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2020/21 Plan Summary & Future Activities

Natalia de Leon
G2F Workshop

Phenome 2020 Conference
February, 24th

www.Genomes2Fields.org

Aspirational Objectives:

- ✧ Leverage the National Plant Genome Initiative investment in genome data with new phenotyping tools to deliver new products to farmers
- ✧ Desired Outcomes:
  - ✧ Identify phenes and genes that control variation for plant performance in diverse environments ("GxE" Project)
  - ✧ Improve our ability to predict plant performance to enhance agronomic production, accelerate plant breeding, and support business and policy interests
  - ✧ Enhance and organize the broader research community
    - ✧ Integrated and annotated public data sets
    - ✧ Development of data management resources
    - ✧ Facilitate synergies and interactions within the community

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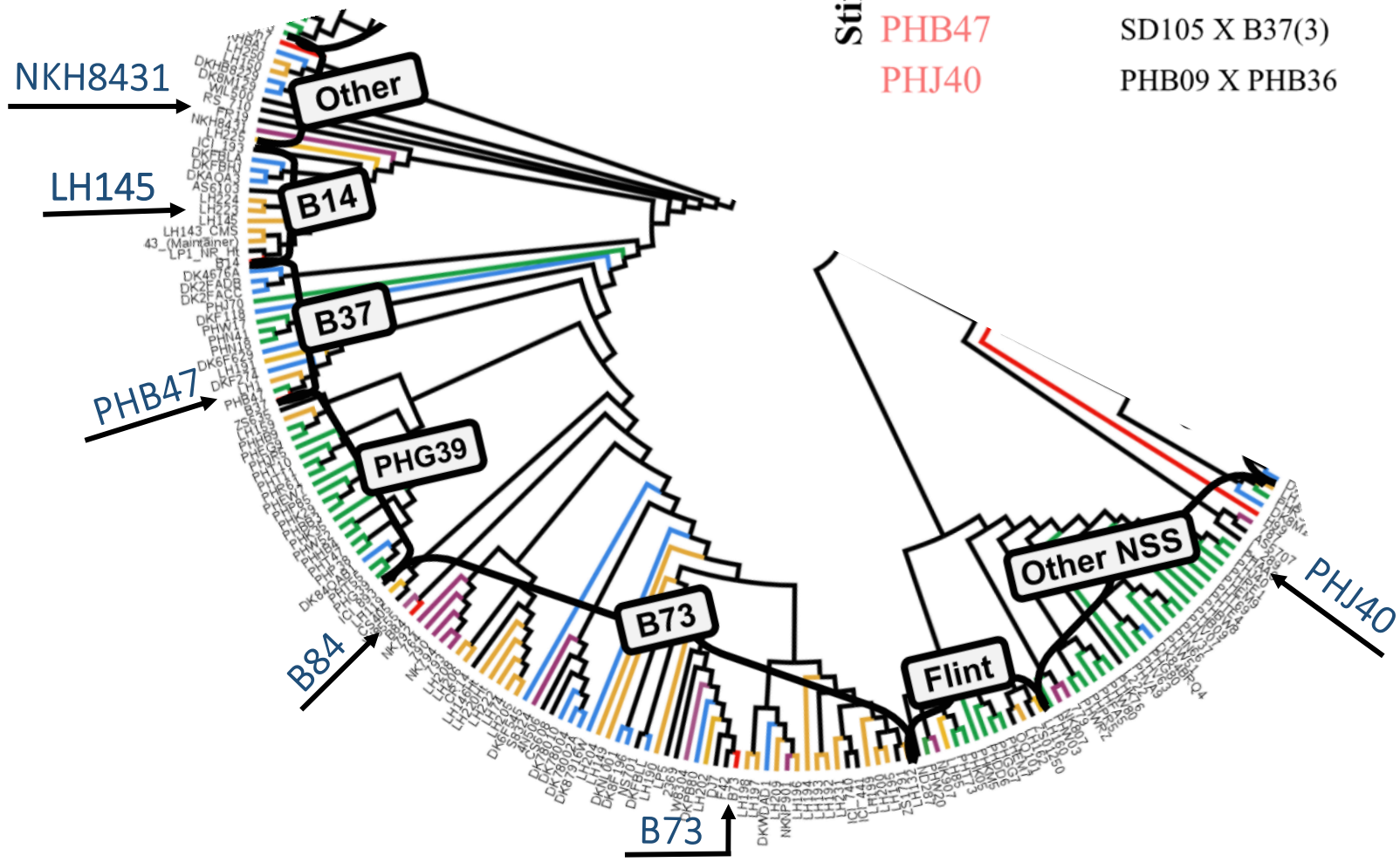
Opportunities:

- ✧ G2F has focused on developing a flexible and distributed infrastructure that can adjust to address emerging problems
- ✧ Importance of sharing unique resources and data
- ✧ Develop standards and data accessibility tools
- ✧ Work at a scale that instigates interest from interdisciplinary collaborators way beyond the plant sciences
- ✧ Develop a framework for effective interdisciplinary training

2020-21 Population:

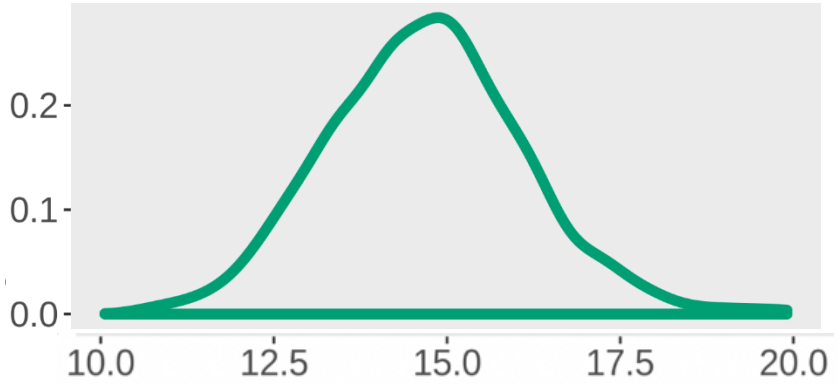
- Stiff Stalk MAGIC
- Diallel of 6 parents per population, followed by intermating of F_1 hybrids, bulked seed was randomly intermate for subsequent DH generation

Stiff Stalk		
	B73	C5 of Iowa Stiff Stalk Synthetic (BSSS)
	B84	BSSS(HT)C7
	LH145	A632Ht X CM105
	NKH8431	NK377 X NKB386 X NK347
	PHB47	SD105 X B37(3)
	PHJ40	PHB09 X PHB36

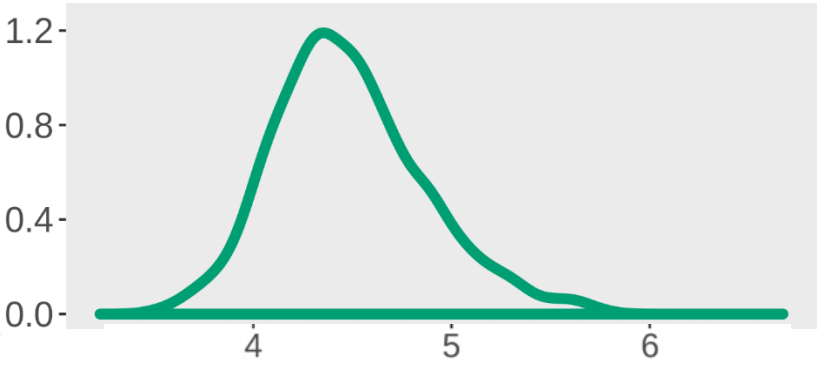


Evaluation of Stiff Stalk MAGIC Inbred Population:

Kernel Row Number



Kernel Thickness



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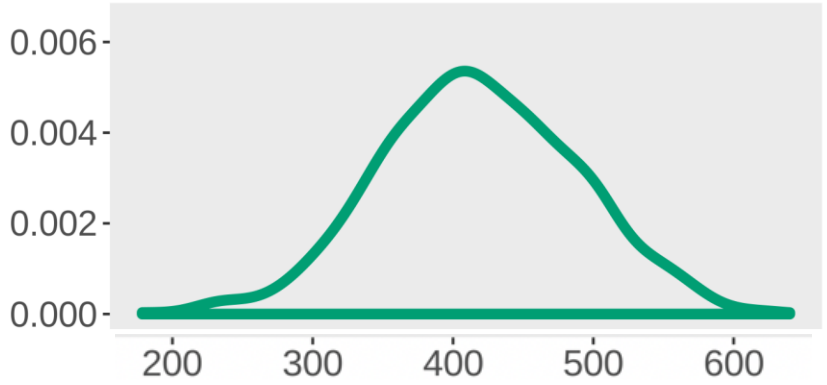

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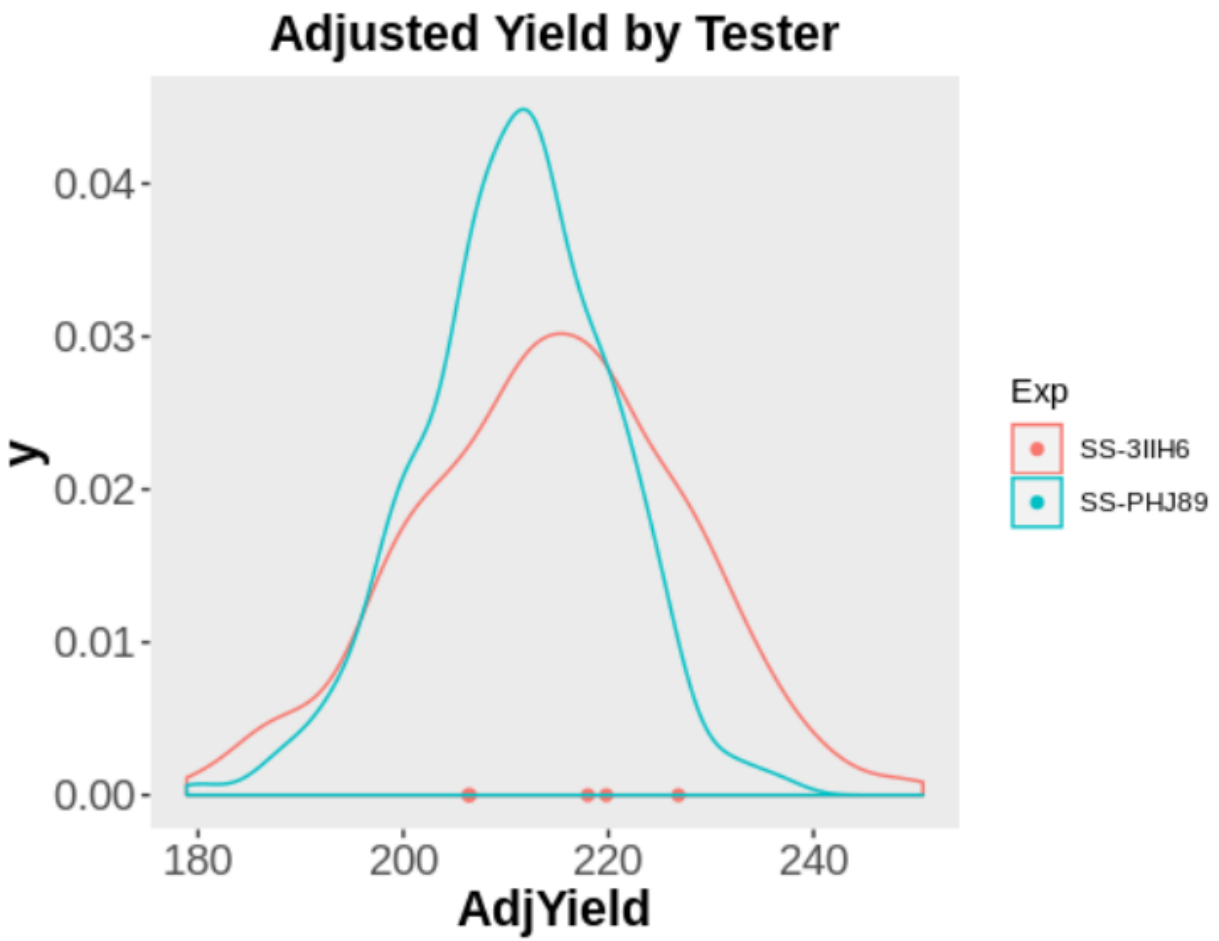
Evaluation of Stiff Stalk MAGIC Hybrids:



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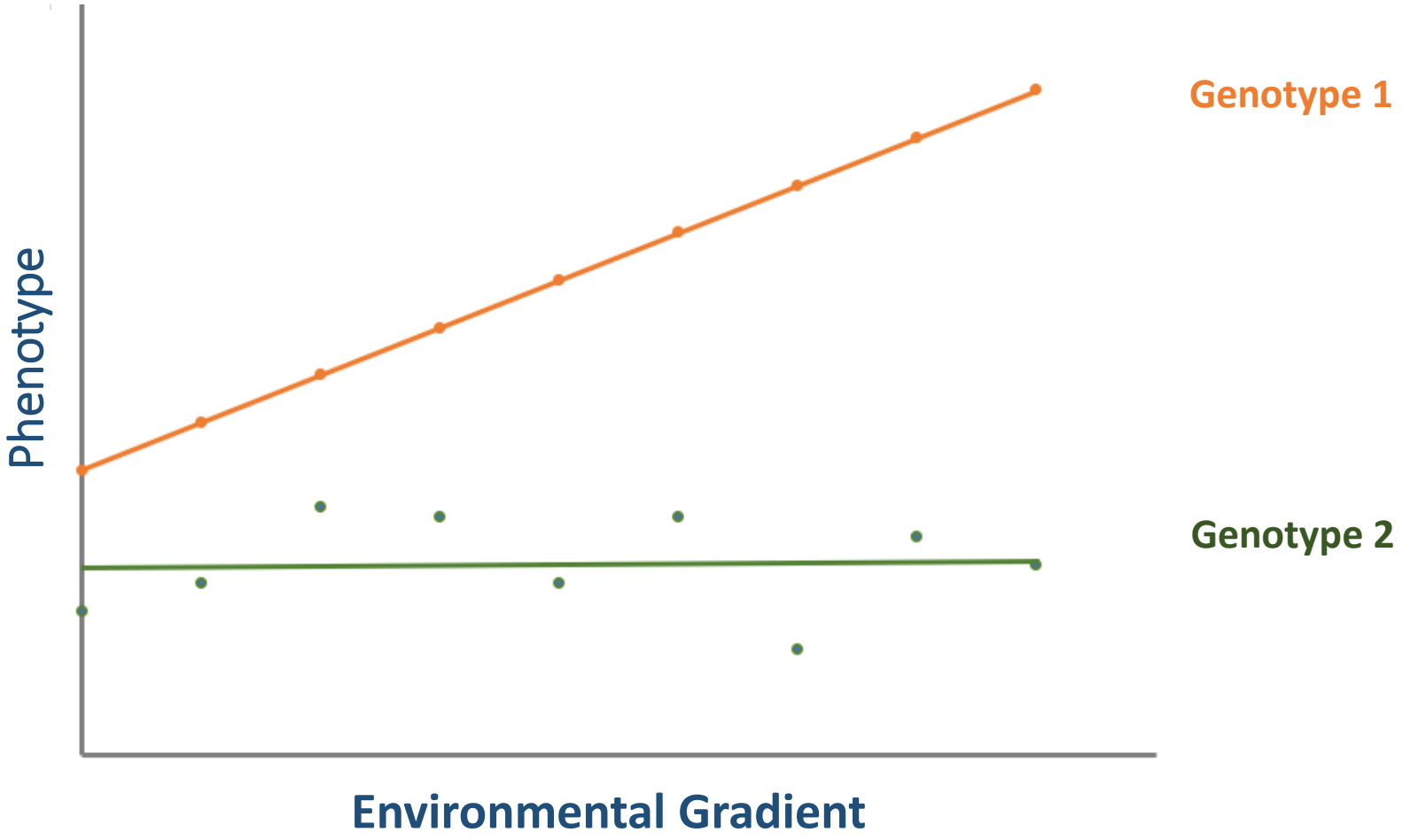
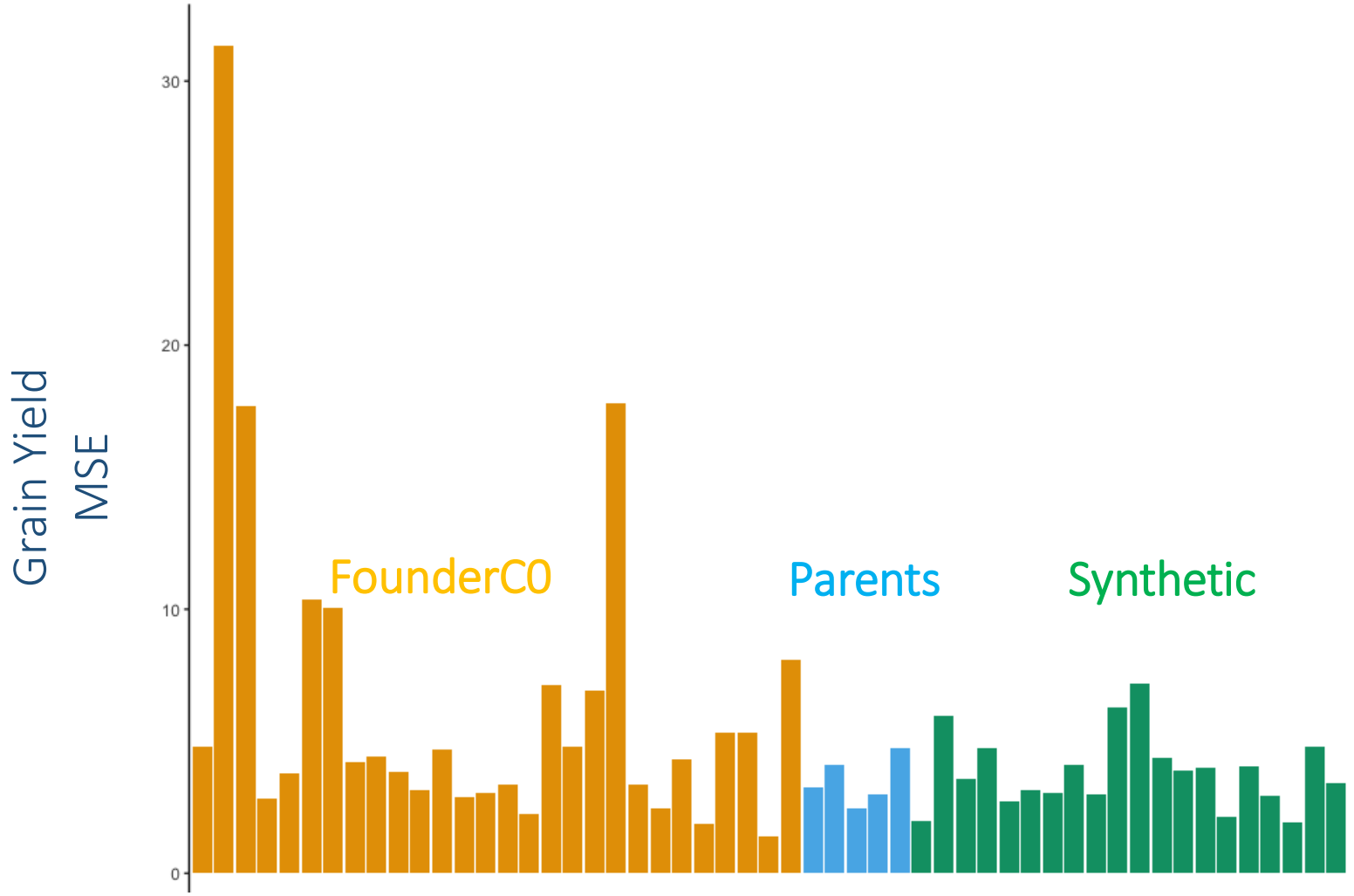
Quantifying Stability – Finlay-Wilkinson Method:



- Type I/II Stability: quantified by regression slope (0 or 1)
- Type III Stability: quantified by variance around the regression (MSE)

Recombination on Stability:



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2020-21 Plan:

- Stiff Stalk MAGIC population
- Lines genotyped with exome capture
- Set of ~375 different DHs
- Three testers:
  - **PHZ51** (Lancaster - PH814 X PH848 - late tester)
  - **PHP02** (Iodent - PHG44 X PHG29 - early tester)
  - **PHK76** (Lancaster C103 - PHAD18 X PHB02 - intermediate tester)
- Common set of checks (yellow stripe) across locations
- Approximately 30 locations in 2020
- Repeat experiment in 2021

2022-23 Plan:

- ✧ Use predictions made based on data 2014 to 2019
- ✧ Identify set of hybrids that perform well based on specific criteria
- ✧ Test set of materials based on prediction to evaluate consistency

High Intensity Phenotyping Sites (HIPS):

- ✧ Sites where specific tools, conditions or processes are used on a smaller (common set of materials) to assess utility
- ✧ Reduced number of sites use 22 Hybrids and 22 Inbreds
- ✧ Test new phenotyping technologies/methods

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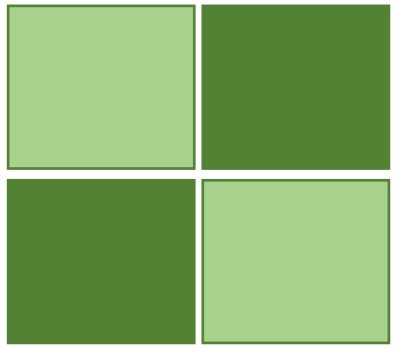
High Intensity Phenotyping Sites Germplasm:

✧ Hybrids and Inbreds suggested by the cooperators due to their relevance in other projects and activities

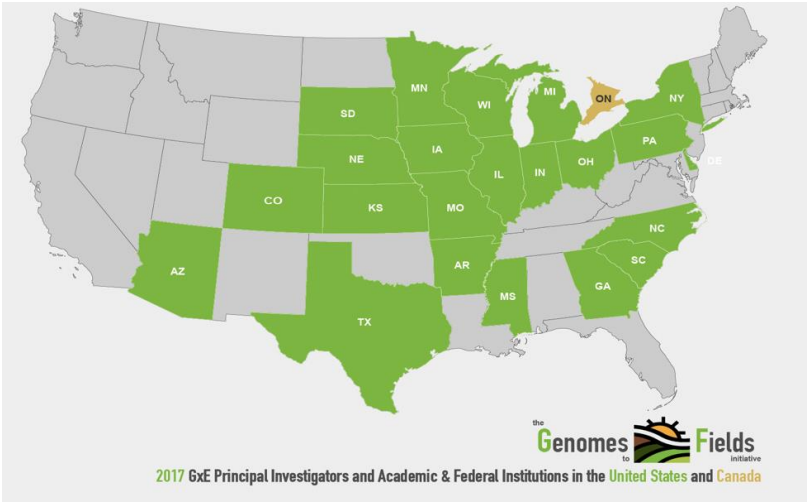
Hybrids	Hybrids	Inbreds	Inbreds
Tx714 X PHZ51	PHB47 X PHZ51	B73	PHJ89
B73 X Mo17	PHB47 X PHK76	B84	PHP02
B73 X PHN82	LH244 X Mo17	LH145	PHR03
B73 X PHZ51	LH244 X PHN82	LH185	PHRE1
B73 X PHK76	LH244 X PHZ51	LH195	PHT69
LH195 X PHZ51	LH244 X PHK76	LH82	PHTD5
LH195 X Mo17	PHJ89 X PH207	Mo17	PHW65
LH195 X PHN82	LH145 X LH82	PH207	PHZ51
LH195 X PHK76	PHG29 X PHG47	PHAJ0	Tx714
PHB47 x Mo17	PHRE1 X PHTD5	PHB47	LH244
PHB47 X PHN82	PHJ40 X PHAJ0	PHJ40	W22-Uniform Mu strain

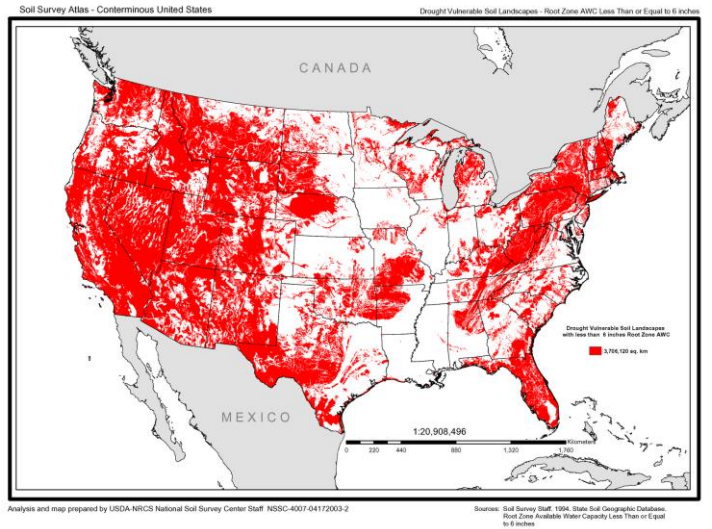
Use of Controlled Environment Testing:

- ✧ Dissect into components
- ✧ Modeling



Controlled environments





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Drones 2020:

- ✧ Pilot study involving 6 to 8 locations to fly drones over fields weekly
- ✧ Follow SOP
- ✧ Develop the data management infrastructure to gather data from geographically distributed sites
- ✧ Consolidate initial steps of data processing (QC and stitching, etc)
- ✧ Make data available initially to involved groups and then publicly

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)
- Sanzchen 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)

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