



Phenome2020 - G2F Workshop

Alejandro Castro Aviles
Tucson, AZ
February 24th, 2020

www.Genomes2Fields.org

WELCOME!

- ❖ Participants:
 - ❖ 37 national
 - ❖ 23 international
 - ❖ 53 public sector
 - ❖ 7 private sector

AGENDA:

- 11:15 – 11:25AM – Welcome and Introductions
- 11:25 – 12: 10PM – G2F Updates presentations
- 12:10 – 12:40PM – *Break and executive lunch served*
- 12:40 – 2:20PM – Research Presentations – first session
- 2:20 – 2:45PM – *Coffee break*
- 2:45 – 4:00PM – Research Presentations – second session
- 4:00PM – *Adjourn*

ACKNOWLEDGMENTS:

- ❖ Teresa Myers – ASPB Meetings Coordinator
- ❖ All G2F Cooperators and Collaborators
- ❖ All Presenters and Participants
- ❖ G2F Executive Committee



Genomes To Fields Collaborators and Cooperators

- Tim Beissinger (Göttingen)
- Martin Bohn (UIUC)
- Ed Buckler (ARS)
- Darwin Campbell (ISU)
- Alejandro Castro (UW)
- Ignacio Ciampitti (KSU)
- Liang Dong (ISU)
- Jode Edwards (ARS)
- David Ertl (IA Corn)
- Sherry Flint-Garcia (ARS)
- Christopher Graham (SDSU)
- Candy Hirsch (UMN)
- Jim Holland (ARS)
- Elizabeth Hood (AR State)
- David Hooker (Guelph)
- Joseph Gage (Cornell)
- Jack Gardiner (ISU)
- Fiona Goggin (AR State)
- Byron Good (Guelph)
- Mike Gore (Cornell)
- Patricio Grassini (UNL)
- Jerry Hatfield (ARS)
- Diego Jarquin (UNL)
- Shawn Kaeppler (UW)
- Joe Knoll (ARS)
- Greg Kruger (UNL)
- Nick Lauter (ARS)
- Carolyn Lawrence-Dill (ISU)
- Liz Lee (Guelph)
- Natalia de Leon (UW)
- Sanzhen Liu (Kansas)
- Argelia Lorence (AR State)
- Aaron Lorenz (UMN)
- Jonathan Lynch (PSU)
- Bridget McFarland (UW)
- John McKay (Colorado)
- Nathan Miller (UW)
- Steve Moose (UIUC)
- Seth Murray (TAMU)
- Rebecca Nelson (Cornell)
- Torbert Rocheford (Purdue)
- Oscar Rodriguez (UNL)
- Cinta Romay (Cornell)
- James Schnable (UNL)
- Pat Schnable (ISU)
- Brian Scully (ARS)
- Rajandeep Sekhon (Clemson)
- Kevin Silverstein (UMN)
- Maninder Singh (MI State)
- Margaret Smith (Cornell)
- Edgar Spalding (UW)
- Nathan Springer (UMN)
- Srikant Srinivasan (ISU)
- Yiwei Sun (ISU)
- Kelly Thorp (ARS)
- Kurt Thelen (MSU)
- Peter Thomison (OSU)
- Addie Thompson (MI State)
- Mitch Tuinstra (Purdue)
- Jason Wallace (UGA)
- Rod Williamson (IA Corn)
- Randy Wisser (UDel)
- Wenwei Xu (TAMU)
- Jianming Yu (ISU)



Genomes To Fields Sponsors



United States Department of Agriculture
National Institute of Food and Agriculture



MinnesotaCorn
RESEARCH & PROMOTION COUNCIL





Genomes to Fields (G2F) Initiative Description and 2019 Data Summary

Alejandro Castro, G2F Collaborators

Phenome 2020 Conference

February 24

the Genomes to Fields initiative

- ❖ A publicly led research initiative to catalyze and coordinate research linking genomics and predictive phenomics to achieve advances that generate economical and societal benefits
- ❖ Overall goal is to create crop varieties that are more resilient and better adapted to current and future variable environments
- ❖ We can achieve this by developing knowledge, tools and technologies that improve phenomic predictability and facilitate deployment of tools and resources that help address fundamental problems

G2F – Executive Committee:



G2F Executive Committee



Patrick Schnable **Co-Lead**
Iowa State University



Natalia de Leon **Co-Lead**
University of Wisconsin



Jonathan Lynch
Pennsylvania State University



Nathan Springer
University of Minnesota



Ed Buckler
USDA-ARS



Shawn Kaeppler
University of Wisconsin



David Ertl
Iowa Corn Growers' Association

- Advocates for federal funding for initiative in area of predictive phenomics
 - Modeling, analytical, and HT phenotyping tools
 - Database development
 - Student training
- As part of the G2F initiative is the **Maize GxE Project**



Alejandro Castro,
Research Coordinator

G2F
Overview

Overview of Maize GXE Project:

- G2F has been able to successfully evaluate a diverse set of hybrids across multiple locations and years to maximize interaction between representative set of material and multiple environments
- Living infrastructure of researchers across disciplines and a network of field phenotyping sites

	2014	2015	2016	2017	2018	2019
No. of unique locations	19	24	34	38	31	35
No. of plots planted	12,679	17,350	16,480	21,252	27,298	27,291
No. of plots post-harvest and data cleaning	12,302	11,956	16,014	15,940	24,379	TBD

Since 2014:

- 182 unique environments
- ~122,350 plots
- ~ 12,000 unique varieties (with genetic sequence)

2019 Principal Investigators

Arkansas (AR)

Beth Hood

Colorado (CO)

John McKay

Delaware (DE)

Randy Wisser

Georgia (GA)

Joe Knoll
Jason Wallace

Illinois (IL)

Martin Bohn

Indiana (IN)

Mitch Tunistra

Iowa (IA)

Jode Edwards
Patrick Schnable

Kansas (KS)

Sanzhen Liu

Michigan (MI)

Maninder Singh
Addie Thompson

Minnesota (MN)

Candice Hirsch
Nathan Springer

Missouri (MO)

Sherry Flint-Garcia

Nebraska (NE)

James Schnable

New York (NY)

Ed Buckler
Michael Gore
Rebecca Nelson

North Carolina (NC)

Jim Holland

Ohio (OH)

Richard Minyo
Peter Thomison

South Carolina (SC)

Rajan Sekhon

Texas (TX)

Seth Murray
Wenwei Xu

Wisconsin (WI)

Natalia de Leon
Shawn Kaeppler

Ontario (ON) – Canada

David Hooker
Elizabeth Lee

Other Investigators

(Not shown on map)

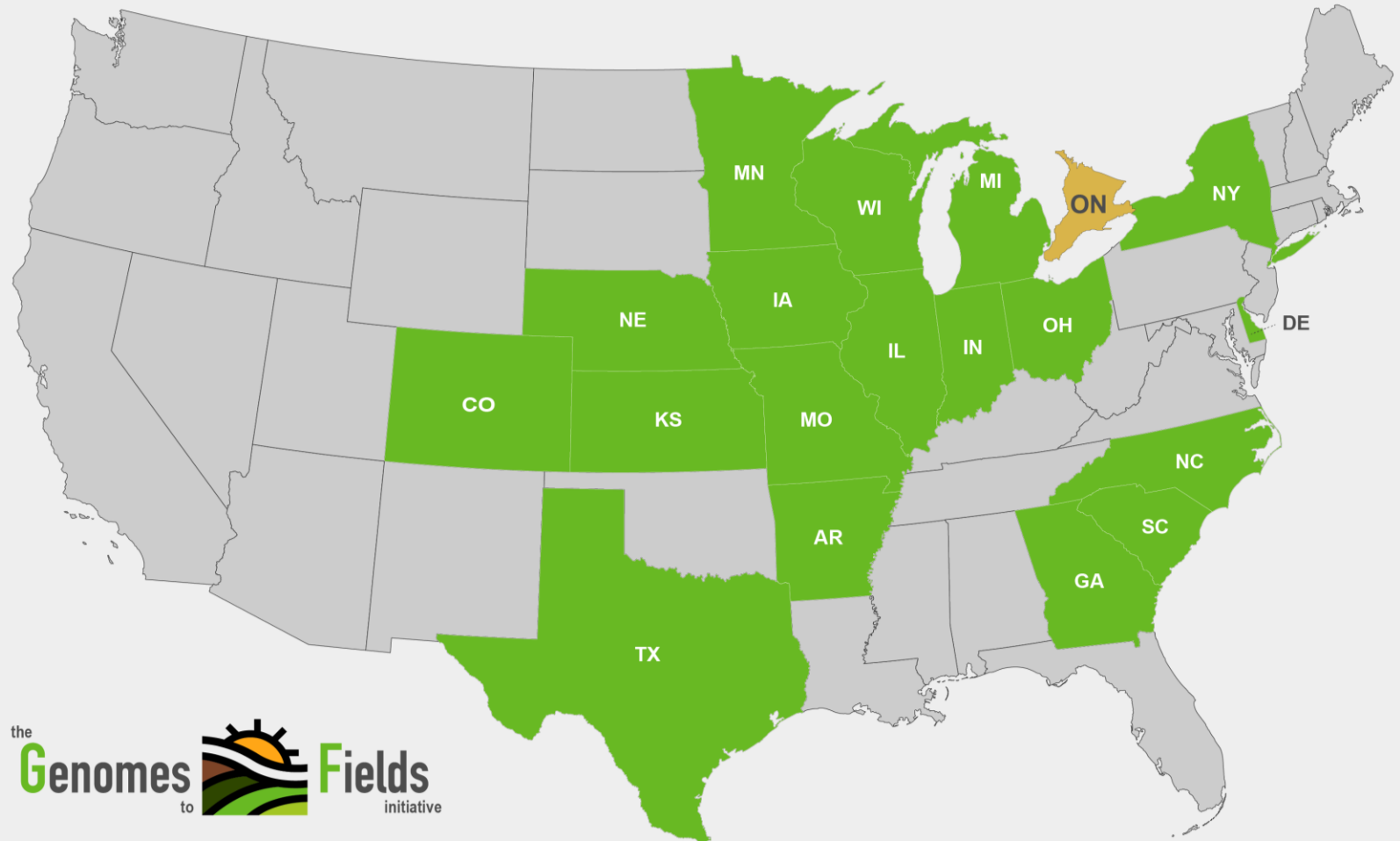
Tim Beissinger (Germany)

Arkansas State University
Clemson University
Colorado State University
Cornell University
Iowa State University
Kansas State University

Michigan State University
North Carolina State University
Ohio State University
Purdue University
Texas A&M University
University of Delaware

University of Georgia
University of Guelph
University of Illinois
University of Minnesota
University of Missouri
University of Nebraska

University of Wisconsin
USDA-ARS
Georg-August-Universität Göttingen
(Not shown on map)



2019 GxE Principal Investigators and Academic & Federal Institutions in the United States and Canada

Maize GXE Project - Field Design:

- Plots per location
 - Each location grows between 500 – 1,500 of various hybrids
 - Mega-location at least 1,500 plots and multiple testers
 - Incomplete blocks per location, overall balanced
 - 2 row plots
- Populations and testers change every two years
 - 2014-2015
 - 2016-2017
 - 2018-2019
- Yellow Stripe (YS) Hybrids
 - Common set of ~30 hybrids replicated in each location
 - Serve as checks across multiple locations and years
 - Ties data together
 - Used for specific research projects

Yellow Stripes
2369/LH123HT
B14A/H95
B14A/MO17
B14A/OH43
B37/H95
B37/MO17
B37/OH43
B73/MO17
B73/PHM49
B73/PHN82
CG119/CG108
CG44/CGR01
F42/H95
F42/MO17
F42/OH43
LH74/PHN82
PHG39/PHN82
PHW52/PHM49
PHW52/PHN82
TX110/87916
TX714/TX779
TX777/LH195
TX779/LH195
B73/TX779
LH132/TX779

Data Collection

- Phenotypic:
 - Plot-level notes of stand count, lodging, flowering, yield, etc. ($n=15$)

Agronomic Characteristics



Yield Components



Flowering/Silking Dates



Plant/Ear Height



Data Collection

- Genotypic:

- 2014 – 2017 Genotyping by Sequencing (GBS)
- 2018 – 2019 Practical Haplotype Graph (PHG), focus on inter-genic region



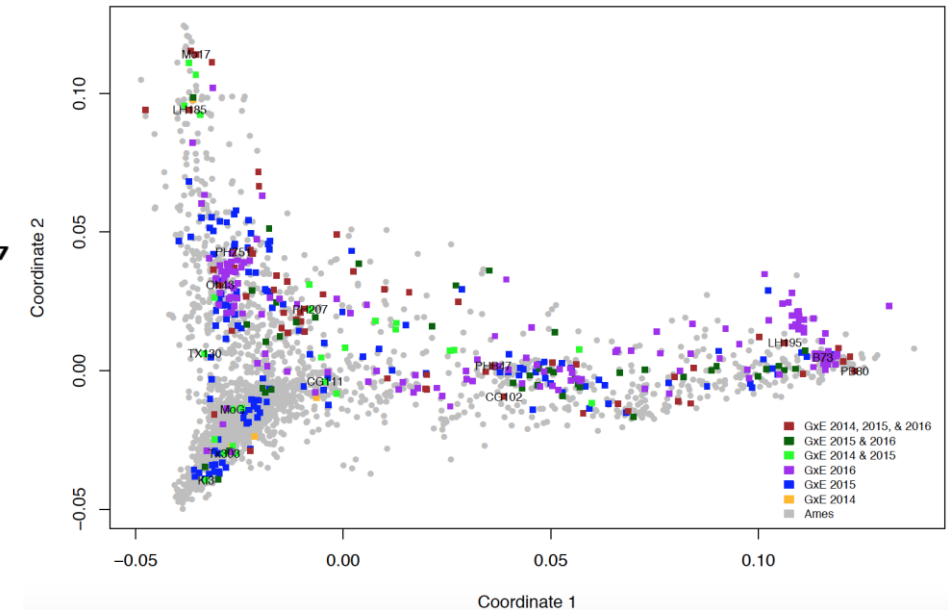
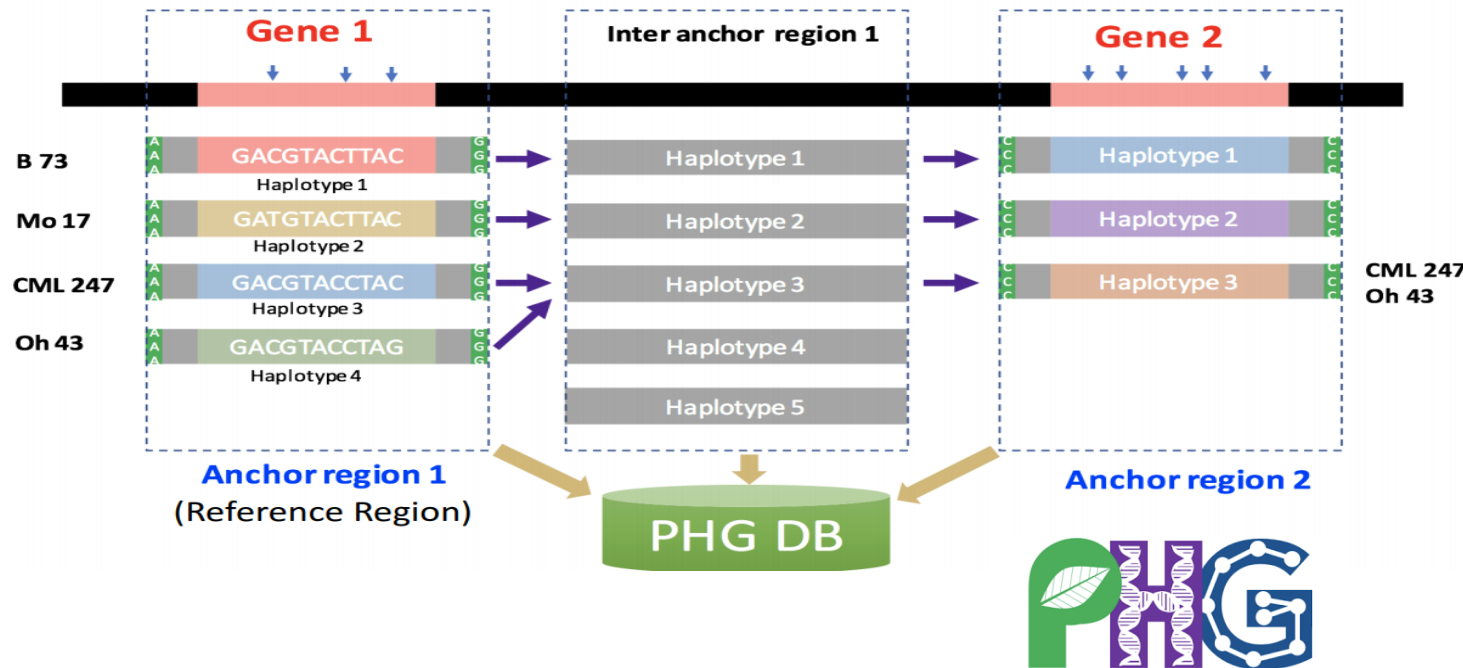
Cinta Romay



Ed Buckler



Cornell University

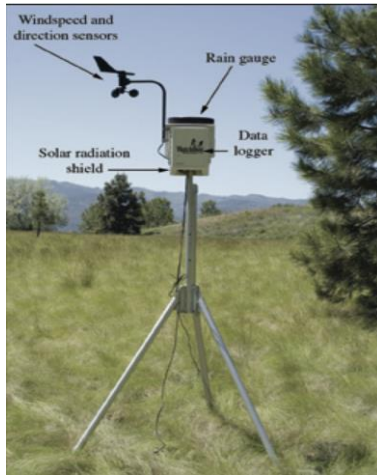


Data Collection

Weather Data:

- Field-level from weather stations temperature, relative humidity, rainfall, wind, PAR, soil temp, photoperiod, etc. ($n=14$)

Main Weather Station



MicroStation



G2F
Overview

Data
Collection

Soil Data:

- Soil Texture
- Soil Composition: %Sand, Silt, and Clay
- N, K, Zn, Fe, Mn, Cu, Ca, Na levels
- Soil pH



MetaData:

- Field applications
- field GPS coordinates,
- specific machinery,
- field layout
- Any issues throughout the season ($n=30+$)

Experiment Code -->	WIH1	
When all values have been recorded, choose "done" --> (Data will not be collected until then)	Done	
Experiment	Treatment	Standard
	City	Madison
	Farm	West Madison Agricultural Research Station
	Field	M1400 N
	Trial ID (Assigned by collaborator for internal reference)	
	Soil taxonomic ID and horizon description, if known	
Weather station information		
WatchDog 2780 weather station		
Weather station serial number (Last four digits, e.g. m2700a####)	8648	
Location		Not Sure?
Weather station location latitude (in decimal numbers NOT DMS)	43.057176	Check it!
Weather station location longitude (in decimal numbers NOT DMS)	-89.531052	
Date weather station placed in service	5/2/2017	
Date weather station removed from service	10/18/2017	
In-field pup weather station (if applicable)		
In-field station serial number	14820	
Location		Not Sure?
In-field station latitude (in decimal numbers NOT DMS)	43.055986	Check it!
In-field station longitude (in decimal numbers NOT DMS)	-89.530831	
In-field pup weather station (if applicable)		
In-field station serial number		
Location		Not Sure?
In-field station latitude (in decimal numbers NOT DMS)	43.07471	Check it!
In-field station longitude (in decimal numbers NOT DMS)	-89.384397	
Additional weather data source (if necessary)		
Link to additional weather source available online		
Plot layout and planter information		
Previous Crop	soybeans	
Pre-plant tillage method(s)	field cultivate	
In-season tillage method(s)	hand weed	Centimeter to Inch converter
Plot length (center-to-center in feet)	15	
Alley length (in inches)	30	0
Row spacing (in inches)	30	
Types of planter (fluted cone, belt cone, air planter)	fluted cone	Inches =
Number kernels planted per plot (>200 seed/pack for cone planters)	80	0

Data Collection – SOP:

- Collaborators are provided a SOP and Phenotype Handbook each year (genomes2fields.org)

Document Contents

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Data Collection – SOP:

Ear Height (EHT)

Description/Procedure:

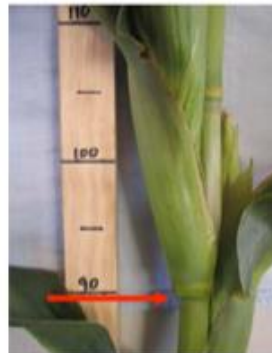
Placing measuring stick on ground next to the root crown, “ear height” is measured at the primary ear bearing node. See *Picture 1*.

Timing: At plant maturity

n = 1 representative plant per plot

Unit: centimeter [cm]

Notes: One plant is considered sufficient since these are inbreds and hybrids and are not segregating for traits.



Picture 1



Data Cleaning – Data Wrangling:

- Group of PIs, data scientists, post docs and grad students
- Eliminates obvious outliers, no bias
- Examples of cleaning steps:
 - Stand count > # of seeds planted, then “NA”
 - Ear height > plant height, then “NA”
 - Plot weight, test weight, grain moisture < 0 or > 400, then “NA”
 - Grain yield > 500, then “NA”
 - Spatial variability using field maps for high/low values
 - Read through metadata to see if additional plots need to be discarded


Weather Data Cleaning:

- Impute missing weather data from:
 - Nearest airport
 - Publicly available weather stations

IOWA STATE UNIVERSITY
Iowa Environmental Mesonet

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ASOS Network / ASOS-AWOS-METAR Data Download

The IEM maintains an ever growing archive of automated airport weather observations from around the world! These observations are typically called 'ASOS' or sometimes 'AWOS' sensors. A more generic term may be METAR data, which is a term that describes the format the data is transmitted as. If you don't get data for a request, please feel free to [contact us](#) for help. The IEM also has a one minute interval dataset for Iowa **ASOS** (2000-) and **AWOS** (1995-2011) sites. This archive simply provides the as-is collection of historical observations, very little quality control is done. "M" is used to denote missing data.

Here is a [python script example](#) that automates the download of data from this interface. A community user has contributed [R language](#) version of the python script.

Please be patient with this page as it will take a number of seconds to process your request and provide the result.

Select Network

1) Select Station/Network by clicking on location:

Select Widget for NC_ASOS Network

Sort Available Stations: ▾

[1A5] FRANKLIN

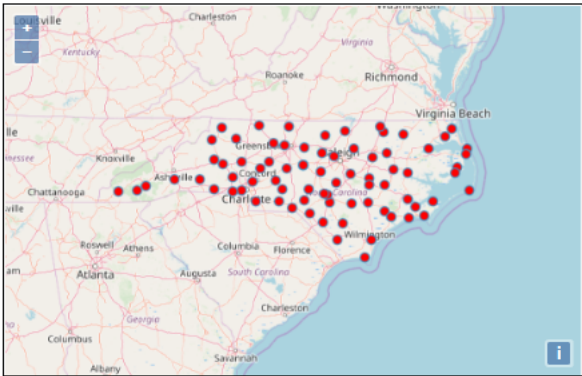
[24A] Sylva

[2DP] Dare County Gunnery Range

[5W8] Silver City

Enter some text here to f

Selected Stations:



2) Select From Available Data:

All Available

Air Temperature [F]

Air Temperature [C]

Dew Point [F]

Dew Point [C]

Relative Humidity [%]

Heat Index/Wind Chill [F]

Wind Direction

Wind Speed [knots]

Wind Speed [mph]

3) Specific Date Range (If needed):

Note: There is up to an hour delay for observations to appear within this service. A process runs at approximately 20 minutes after the hour to copy over the previous hour's worth of data in the backend database behind this service.

Start Date:

End Date:

4) Timezone of Observation Times:

The following options are available for how the observation time is presented.

5) Download Options:

Data Format:

Include Latitude + Longitude?

How to represent missing data?

How to represent Trace reports?

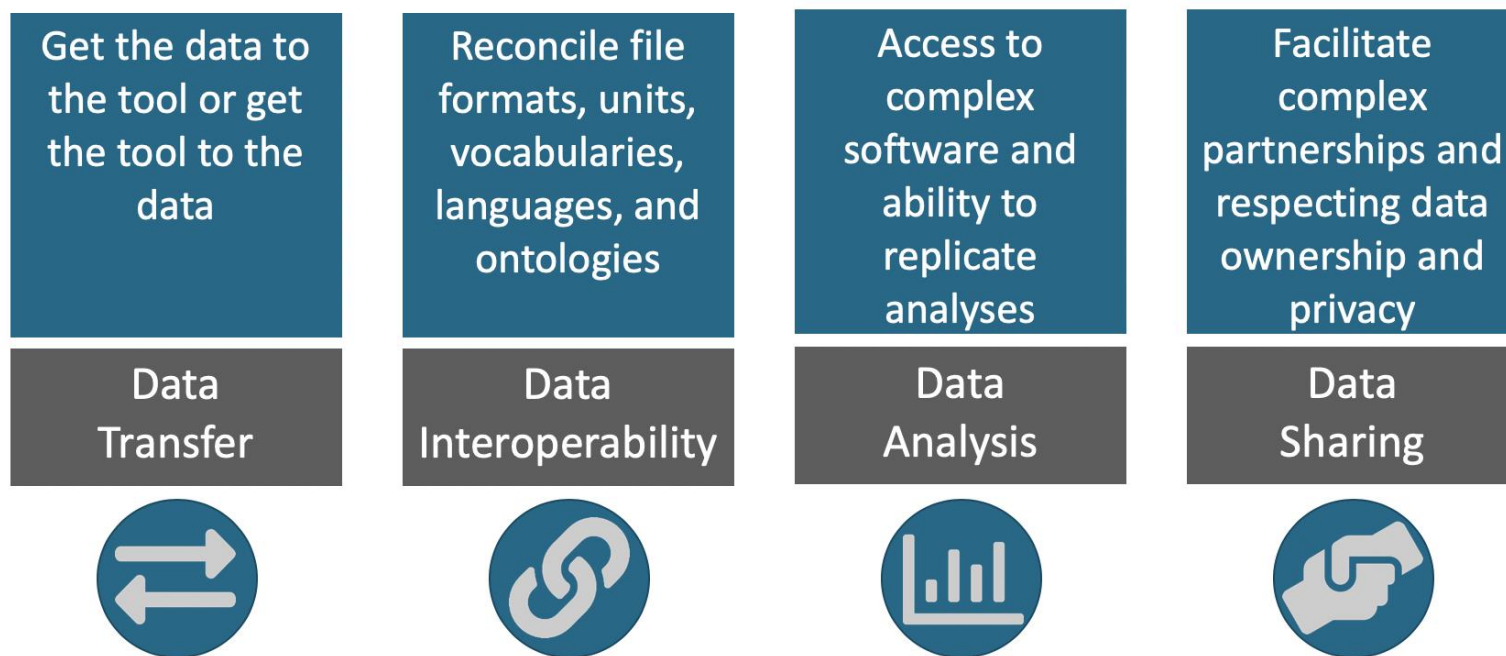
G2F
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Data Processing:

- GEMS is a novel data sharing and big data analytical platform;
- Kevin Silverstein, Bioinformaticist/GEMS Operations Manager



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Data Is Made Publicly Available:

[Home](#)[About](#)[Funded Projects](#)[Publications](#)[Meetings](#)[Resources](#)

Data Downloads

Field Season	Release to Collaborators (ARK)	Release to Public (DOI)
2014	Not Available	https://doi.org/10.7946/P2V888
2015	February 2017	https://doi.org/10.7946/P24S31
2016	February 2017	https://doi.org/10.7946/P3MW27
2017	February 2018	March 2019
N	February of N+1	March of N+2

❗ Please report data errors or inconsistencies that you might identify [using this submission form](#)

2016 Field Season (Available to Public): Phenotypic, genotypic, and environment data for the 2016 field season: <https://doi.org/10.7946/P3MW27>

2015 Field Season (Available to Public): Phenotypic, genotypic, and environment data for the 2015 field season: <https://doi.org/10.7946/P24S31>

2014 Field Season (Available to Public): Phenotypic, genotypic, and environment data for the 2014 field season: <https://doi.org/10.7946/P2V888>

[>Ear Imaging Data](#)[>Data Downlads](#)[>Standard Operating Procedures \(SOP\)](#)[>Newsletters](#)

- › 2018-12-31
- › 2018-07-18
- › 2017-08-11
- › 2017-04-10
- › 2016-06-21

[>Genomes2Fields Links](#)[>Genomes2Fields Logos & Images](#)[>Photos & Videos](#)

Data Is Made Publicly Available:

AlKhalifah et al. BMC Res Notes (2018) 11:452
https://doi.org/10.1186/s13104-018-3508-1

BMC Research Notes

DATA NOTE

Open Access



Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets

Naser AlKhalifah^{1,2,3†}, Darwin A. Campbell^{1†}, Celeste M. Falcon^{2†}, Jack M. Gardiner^{1,2,4†}, Nathan D. Miller^{2†}, Maria Cinta Romay^{2†}, Ramona Walls^{4†}, Renee Walton^{1†}, Cheng-Ting Yeh^{1†}, Martin Bohn⁵, Jessica Bubert⁵, Edward S. Buckler^{3,6}, Ignacio Ciampitti⁷, Sherry Flint-Garcia^{6,8}, Michael A. Gore³, Christopher Graham⁹, Candice Hirsch¹⁰, James B. Holland^{6,11}, David Hooker¹², Shawn M. Kaeppler², Joseph Knoll⁶, Nick Lauter^{1,6}, Elizabeth C. Lee¹³, Aaron Lorenz^{14,25}, Jonathan P. Lynch¹⁵, Stephen P. Moose⁵, Seth C. Murray¹⁶, Rebecca Nelson³, Torbert Rocheford¹⁷, Oscar Rodriguez¹⁴, James C. Schnable¹⁴, Brian Scully¹⁸, Margaret Smith³, Nathan Springer¹⁰, Peter Thomison¹⁹, Mitchell Tuinstra¹⁷, Randall J. Wisser²⁰, Wenwei Xu²¹, David Ertl²², Patrick S. Schnable^{1*}, Natalia De Leon^{2*}, Edgar P. Spalding^{2*}, Jode Edwards^{1,6*} and Carolyn J. Lawrence-Dill^{1*}

Abstract

Objectives: Crop improvement relies on analysis of phenotypic, genotypic, and environmental data. Given large, well-integrated, multi-year datasets, diverse queries can be made: Which lines perform best in hot, dry environments? Which alleles of specific genes are required for optimal performance in each environment? Such datasets also can be leveraged to predict cultivar performance, even in uncharacterized environments. The maize Genomes to Fields (G2F) Initiative is a multi-institutional organization of scientists working to generate and analyze such datasets from existing, publicly available inbred lines and hybrids. G2F's genotype by environment project has released 2014 and 2015 datasets to the public, with 2016 and 2017 collected and soon to be made available.

Data description: Datasets include DNA sequences; traditional phenotype descriptions, as well as detailed ear, cob, and kernel phenotypes quantified by image analysis; weather station measurements; and soil characterizations by site. Data are released as comma separated value spreadsheets accompanied by extensive README text descriptions. For genotypic and phenotypic data, both raw data and a version with outliers removed are reported. For weather data, two versions are reported: a full dataset calibrated against nearby National Weather Service sites and a second calibrated set with outliers and apparent artifacts removed.

Keywords: Maize, Genome, Genotype, Environment, Breeding, Phenotype, Prediction, Soil, Inbred, Hybrid

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[†]Naser AlKhalifah, Darwin A. Campbell, Celeste M. Falcon, Jack M. Gardiner, Nathan D. Miller, Maria Cinta Romay, Ramona Walls, Renee Walton, Cheng-Ting Yeh are joint first authors

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McFarland et al. BMC Res Notes (2020) 13:71
https://doi.org/10.1186/s13104-020-4922-8

BMC Research Notes

DATA NOTE

Open Access



Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets

Bridget A. McFarland^{1†}, Naser AlKhalifah^{1†}, Martin Bohn², Jessica Bubert², Edward S. Buckler^{3,4}, Ignacio Ciampitti⁵, Jode Edwards^{4,6}, David Ertl⁷, Joseph L. Gage³, Celeste M. Falcon¹, Sherry Flint-Garcia^{4,8}, Michael A. Gore³, Christopher Graham⁹, Candice N. Hirsch¹⁰, James B. Holland^{4,11}, Elizabeth Hood¹², David Hooker¹³, Diego Jarquin¹⁴, Shawn M. Kaeppler¹, Joseph Knoll⁴, Greg Kruger¹⁴, Nick Lauter^{4,6}, Elizabeth C. Lee¹³, Dayane C. Lima¹, Aaron Lorenz¹⁰, Jonathan P. Lynch¹⁵, John McKay¹⁶, Nathan D. Miller¹, Stephen P. Moose², Seth C. Murray¹⁷, Rebecca Nelson³, Christina Poudyal¹⁰, Torbert Rocheford¹⁸, Oscar Rodriguez¹⁴, Maria Cinta Romay³, James C. Schnable¹⁴, Patrick S. Schnable⁶, Brian Scully¹⁹, Rajandeep Sekhon²⁰, Kevin Silverstein¹⁰, Maninder Singh²¹, Margaret Smith³, Edgar P. Spalding¹, Nathan Springer¹⁰, Kurt Thelen²¹, Peter Thomison²², Mitchell Tuinstra¹⁸, Jason Wallace²³, Ramona Walls²⁴, David Willis⁹, Randall J. Wisser²⁵, Wenwei Xu¹⁷, Cheng-Ting Yeh⁶ and Natalia de Leon^{1*}

Abstract

Objectives: Advanced tools and resources are needed to efficiently and sustainably produce food for an increasing world population in the context of variable environmental conditions. The maize genomes to fields (G2F) Initiative is a multi-institutional initiative effort that seeks to approach this challenge by developing a flexible and distributed infrastructure addressing emerging problems. G2F has generated large-scale phenotypic, genotypic, and environmental datasets using publicly available inbred lines and hybrids evaluated through a network of collaborators that are part of the G2F's genotype-by-environment (G × E) project. This report covers the public release of datasets for 2014–2017.

Data description: Datasets include inbred genotypic information; phenotypic, climatic, and soil measurements and metadata information for each testing location across years. For a subset of inbreds in 2014 and 2015, yield component phenotypes were quantified by image analysis. Data released are accompanied by README descriptions. For genotypic and phenotypic data, both raw data and a version without outliers are reported. For climatic data, a version calibrated to the nearest airport weather station and a version without outliers are reported. The 2014 and 2015 datasets are updated versions from the previously released files [1] while 2016 and 2017 datasets are newly available to the public.

Keywords: Maize, Genome, Genotype, GBS, G × E, Hybrid, Inbred, Phenotype, Environment, Field metadata

Objective

Genomes to fields (G2F) is a multi-institutional, public collaborative to develop information and tools that support the translation of maize (*Zea mays* L.) genomic information into relevant phenotypes for the benefit of

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[†]Bridget A. McFarland and Naser AlKhalifah are joint first authors

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Published Research Involving G2F Data:

Genomes To Fields (G2F) Publications

Symbol Legend: * Authors contributed equally to the article



[Field Crops Research](#). 2020, 249: 107737 | 1 April 2020
[doi:10.1016/j.fcr.2020.107737](#)

Stalk bending strength is strongly associated with maize stalk lodging incidence across multiple environments

Rajandeep S. Sekhon, Chase N. Joyner, Arlyn J. Ackerman, Christopher S. McMahan, Douglas D. Cook, Daniel J. Robertson

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[BMC Research Notes](#). 2020, 13: 71 | 12 February 2020
[doi:10.1186/s13104-020-4922-8](#)

Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets

Bridget A. McFarland*, Naser AlKhalifah*, Martin Bohn, Jessica Bubert, Edward S. Buckler, Ignacio Ciampitti, Jode Edwards, David Ertl, Joseph L. Gage, Celeste M. Falcon, Sherry Flint-Garcia, Michael A. Gore, Christopher Graham, Candice N. Hirsch, James B. Holland, Elizabeth Hood, David Hooker, Diego Jarquin, Shawn M. Kaeppler, Joseph Knoll, Greg Kruger, Nick Lauter, Elizabeth C. Lee, Dayane C. Lima, Aaron Lorenz, Jonathan P. Lynch, John McKay, Nathan D. Miller, Stephen P. Moose, Seth C. Murray, Rebecca Nelson, Christina Poudyal, Torbert Rocheford, Oscar Rodriguez, Maria Cinta Romay, James C. Schnable, Patrick S. Schnable, Brian Scully, Rajandeep Sekhon, Kevin Silverstein, Maninder Singh, Margaret Smith, Edgar P. Spalding, Nathan Springer, Kurt Thelen, Peter Thomison, Mitchell Tuinstra, Jason Wallace, Ramona Walls, David Wills, Randall J. Wisser, Wenwei Xu, Cheng-Ting Yeh, Natalia de Leon

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[Frontiers in Plant Science](#). 2019, 10: 1550 | 12 December 2019
[doi:10.3389/fpls.2019.01550](#)

Millimeter-Level Plant Disease Detection From Aerial Photographs via Deep Learning and Crowdsourced Data

Tyr Wiesner-Hanks, Harvey Wu, Ethan Stewart, Chad DeChant, Nicholas Kaczmar, Hod Lipson, Michael A. Gore, Rebecca J. Nelson

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[The Plant Genome Journal](#). 2019, 2(1): 190011 | 22 November 2019
[doi:10.2135/tppj2019.07.0011](#)

In-Field whole-plant maize architecture characterized by subcanopy rovers and latent space phenotyping

Joseph L. Gage, Elliot Richards, Nicholas Lepak, Nicholas Kaczmar, Chinmay Soman, Girish Chowdhary, Michael A. Gore, Edward S. Buckler

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[The Plant Phenome Journal](#). 2019, 2(1) | 7 November 2019
[doi:10.2135/tppj2019.03.0006](#)

Autonomous detection of plant disease symptoms directly from aerial imagery

Harvey Wu, Tyr Wiesner-Hanks, Ethan L. Stewart, Chad DeChant, Nicholas Kaczmar, Michael A. Gore, Rebecca J. Nelson, Hod Lipson

Overview of 2019:

- 21 Academic and Federal Institutions
- 30 PIs
- 35 unique locations

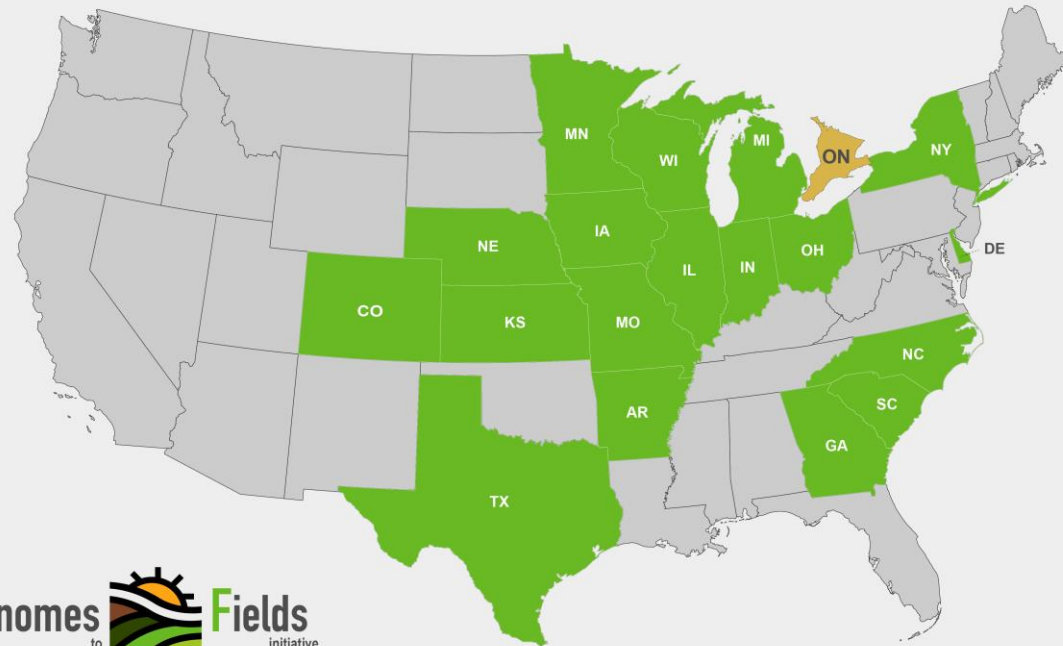
2019 Academic & Federal Institutions

Arkansas State University
Clemson University
Colorado State University
Cornell University
Iowa State University
Kansas State University

Michigan State University
North Carolina State University
Ohio State University
Purdue University
Texas A&M University
University of Delaware

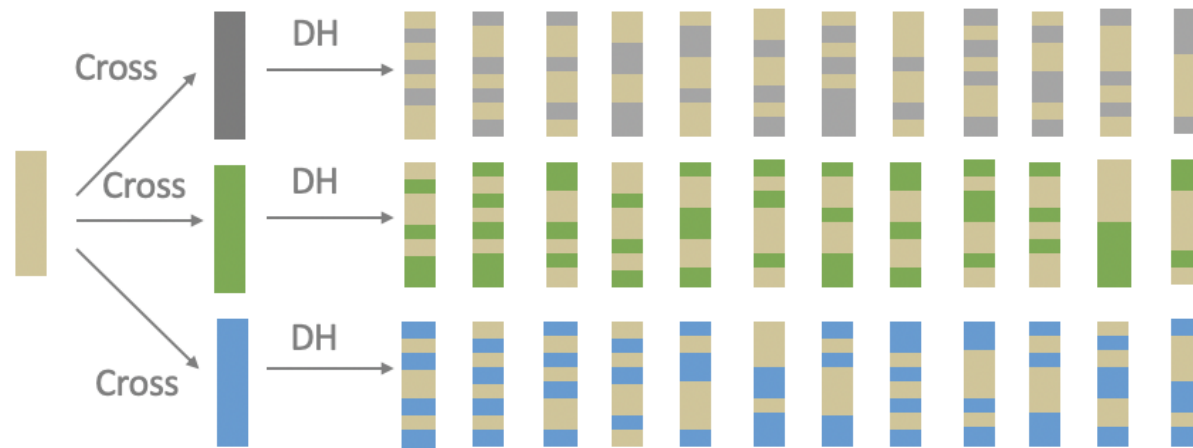
University of Georgia
University of Guelph
University of Illinois
University of Minnesota
University of Missouri
University of Nebraska

University of Wisconsin
USDA-ARS
Georg-August-Universität Göttingen
(Not shown on map)



PHW65 mini-NAM Maize Population:

- PHW65 NAM-type population
 - PHW65 reference crossed with 3 lines contrasting levels of selection
 - DHs were derived from crosses
 - Location-specific testers were used to generate hybrids



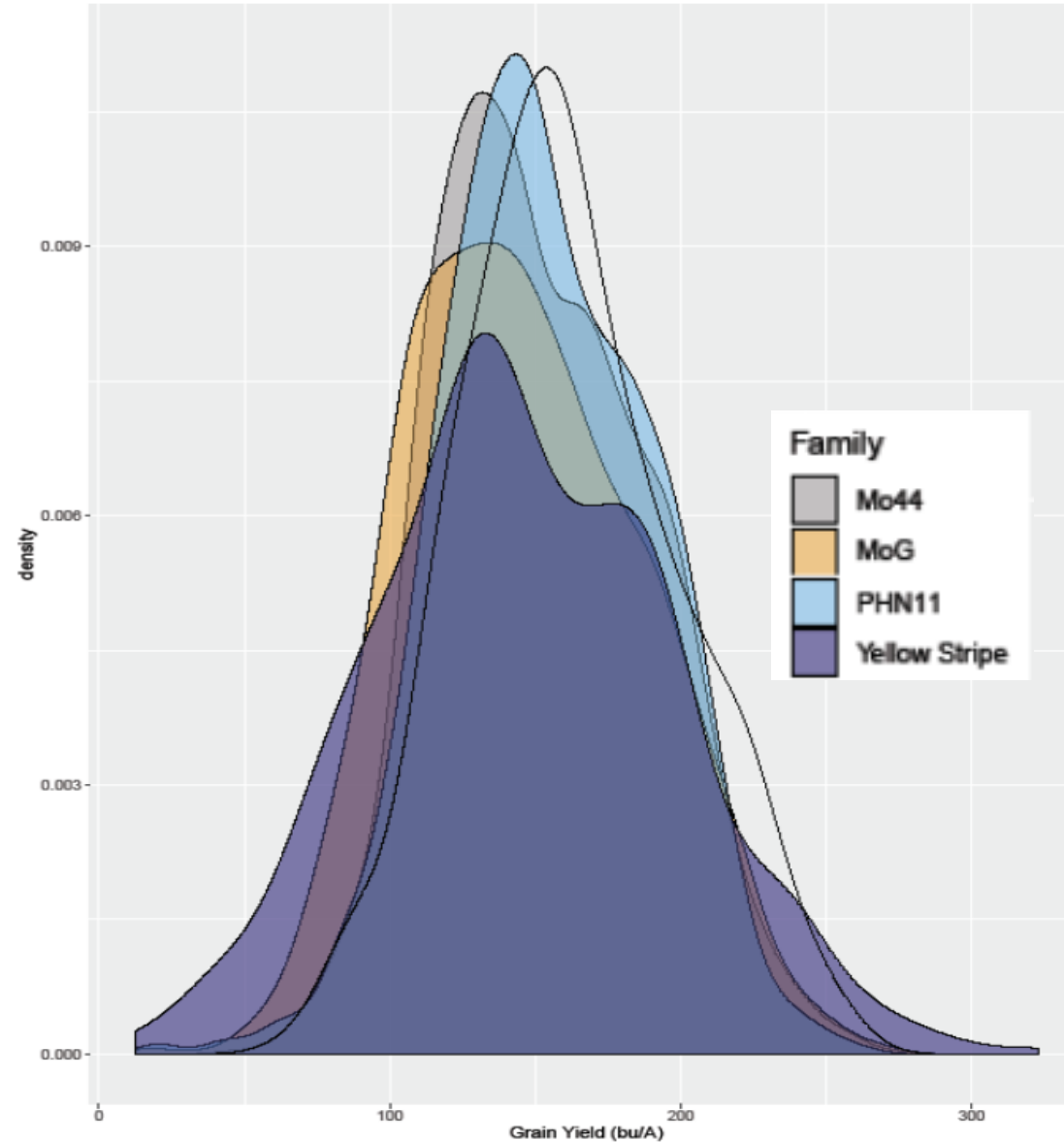
G2F
Overview

Data
Collection

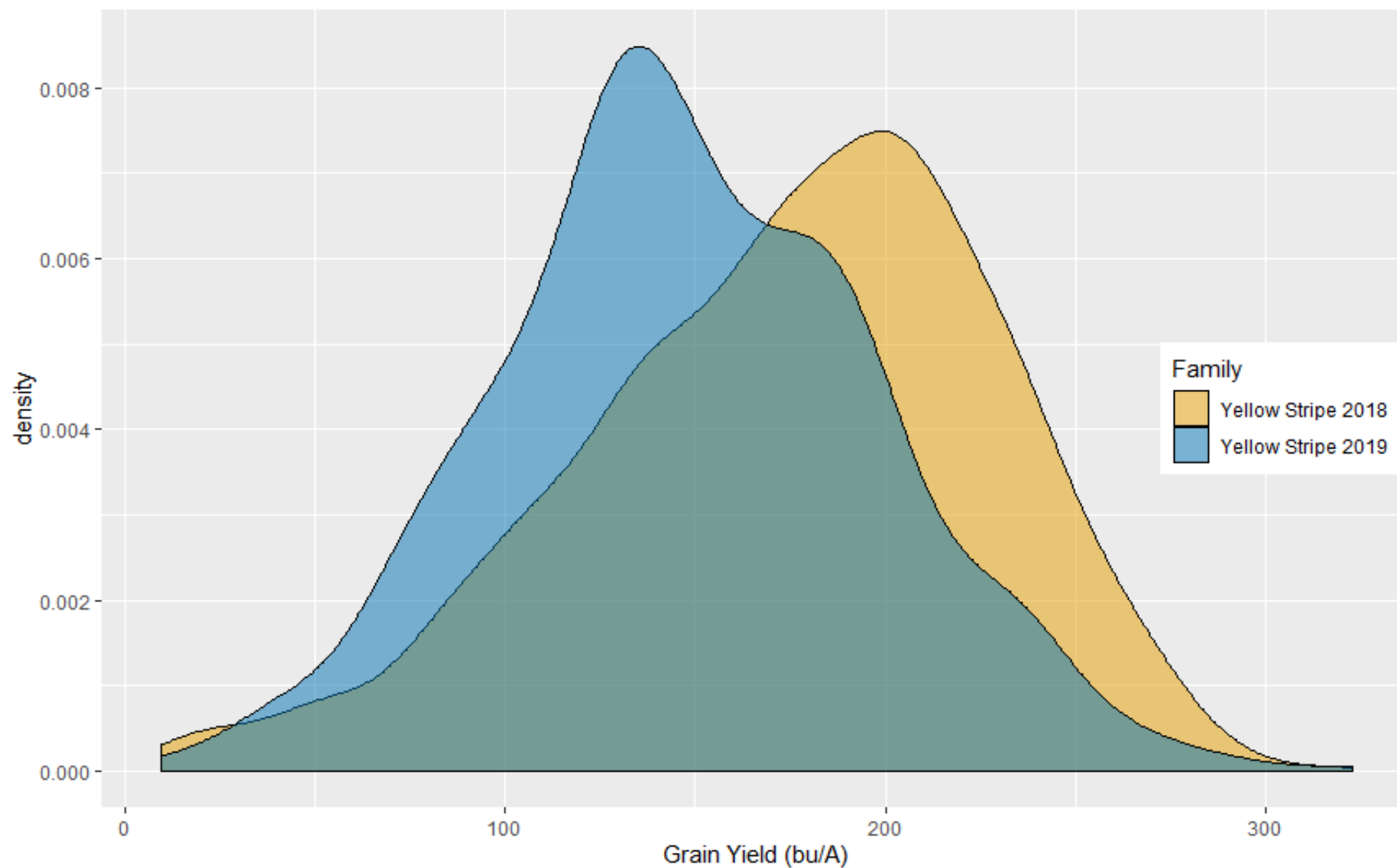
Data Cleaning

2019 Recap

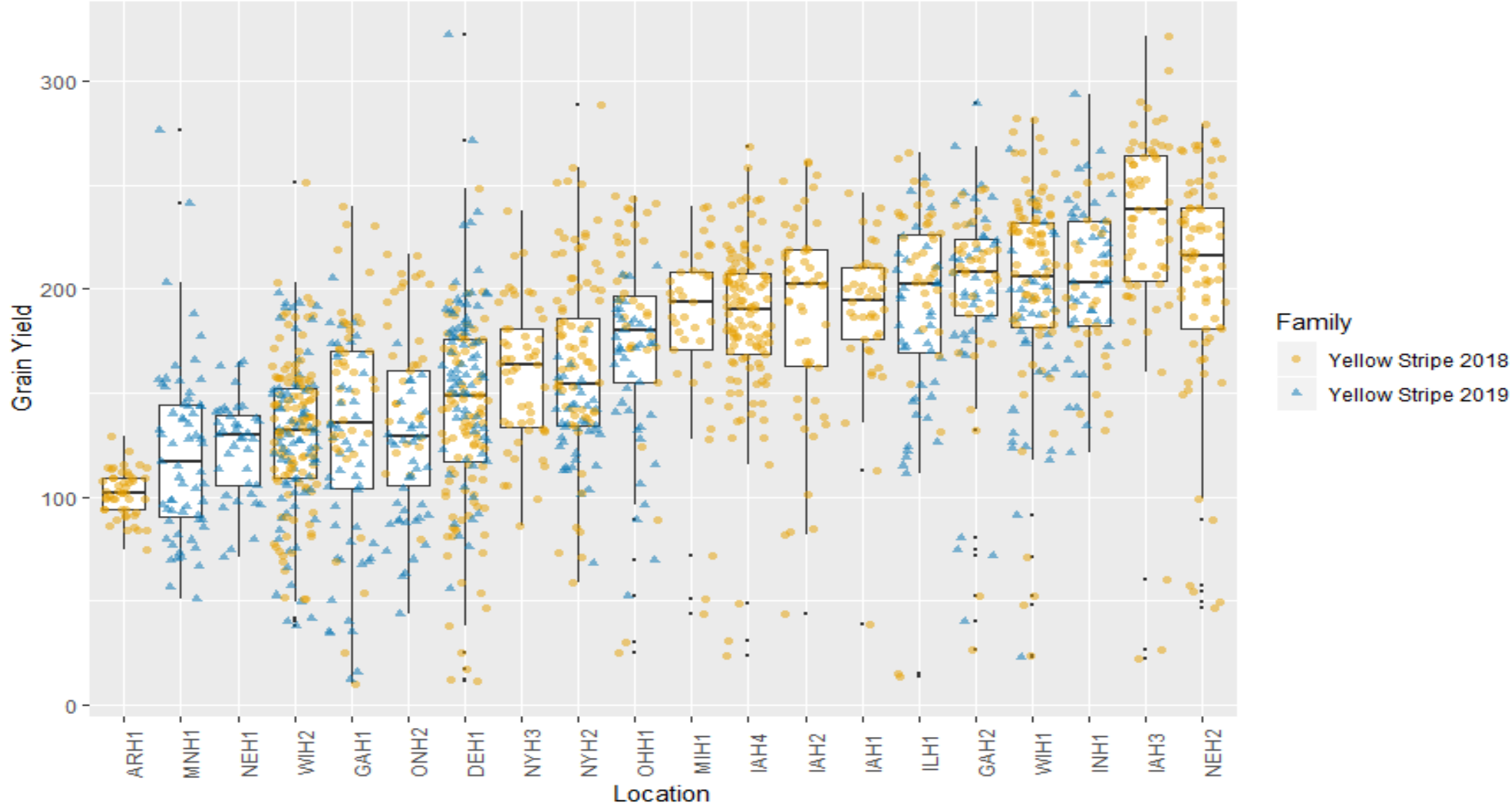
Grain Yield – Per Family 2019:



Grain Yield – Yellow Stripe:



Grain Yield of Yellow Stripe.- Regression:



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- Ed Buckler (ARS)
- Darwin Campbell (ISU)
- Alejandro Castro (UW)
- Ignacio Ciampitti (KSU)
- Liang Dong (ISU)
- Jode Edwards (ARS)
- David Ertl (IA Corn)
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