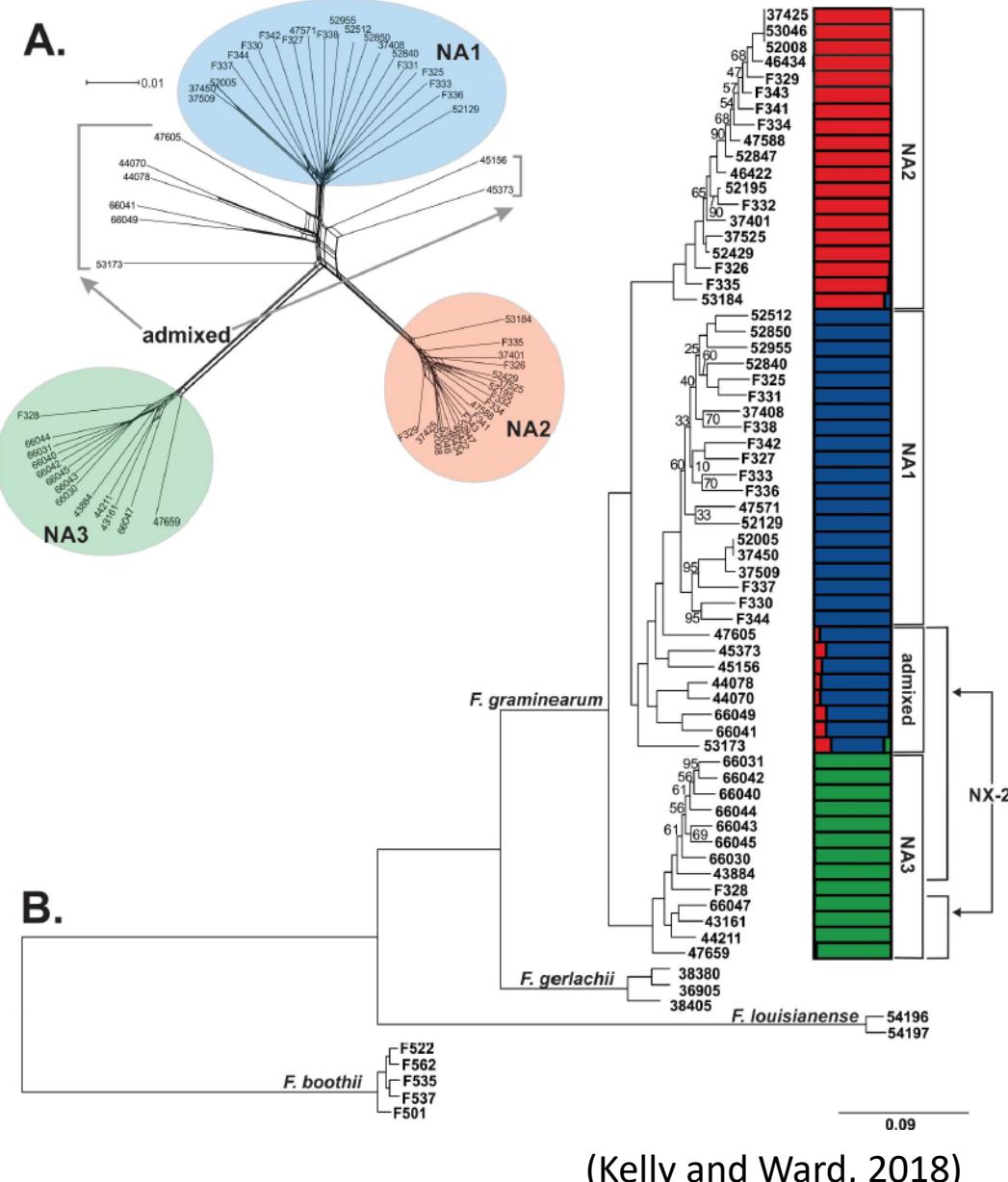
**Martha M. Vaughan, Todd Ward, Miroslava Cuperlovic-Culf,  
Susan P. McCormick and Matthew G. Bakker**



# Three North American Populations of *F. graminearum*



(Bakker et al., 2018)



# Three North American Populations of *F. graminearum*

Genetic Background	Chemotype in culture	Chemotype in planta
NA1	15-ADON	DON
NA2	3-ADON	DON
NA3	NX-2	NX-3

Are there population specific differences during wheat infection?



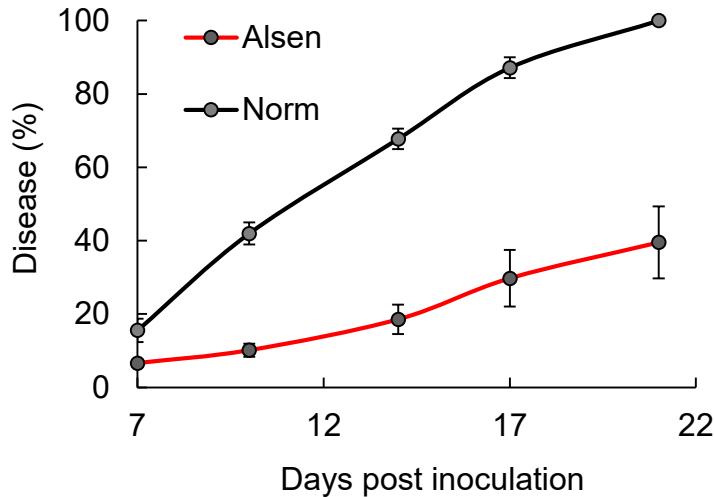
	NA1	NA2	NA3
1	38746	37525	43161
2	38762	38763	43884
3	38811	38851	44211
4	38986	38964	47659
5	47571	38980	66030
6	52005	46422	66031
7	52512	47588	66037
8	52955	52008	66039
9	06-219	52195	66040
10	06-225	52429	66042
11	06-270	53046	66043
12	13MN1-6	00-588	66044
13	F333	12SD6-2	66045
14	F342	06-239	66047
15	F344	06-240	F322

15-ADON

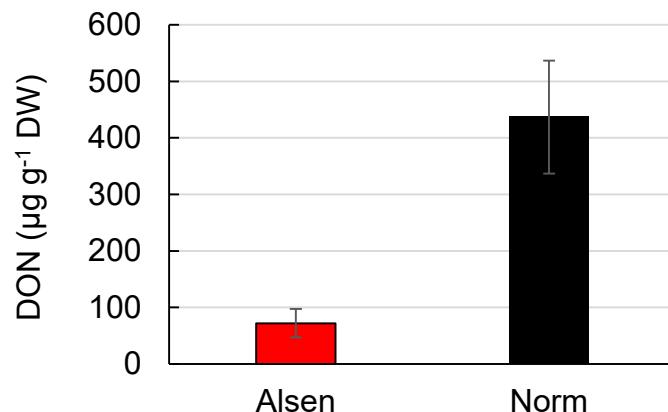
3-ADON

NX

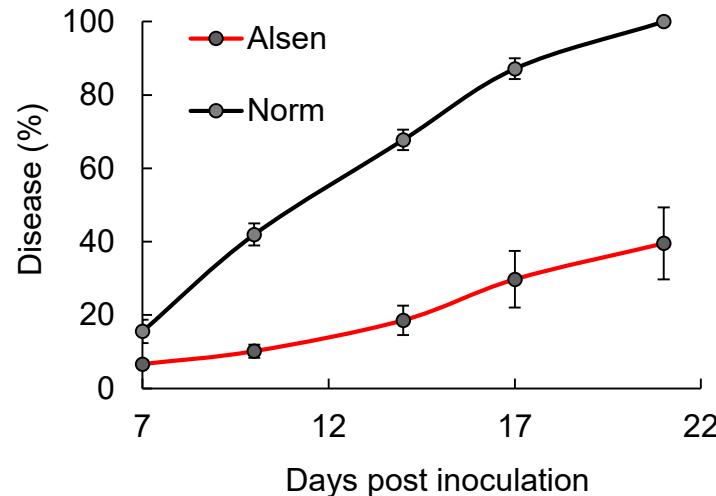
# Population specific differences on moderately resistant wheat variety Alsen



- **Moderately resistant variety Alsen** contains loci derived from the Chinese spring wheat cultivated variety Sumai 3 (Bai, 1996)
  - *Fhb1* confers type II resistance
  - *Fhb5* confers type I resistance

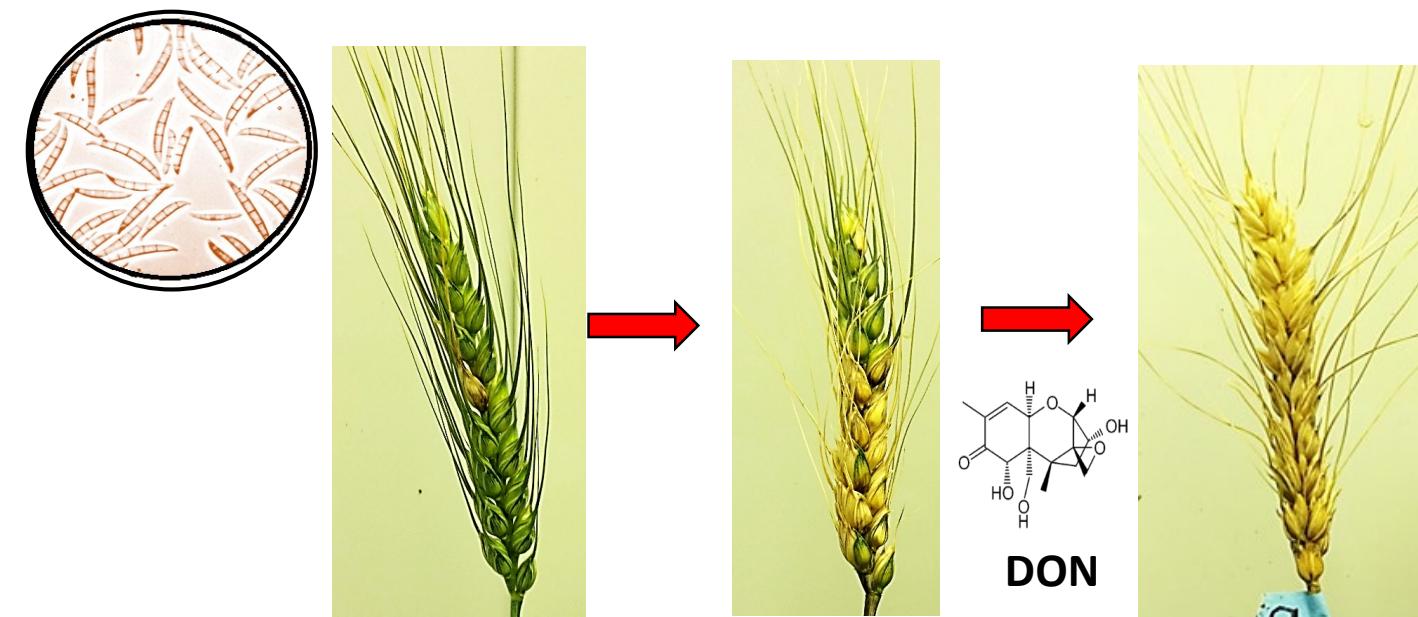
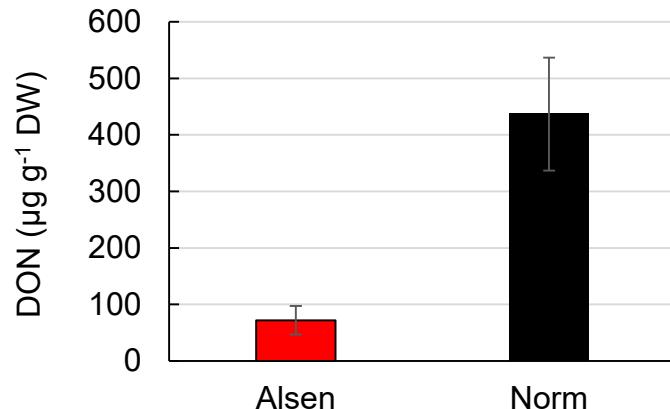


# Population specific differences on moderately resistant wheat variety Alsen



- **Moderately resistant variety Alsen** contains loci derived from the Chinese spring wheat cultivated variety Sumai 3 (Bai, 1996)
  - *Fhb1* confers type II resistance
  - *Fhb5* confers type I resistance

- **Type I: Resistance to initial infection**
- **Type II: Resistance to spread**

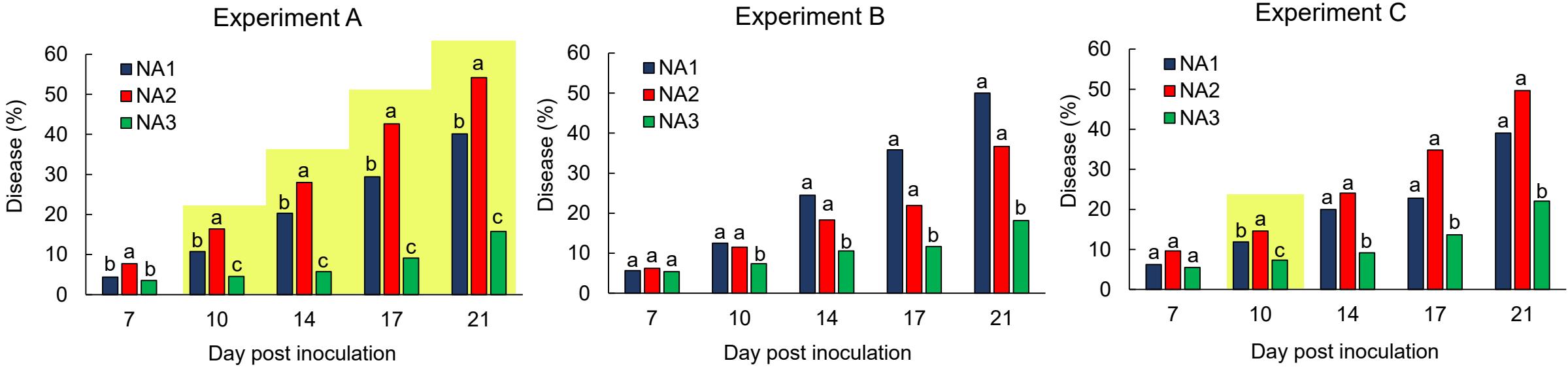


# Experimental Design

	NA1	NA2	NA3
1	38746	37525	43161
2	38762	38763	43884
3	38811	38851	44211
4	38986	38964	47659
5	47571	38980	66030
6	52005	46422	66031
7	52512	47588	66037
8	52955	52008	66039
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10	06-225	52429	66042
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14	F342	06-239	66047
15	F344	06-240	F322

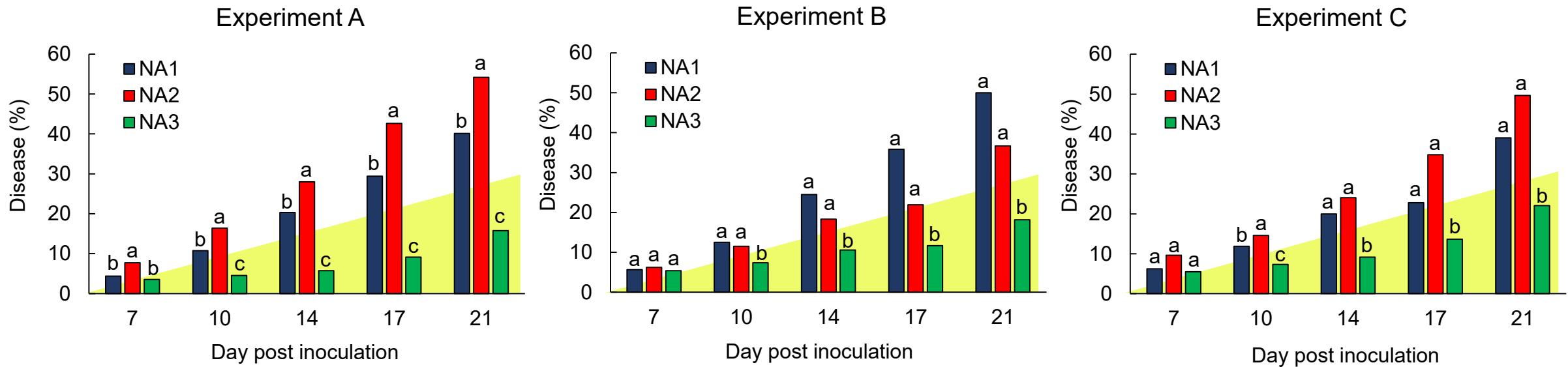
- 6 flowering Alsen wheat heads per strain
- Total of 90 heads per population
- Destructive sampling of 1 head per strain at timepoints Day 7, 14 and 21 for toxin and molecular analyses.
- Combined three random heads so that n=5 at each timepoint

# Are there population specific differences during infection of moderately resistant wheat?

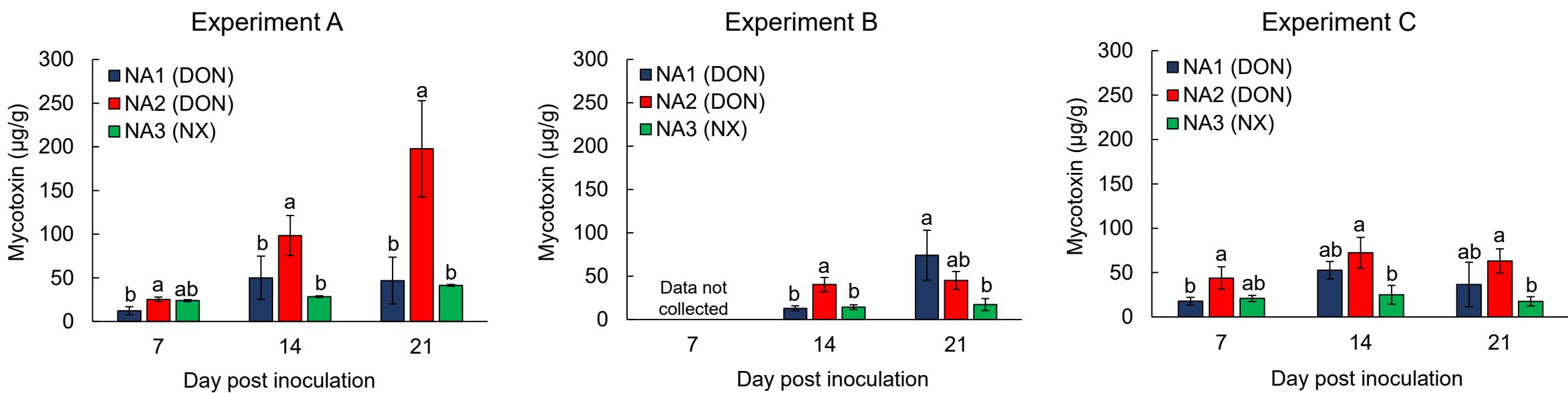
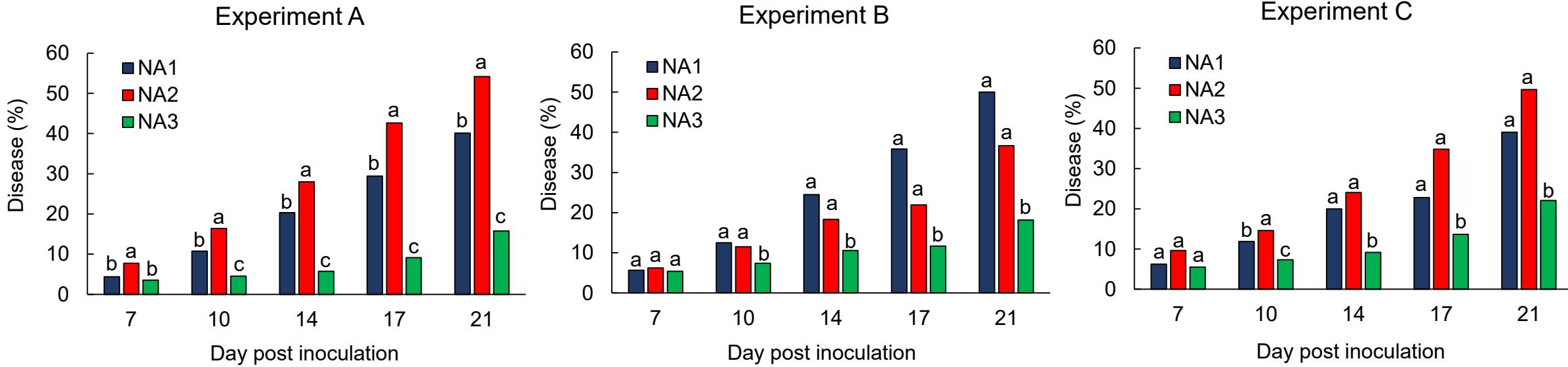


Data from 3 experiments were analyzed to compare 3 populations (NA1, NA2, and NA3) for % diseased florets as a function of time (7, 10, 14, 17, and 21 days) using weighted regression analysis.

# Are there population specific differences during infection of moderately resistant wheat?



**NA1 or NA2 > NA3**



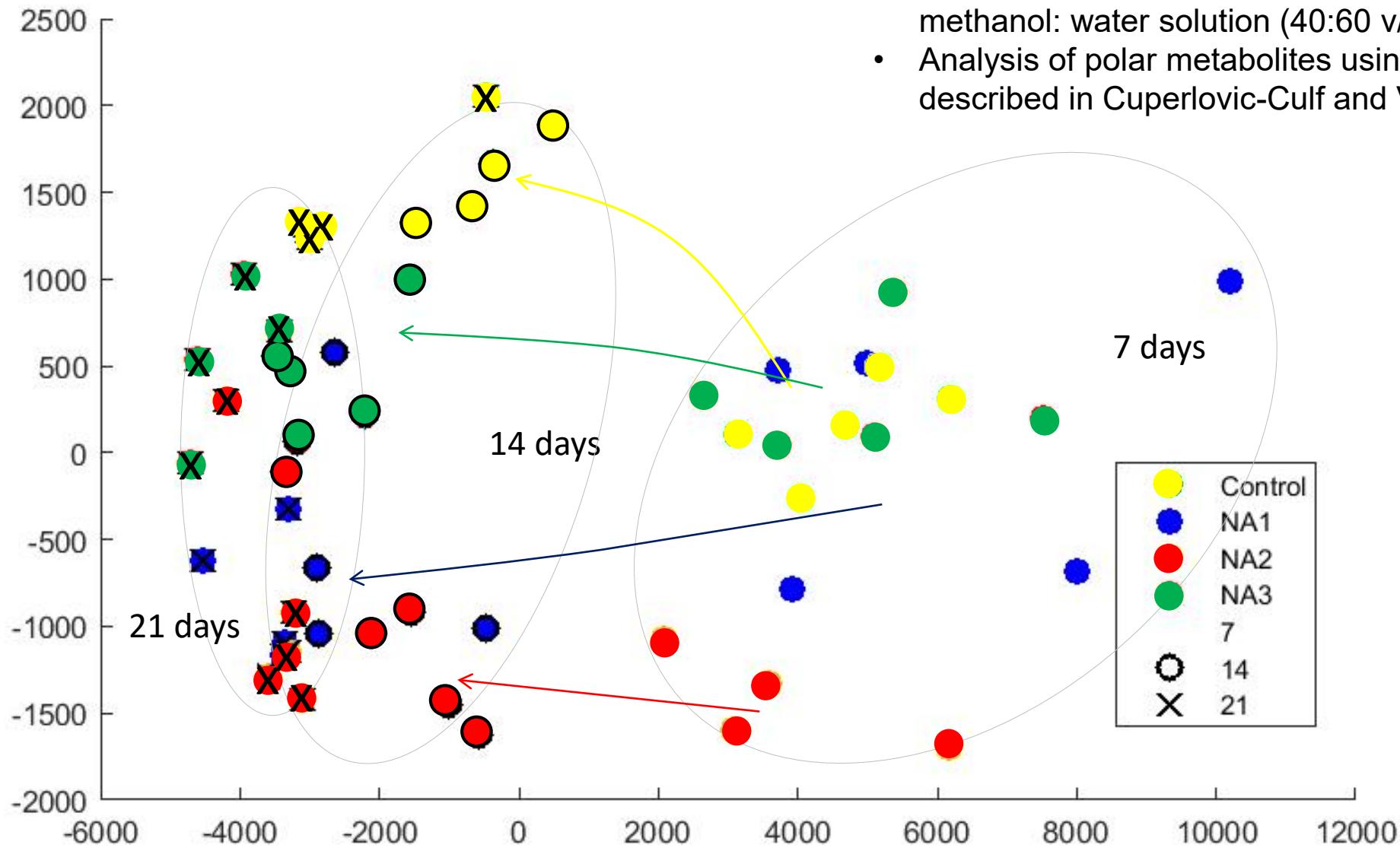
# **Why does NA3 cause less disease?**

**Hypotheses:**

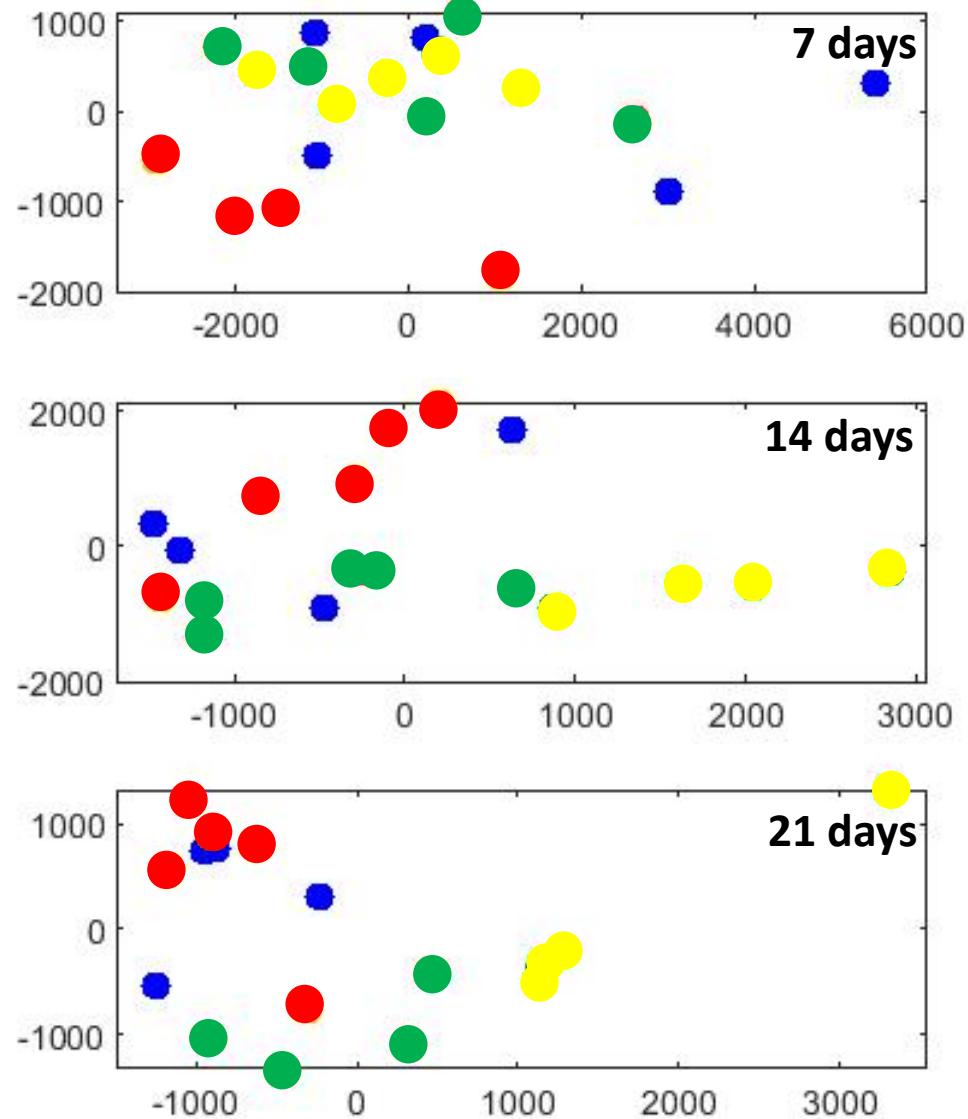
- 1. Host plant response against NA3 strains is stronger and more effective at controlling disease spread.**
  
- 2. NA3 strains are less virulent.**

# Metabolomic Analysis (NMR)

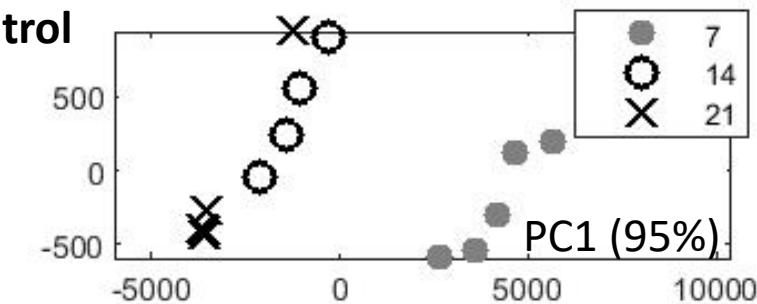
- Metabolite Extraction from plant tissues using methanol: water solution (40:60 v/v)
- Analysis of polar metabolites using NMR methods described in Cuperlovic-Culf and Vaughan et al., 2018



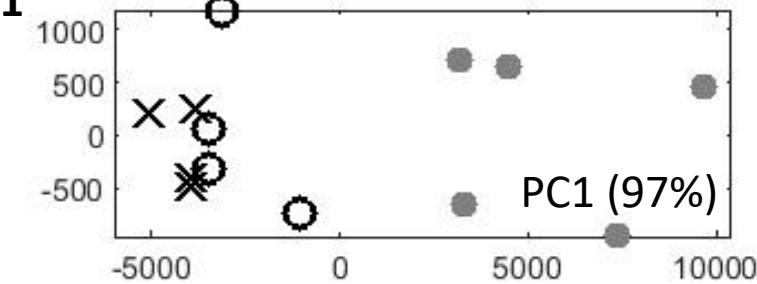
Control  
NA1  
NA2  
NA3



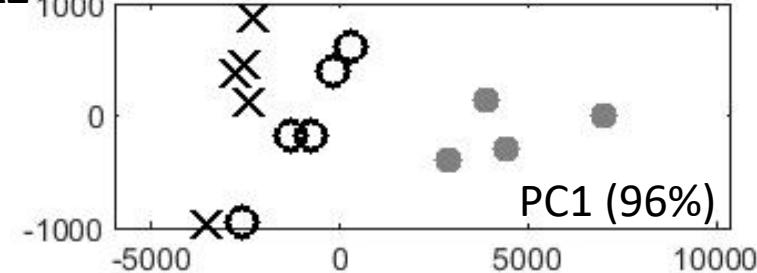
Control



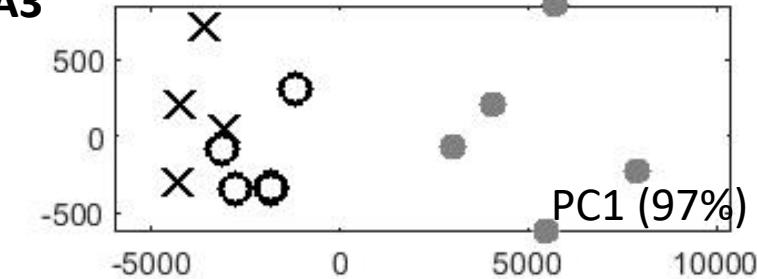
NA1



NA2



NA3



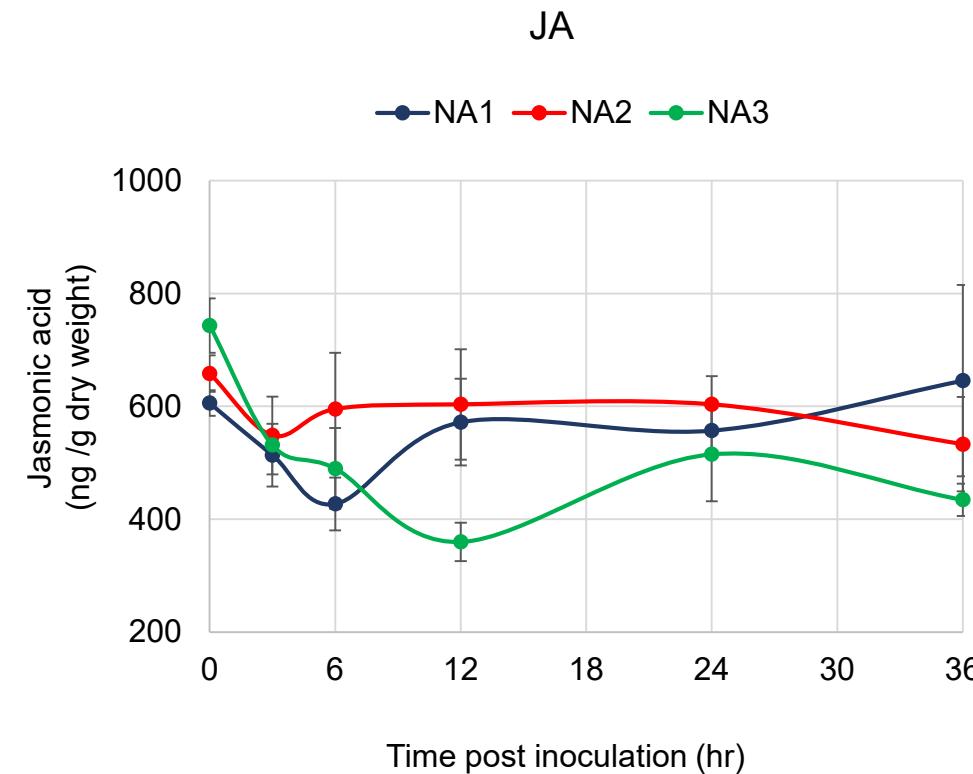
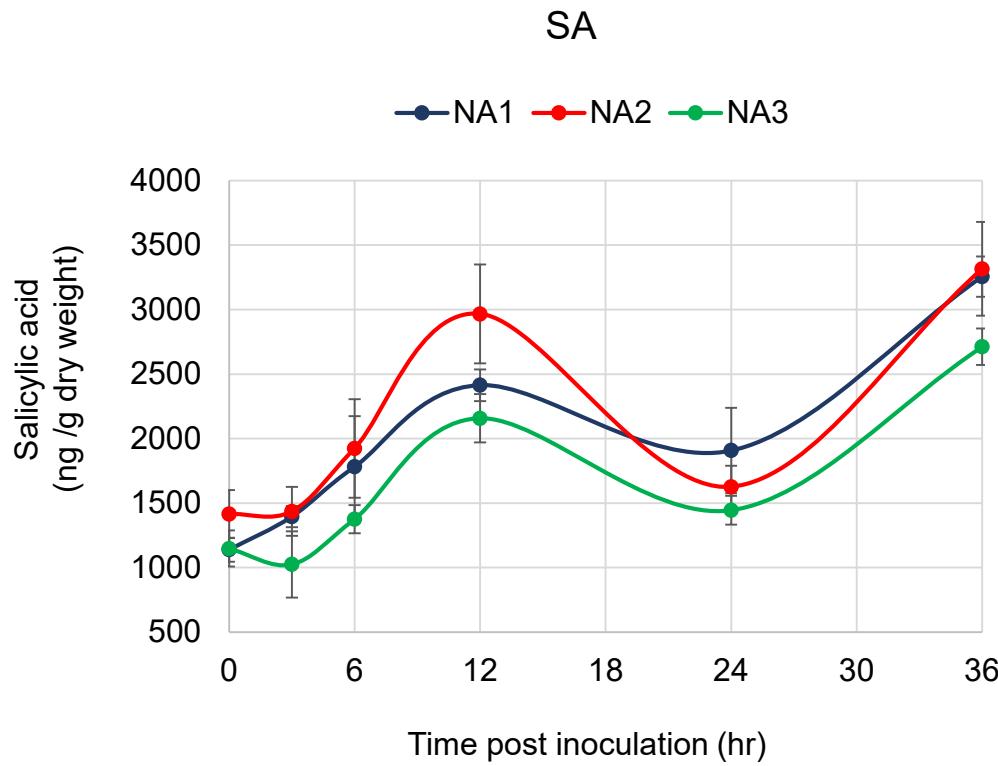
Unsupervised Principle Components Analysis

# Further analysis of Host Defense Response Experimental Design

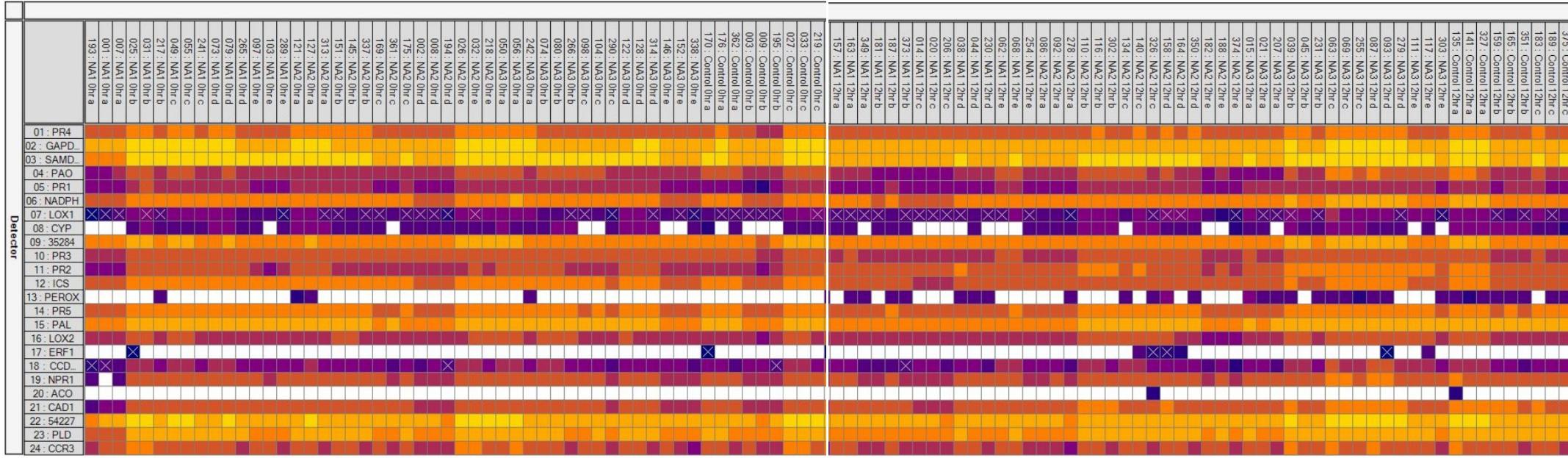
	NA1	NA2	NA3
1	38746	37525	43161
2	38762	38763	43884
3	38811	38851	44211
4	38986	38964	47659
5	47571	38980	66030
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11	06-270	53046	66043
12	13MN1-6	00-588	66044
13	F333	12SD6-2	66045
14	F342	06-239	66047
15	F344	06-240	F322

- Conducted whole head inoculations (via dip method)
- Collected samples at Early Time points:
  - 0, 3, 6, 12, 24, 36 hr
- 15 representative strains from each population
  - (NA1, NA2, NA3)
- 6 flowering Alsen wheat heads per strain
- Total of 90 heads per population
- Destructive sampling of 1 head per strain at each timepoint.
- Combined three random heads so that n=5 at each timepoint
- Phytohormone and Transcriptional Analyses

# Phytohormone response to *F. graminearum* populations



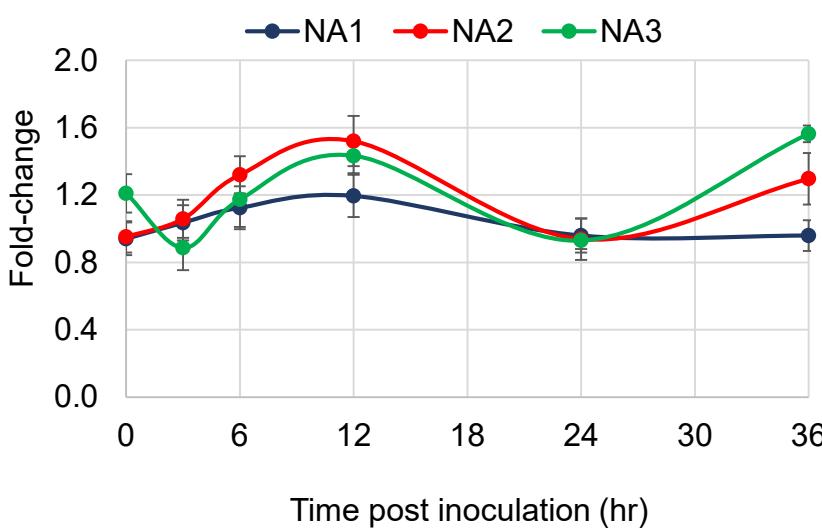
# Transcriptional Analysis of Host Defense Response Genes



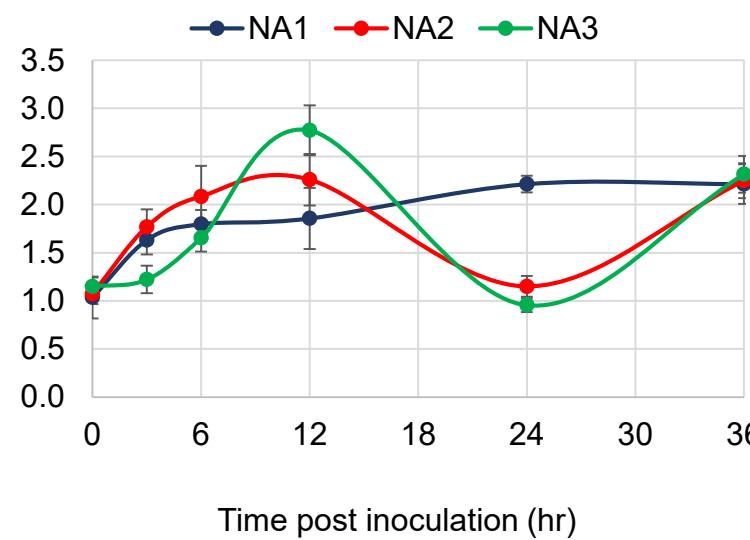
- 20 selected defense related genes
- Time points: 0, 3, 6, 12, 24, 36 hr post whole head inoculation method
- 15 representative strains from each population (NA1, NA2, NA3)

# Transcription of Host Defense Response Genes

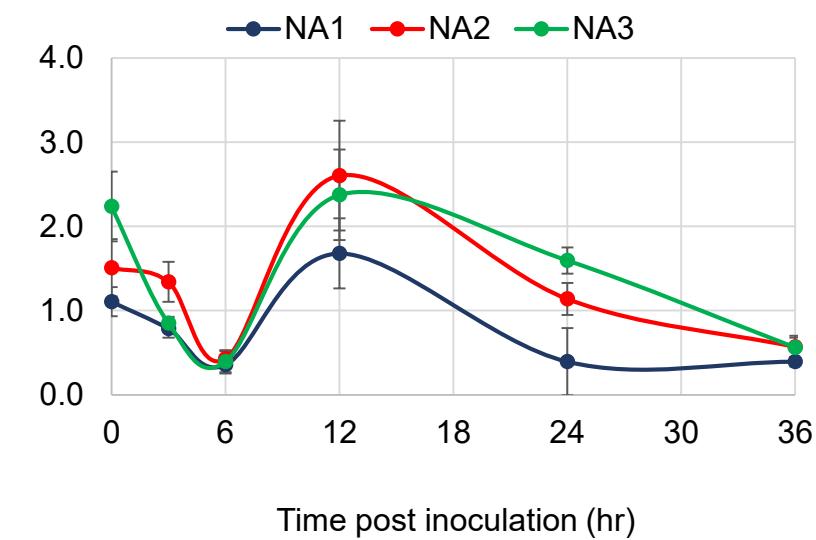
Phenylalanine ammonia lyase (PAL)



Nonexpressor of PR genes 1 (NPR1)



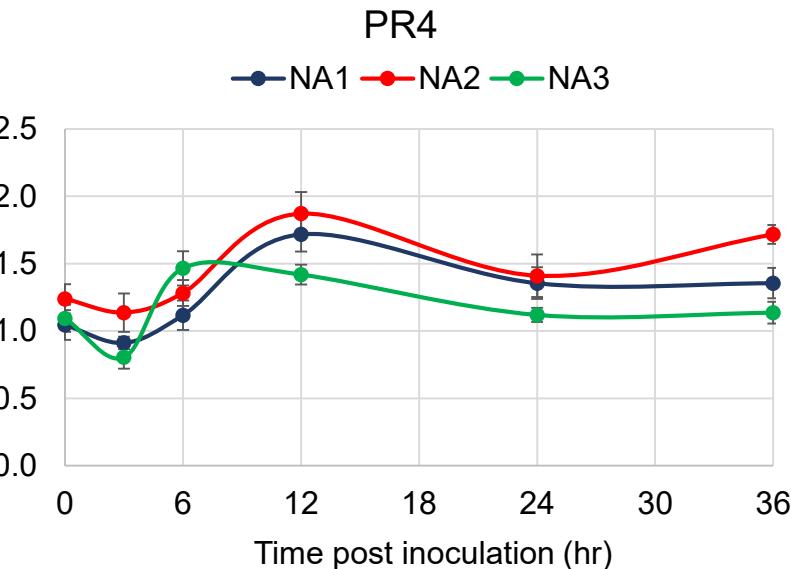
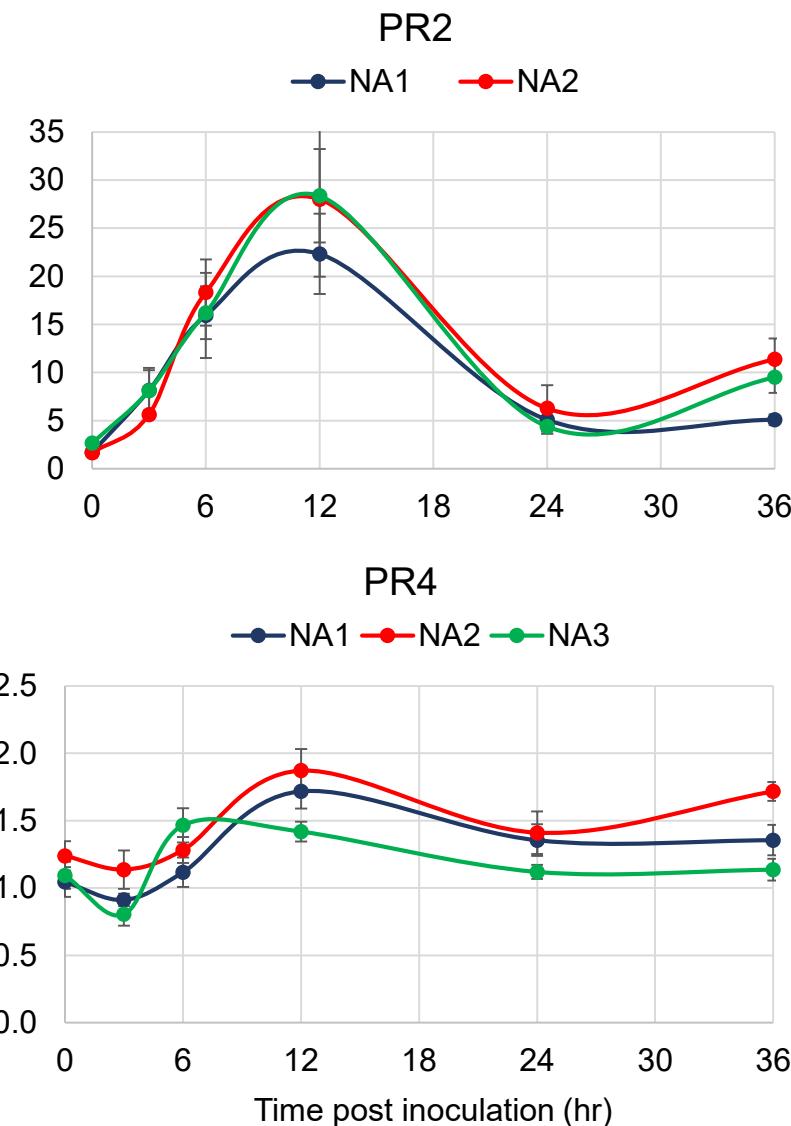
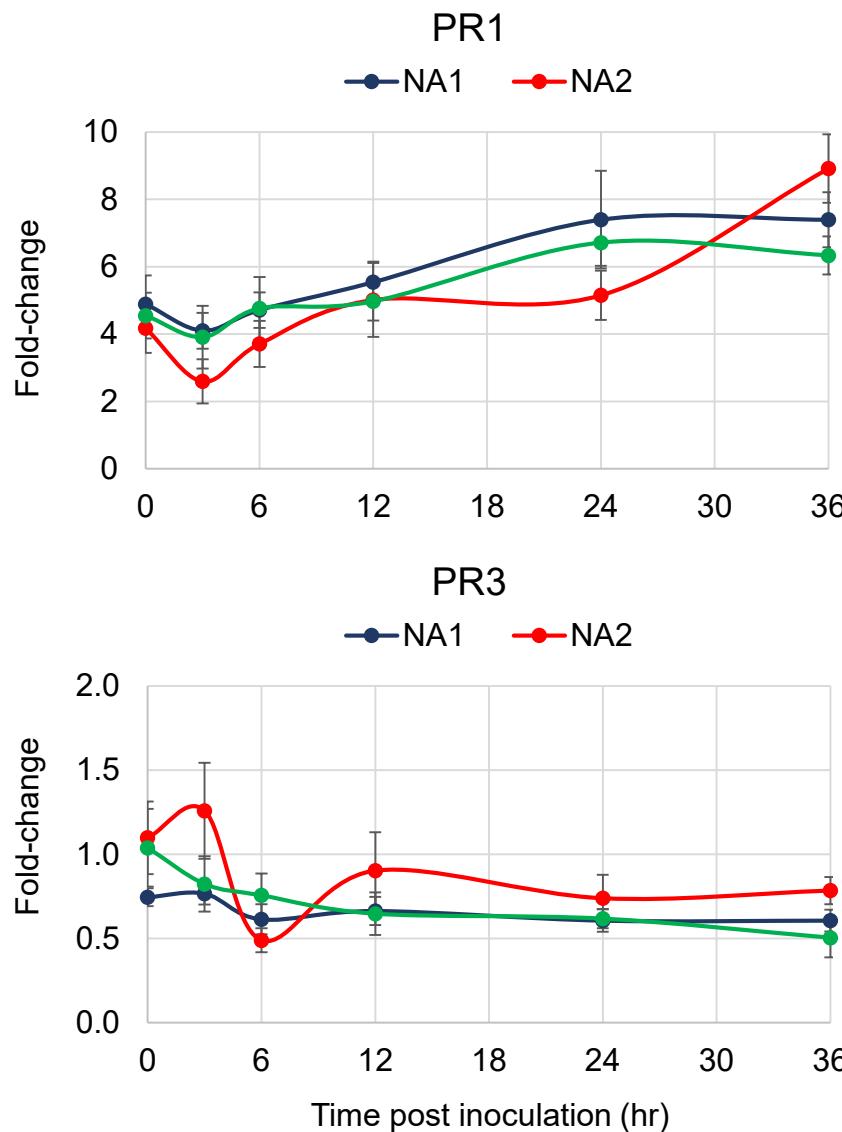
Lipoxygenase 2 (LOX2)



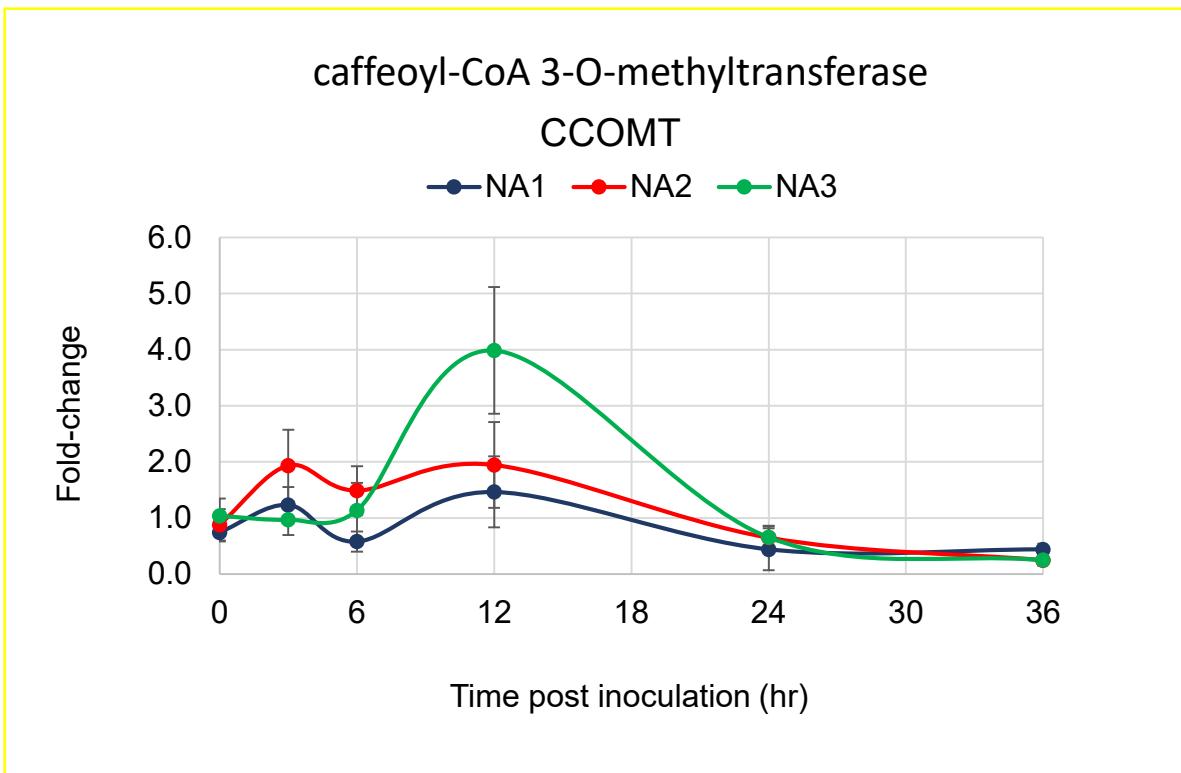
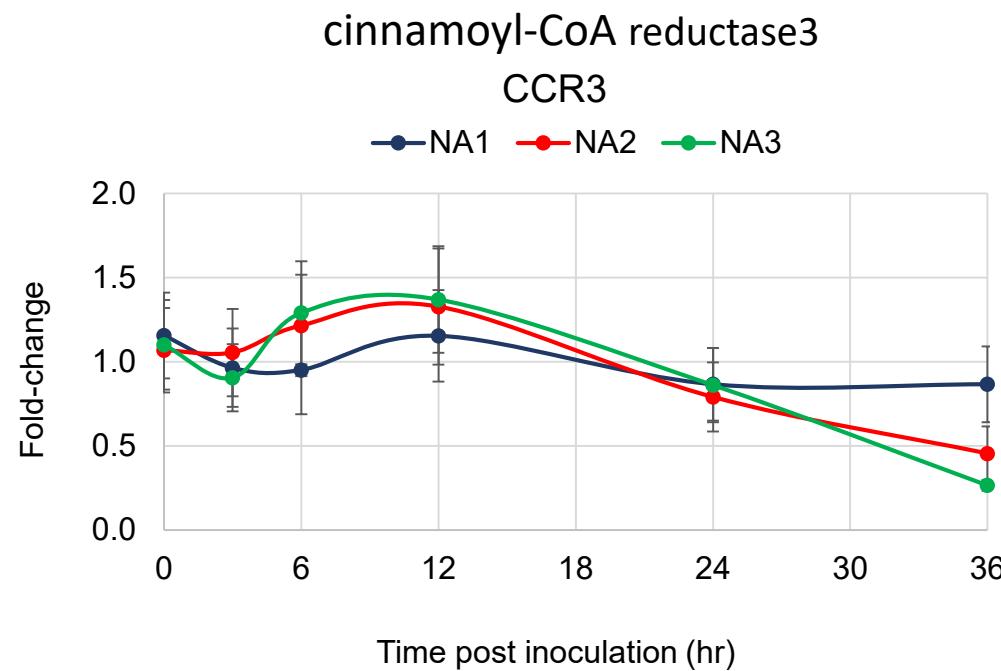
Involved in SA pathway

Involved in JA pathway

# Transcription of Pathogenesis Related (PR) genes



# Transcription of genes involved in lignin deposition



# **Why does NA3 cause less disease?**

**Hypotheses:**

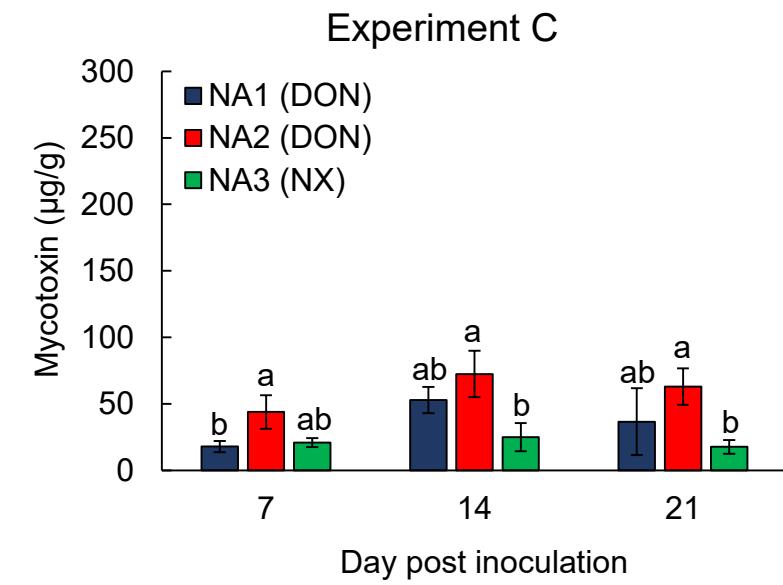
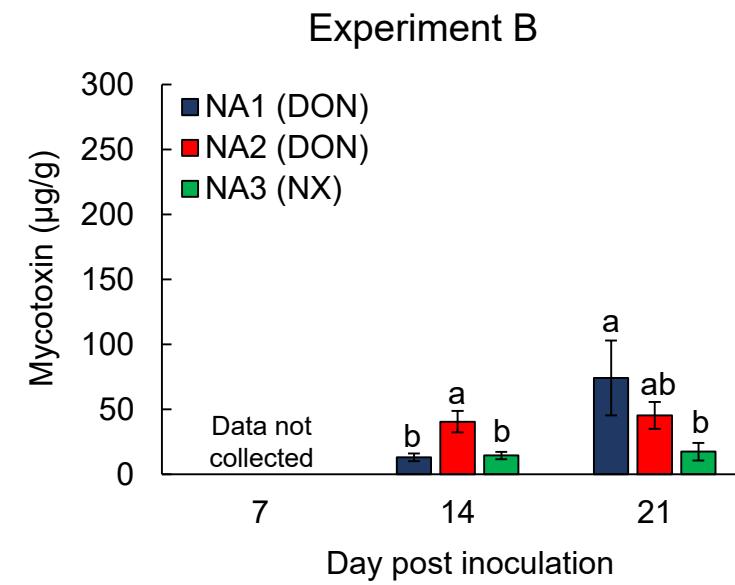
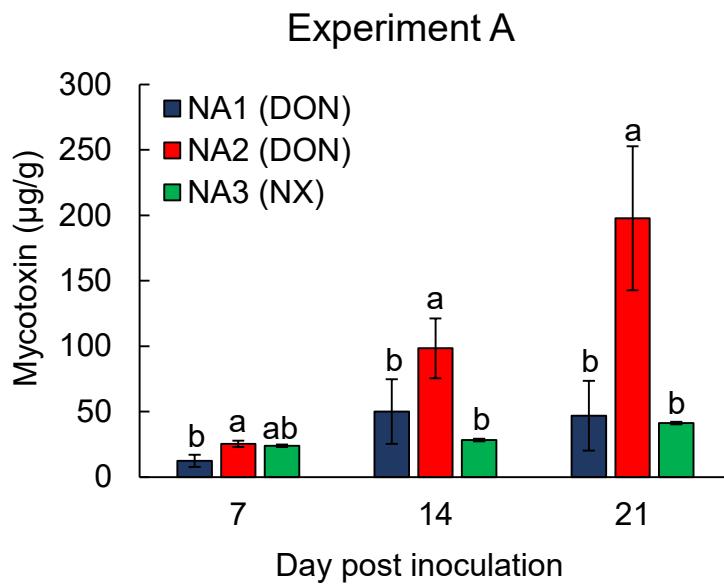
- 1. Host plant response against NA3 strains is stronger and more effective at controlling disease spread.**
  
- 2. NA3 strains are less virulent.**

# Are NA3 strains less virulent?

Hypothesis:

NA3 produces less toxin?

Not always significantly less



# NA3 may be less virulent because of NX chemotype?

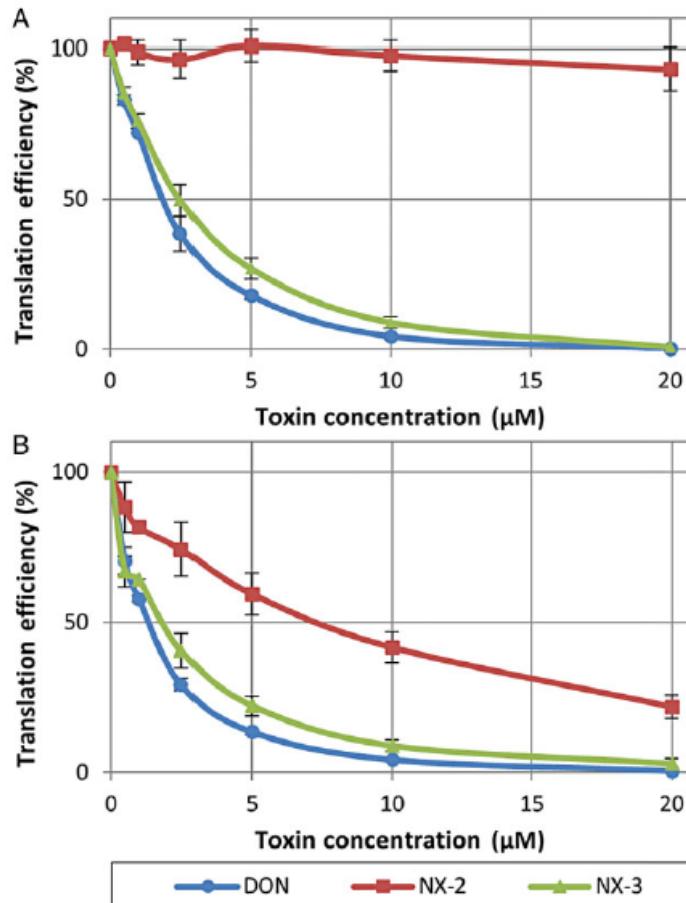


Fig. 3. *In vitro* toxicity of deoxynivalenol and the novel metabolites NX-2 and NX-3 in (A) rabbit reticulocyte lysate and (B) wheat germ extract based translation assays. Error bars show  $\pm$  standard deviations.



**Supporting Information Fig. 3.** *Chlamydomonas reinhardtii* grown in the presence of 100  $\mu$ M trichothecenes. Average culture doublings after 4 days were 4.0 (3-acetyl-deoxynivalenol—3-ADON), 0.2 (deoxynivalenol—DON), and 4.5 (NX-2), 1.5 (NX-3) for the novel compounds, compared to 4.8 for an acetone control.

(Varga et al., 2015)

# NA3 may be less virulent because of NX chemotype?

Less-toxic rearrangement products of NX-toxins are formed during storage and food processing

Elisabeth Varga<sup>a,1</sup>, Gerlinde Wiesenberger<sup>b,1</sup>, Lydia Woelflingseder<sup>b,c</sup>, Krisztian Twaruscheck<sup>b</sup>, Christian Hametner<sup>d</sup>, Marta Vaclaviková<sup>a</sup>, Alexandra Malachová<sup>a</sup>, Doris Marko<sup>c</sup>, Franz Berthiller<sup>a,\*</sup>, Gerhard Adam<sup>b</sup>

<sup>a</sup> Christian Doppler Laboratory for Mycotoxin Metabolism and Center for Analytical Chemistry, Department of Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences, Vienna (BOKU), Tulln, Austria

<sup>b</sup> Department of Applied Genetics and Cell Biology, University of Natural Resources and Life Sciences, Vienna (BOKU), Tulln, Austria

<sup>c</sup> Department of Food Chemistry and Toxicology, University of Vienna, Vienna, Austria

<sup>d</sup> Institute of Applied Synthetic Chemistry, Vienna University of Technology, Vienna, Austria

## GRAPHICAL ABSTRACT

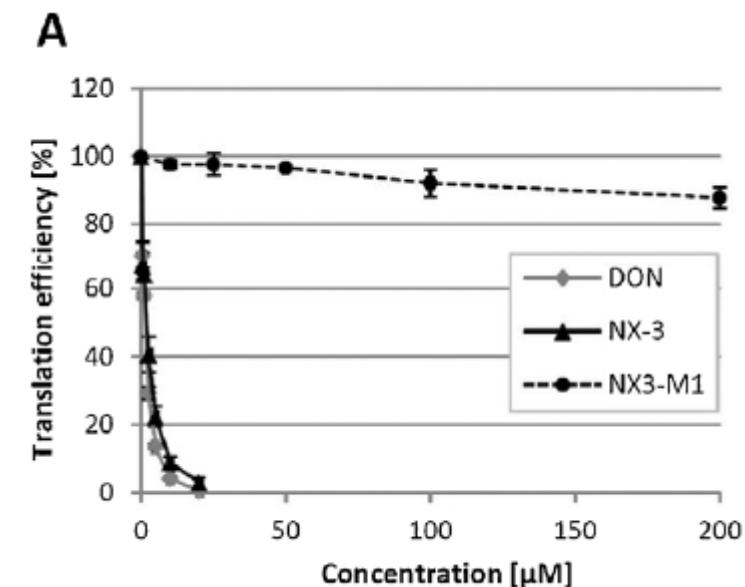
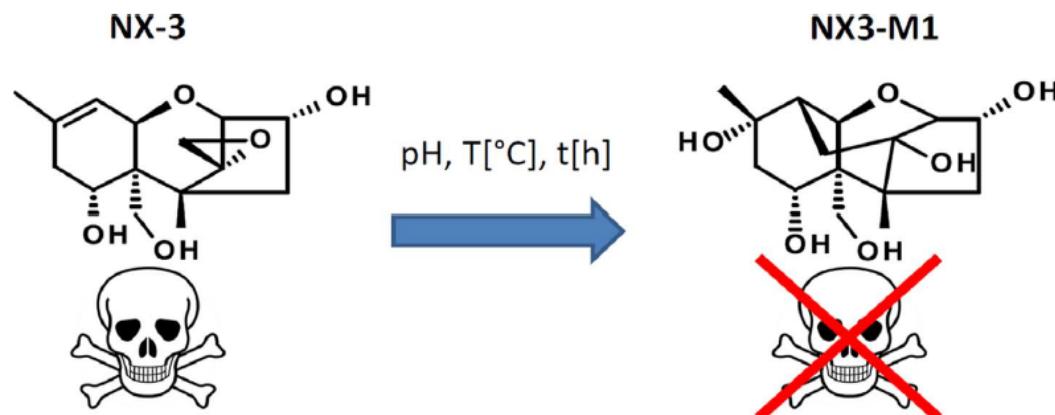


Fig. 2. *In vitro* toxicity of deoxynivalenol (DON) and NX-3 and NX3-M1 in A) wheat germ extract and B) rabbit reticulocyte lysate based translation assays. Error bars show standard deviations of replicates.

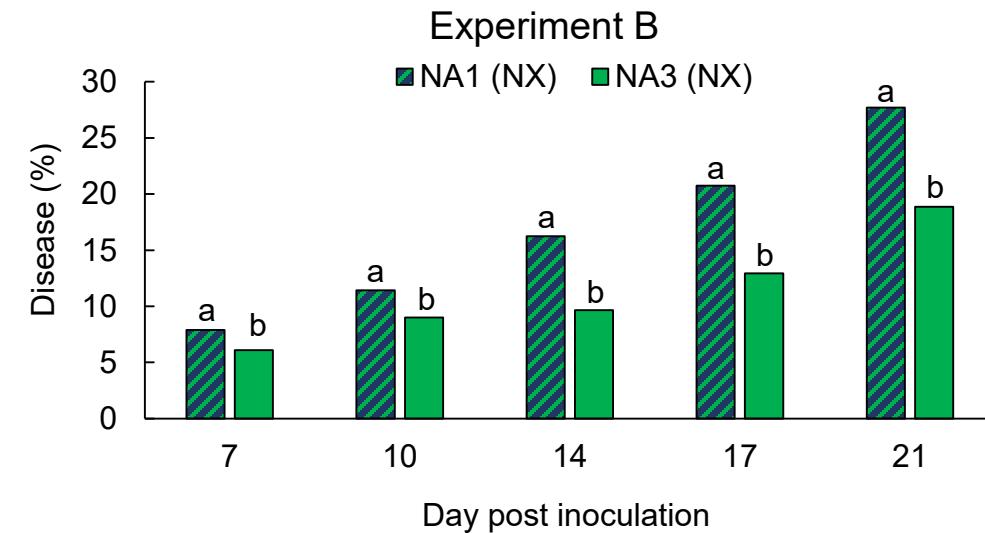
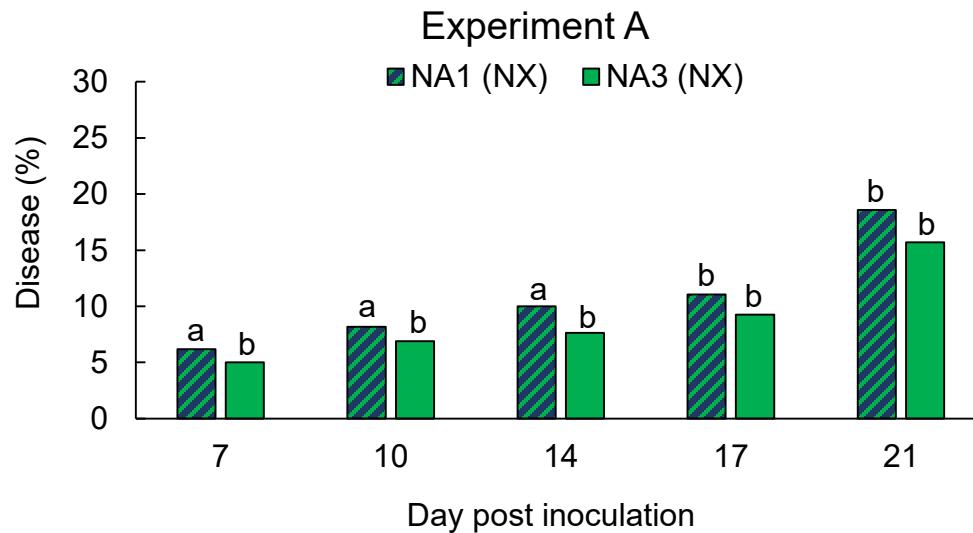
(Varga et al., 2018)

# Are NA3 less virulent because of NX chemotype?

- 6 flowering Alsen wheat heads per strain
- Total of 48 heads per population
- Point inoculation method
- Tracked % disease progression

	Strain Name	Pop/Background	Chemotype
1	43161	NA3	NX
2	44211	NA3	NX
3	47659	NA3	NX
4	66030 (F277)	NA3	NX
5	66044 (F272)	NA3	NX
6	66047 (F268)	NA3	NX
7	66039 (F270)	NA3	NX
8	F322	NA3	NX
1	47605	NA1	NX
2	45373	NA1	NX
3	45156	NA1	NX
4	44078	NA1	NX
5	44070	NA1	NX
6	66049	NA1	NX
7	66041	NA1	NX
8	53173	NA1	NX

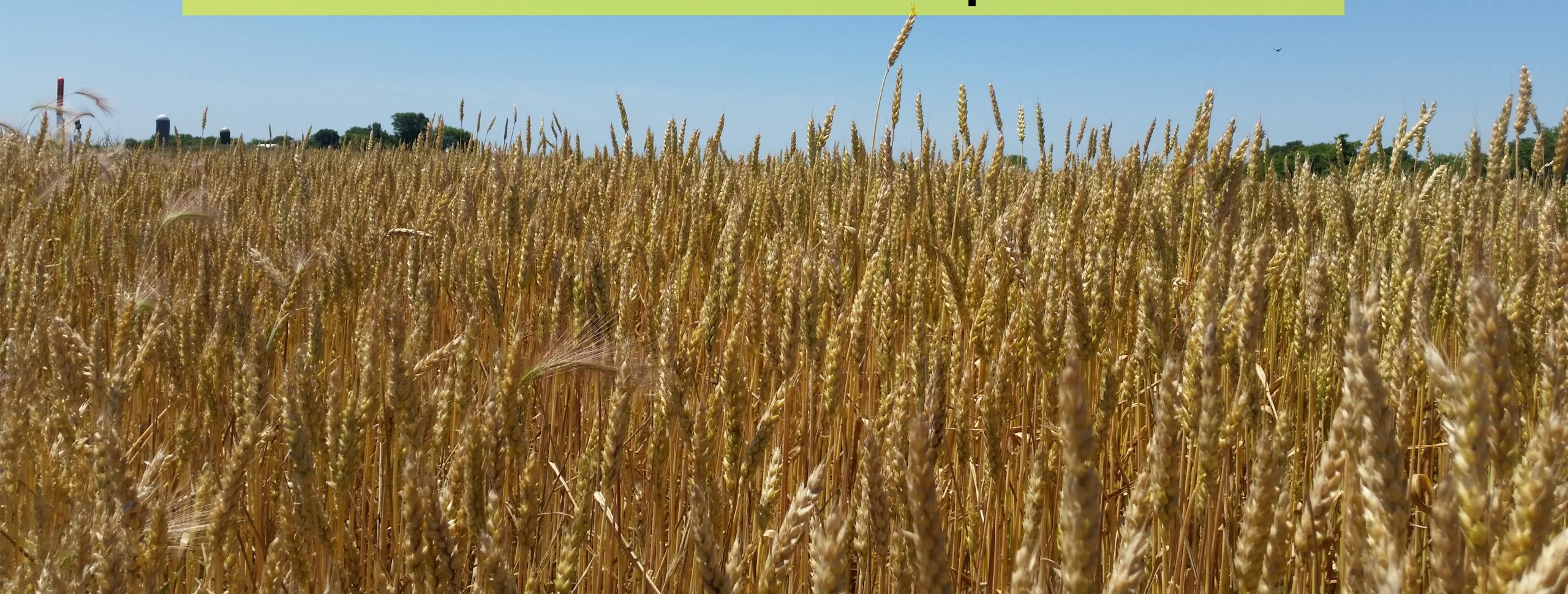
# Population genetic background influences disease development



Data analyzed to compare 2 populations (NA1 and NA3) for % diseased florets as a function of time (7, 10, 14, 17, and 21 days) using weighted regression analysis.

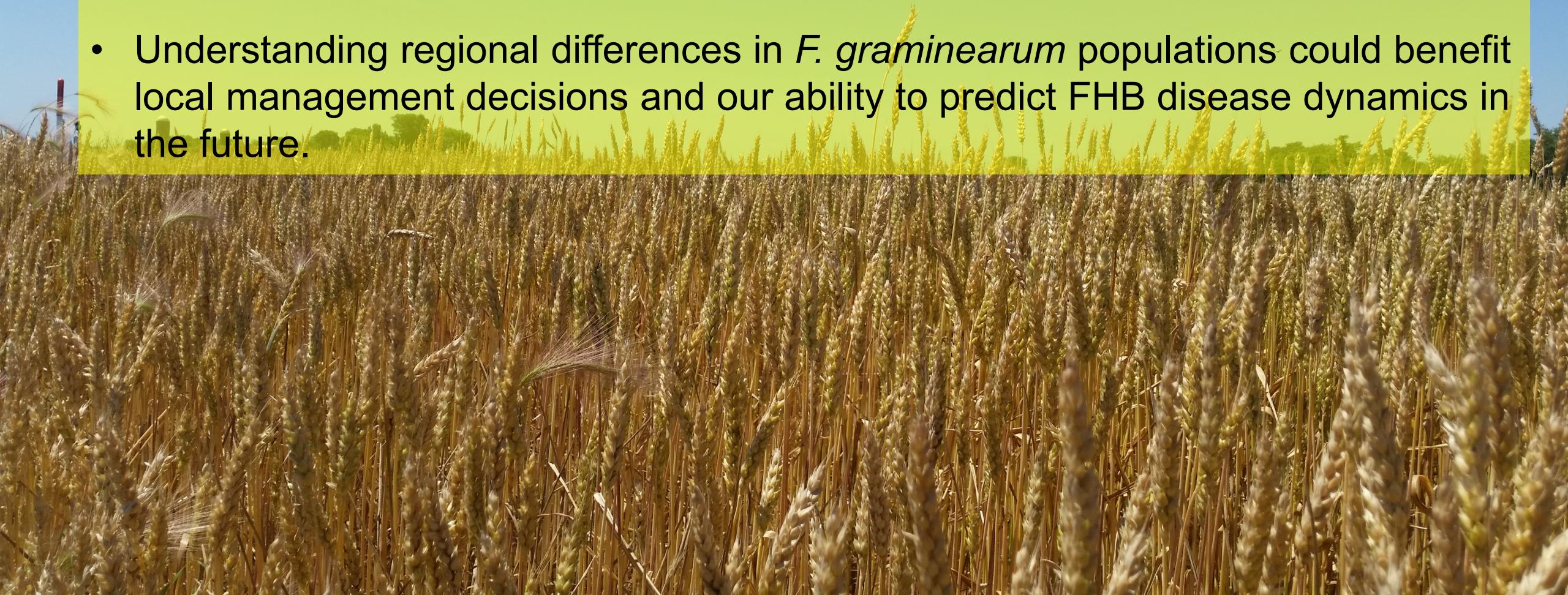
# Summary

- *F. graminearum* population and chemotype influence FHB development.



# Summary

- Understanding population-specific differences during wheat Infection could have important implications for FHB management and research.
- Understanding regional differences in *F. graminearum* populations could benefit local management decisions and our ability to predict FHB disease dynamics in the future.



# Acknowledgements:



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Susan McCormick



Miroslava Cuperlovic-Culf  
National Research Council Canada



Matt Bakker



Amy Kelly

## Technical Support:

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Nathane Orwig  
Thomas Usgaard  
Jacob Brown  
Stephanie Folmar  
Christine Hodges

Statistics  
Deb Palquest

Good things happen when we put our heads together