Genomes to Fields

2018/19 Project & 2020/21 Plan

ASTA G X E Cooperators' Meeting

December 5th, 2017

www.Genomes2Fields.org

Project Concept for 2018-19 Testing Years:

- ✧ Sample alleles for G X E from ex-PVP, old, and unselected pool
- ✧ Dissect Good G X E (mechanisms allowing specific adaptation) vs Bad G X E (poor performance in specific environments due to poor alleles such as disease susceptibility)

Parameters:

- Substrate for:
  - Phenotyping
  - Modeling/Genome Prediction

- Use materials with a relatively narrow maturity window
  - Reduce impact of flowering time on results
  - More uniform data
  - Simplify plot management for collaborators

- Use same genetics across all locations
  - Division of 2016-17 experiments within G X E is not fully leveraging the breadth of environments

Project Plan:

- Populations - mini-NAM DH:
  - PHW65 X PHN11 (ex-PVP x ex-PVP) – “Good” allele source
  - PHW65 X Mo44 (ex-PVP x Old) - “Bad” allele source
  - PHW65 X MoG (ex-PVP x Unselected) – “Ugly” allele source
- Tester:
  - LH195 (B37 X B73) Midwest to South
  - PHT69 (B14 X B37) for North
- Yellow Stripe hybrids (30 plots/location)
  - Accumulate G X Y data and link previous work to new locations
- Continue a small component of the ex-PVP Design II hybrids or TX714 vs B73 and NILAS testing (~100 plots at a subset of locations)

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Things to Still Think About:

- Allocation of PHT69 vs LH195 hybrids
- Proportion (10 – 20%) of hybrids replicated at each site
  - Possibly those hybrids already included in the 2014 & 15 experiment to allow calculation of G X Y estimates
  - Same hybrids replicated across locations
- Design?
  - Randomizing across populations allow direct comparison or block by population?
- Phenotyping
  - Can we implement phenotyping technologies across sites – EarthSense rover
- Mini-weather stations within canopy
  - Interest in the data?

Parameters for the G2F G X E Scientific Project - 2020/21 and Beyond Plan:

- ✧ Research should be founded on relevant research questions
- ✧ Materials (germplasm) used should be publicly available
- ✧ We need to be able to generate hybrid seed for (at least) 500 plots across (at least) 35 locations within the needed timeframe
- ✧ Generate good experiments: minimize the potential for external confounding factors on performance (experiments that fall apart, maturity, tester, etc)

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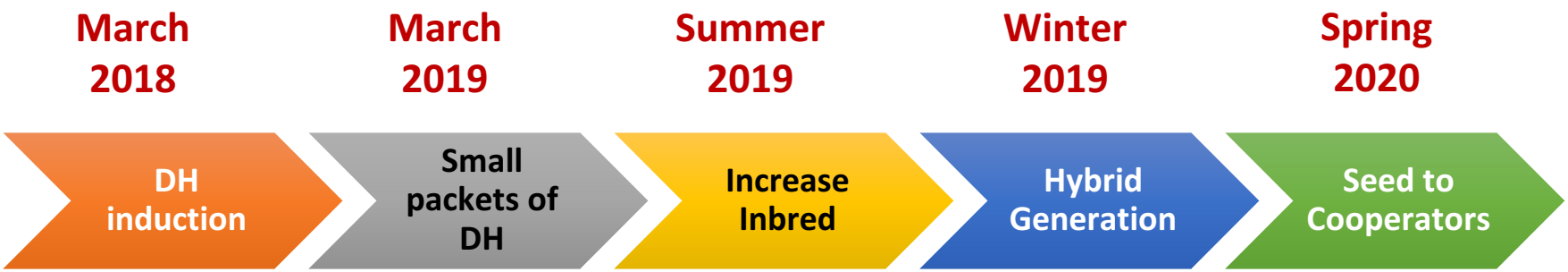
Proposal for G2F G X E Science Project & Timeline:

- ✧ Can we characterize Midwest alleles well enough to determine the value of exotic alleles for productivity
- ✧ The idea is that molecular information allows us to determine what is different but not necessarily what is useful
- ✧ Immediately:



- ✧ Longer term: Develop a germplasm generation infrastructure that provides useful resources to the community over time

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Proposed Plan: North America Germplasm-Based Genetic Modelling and Allele Characterization

Core Inbred pool
ex-PVP and public breeding inbreds

Stiff Stalk
- ex-PVP
- Public

Non-Stiff Stalk
- ex-PVP
- Public

Iodent
- ex-PVP
- Public

New Allele Sources
- GEM selects
- Particular lines from cooperators (yield component traits)
- Donations from industry screening
- Other sources

- Model per se allelic effects
  - Prediction of breeding crosses
  - Prediction of "ideal" inbreds
- Hybrid Prediction
- Traits of focus
- GxE
- Integrating phenotyping, etc.

- Determine how to characterize alleles in the context of Core Inbred Pool
  - Genetic context
  - Recombination/resolution
  - Managed biotic and abiotic stress targets

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A Start:

STIFF STALK SET	PHBW8 *PHJ40 type*	3AZA1 *B14 type*	PHB47 *B37 type*	FBLL *B73 type*
GEMS-0061 *Cristalino Colorado*	DH1	DH2	DH3	DH4
GEMS-0113 *Tuxpeño*	DH5	DH6	DH7	DH8
GEMS-0219 *GEM x GEM derived*	DH9	DH10	DH11	DH12
GEMS-0227 *Inbred-tropical*	DH13	DH14	DH15	DH16

NON STIFF STALK SET	PHP02 *Iodent type*	PHJ89 *PHT77 X PHG47*	PHN46 *PH848/814 /595 type*	LH212Ht *Mo17 type*	PHK76 *PHK76 type*
GEMN-0096 *Hybrid-tropical*	DH17	DH18	DH19	DH20	DH21
GEMN-0097 *Mixed*	DH22	DH23	DH24	DH25	DH26
GEMN-0192 *Tusón*	DH27	DH28	DH29	DH30	DH31
GEMN-0225 *Composite (Suwan)*	DH32	DH33	DH34	DH35	DH36

Other Things to Consider:

- ✧ Is there value on evaluating similar sets of materials across environments

- ✧ Utility of managed locations to identify extreme genotypes for testing

- ✧ Deploying common technologies across sites

Deliverables:

- 2014 data publication - Nature Communications 8: 1348 (2017)
- Summary of 2014-15 data – Diego Jarquin & Aaron Lorenz
- Others:
  - Inbred evaluation - Celeste Falcon
  - 2014-2016/7 – hybrid combined analysis – Jim Holland & Anna Rogers
  - Maize Atlas NILAS project – Randy Wisser
  - NIL data – Zhi Li, Candy Hirsch & Nathan Springer
  - BSSS experiment – Bridget McFarland
  - Stalk lodging GWAS – Alex Lipka
  - ”Yellow Stripe” manuscript – Liz Lee
  - Diallel set – Jode Edwards, Liz Lee, Martin Bohn

Field Season	Release to Collaborators (ARK)	Release to Public (DOI or ARK)
2014		http://dx.doi.org/10.7946/P2201Q
2015	February 2017	https://doi.org/10.7946/P24S31
2016	March 2017	ARK
N	March of N+1	March of N+2
Ears Imaging		Through Cyverse

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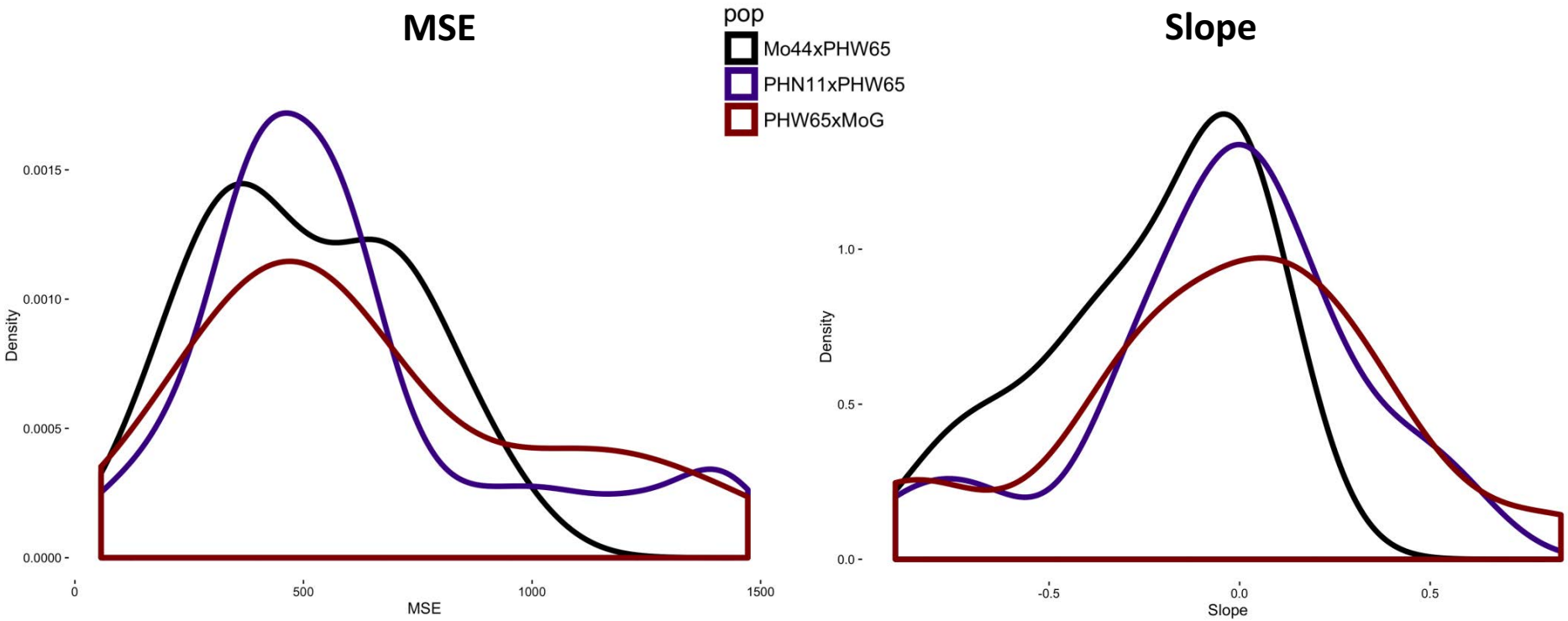
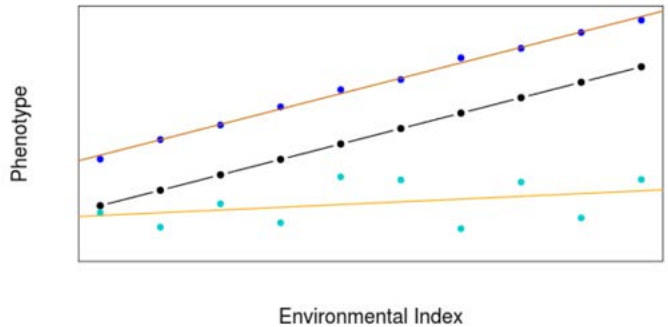
2014/15 Summary – Hybrids Span Range of Slope and MSE Across Testers – Grain Yield:



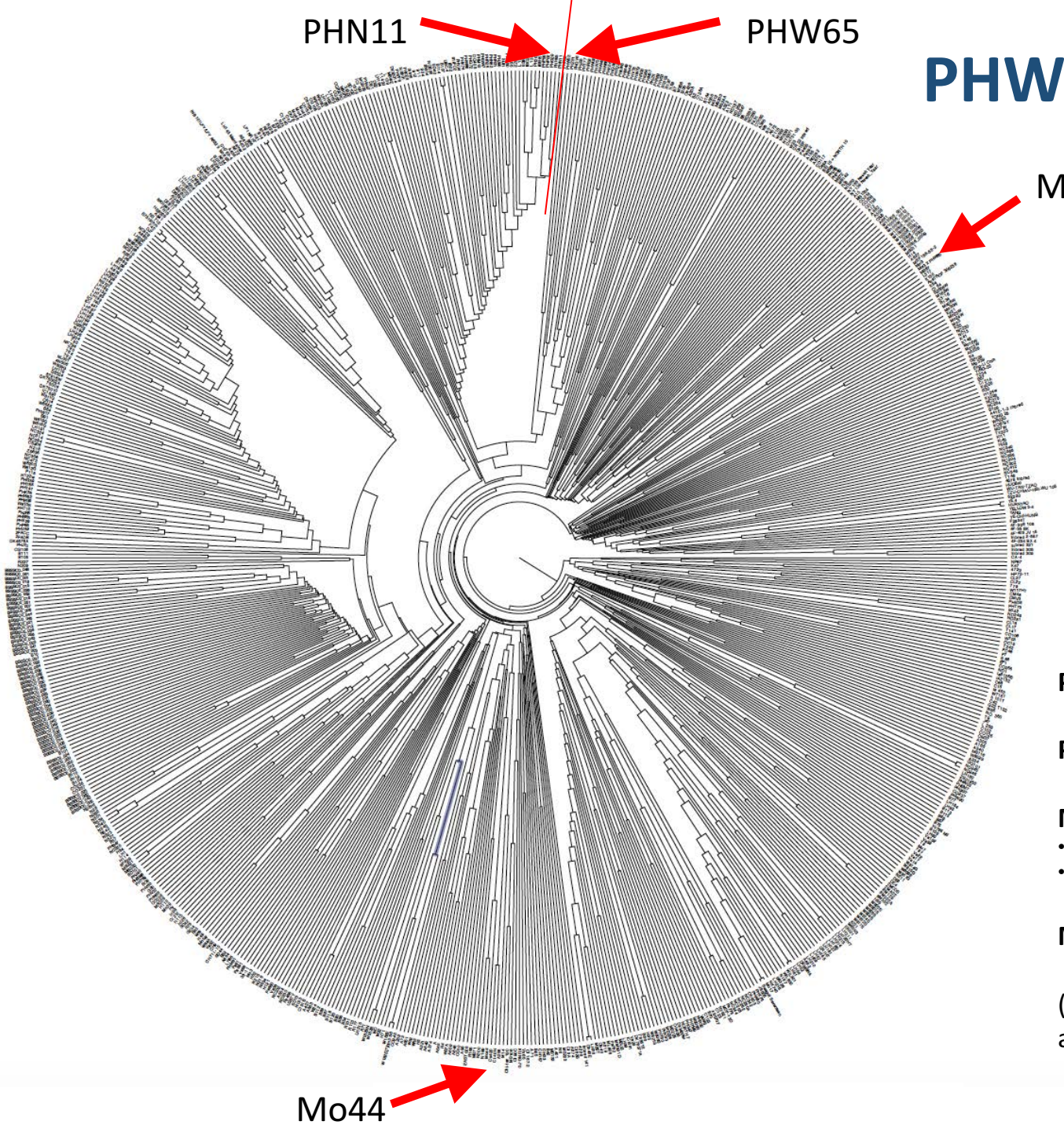
- 6 to 8 location per hybrid



2016 Testcross Data: 313 lines by PHB47

	Yield (bu/A)			Moist (%)		
	AVE	MAX	MIN	AVE	MAX	MIN
PHN11 X PHW65	183.4	135.8	208.5	17.8	16.2	19.4
Mo44 X PHW65	177.7	134.6	204.0	18.1	16.1	19.6
PHW65 X MoG	166.1	134.6	193.6	17.8	16.1	19.3

PHW65 Populations



PHW65: PH861 X PH595

PHN11: PH806 X PH207(2)

Mo44: Mo22 X Pioneer Mex Syn 17

- Mo22: Laguna
- Mo18W (NAM Parent): Wf9 x Mo22(2)

MoG: Mastadon

(All lines resequenced; PH207 assembly)

PHW65 Populations – ex-PVPs Comparison:

PHW65: PH861 x PH595

PHN11: PH806 x PH207(2)

Mo44: Mo22 x Pioneer Mex Syn 17

- Mo22: Laguna
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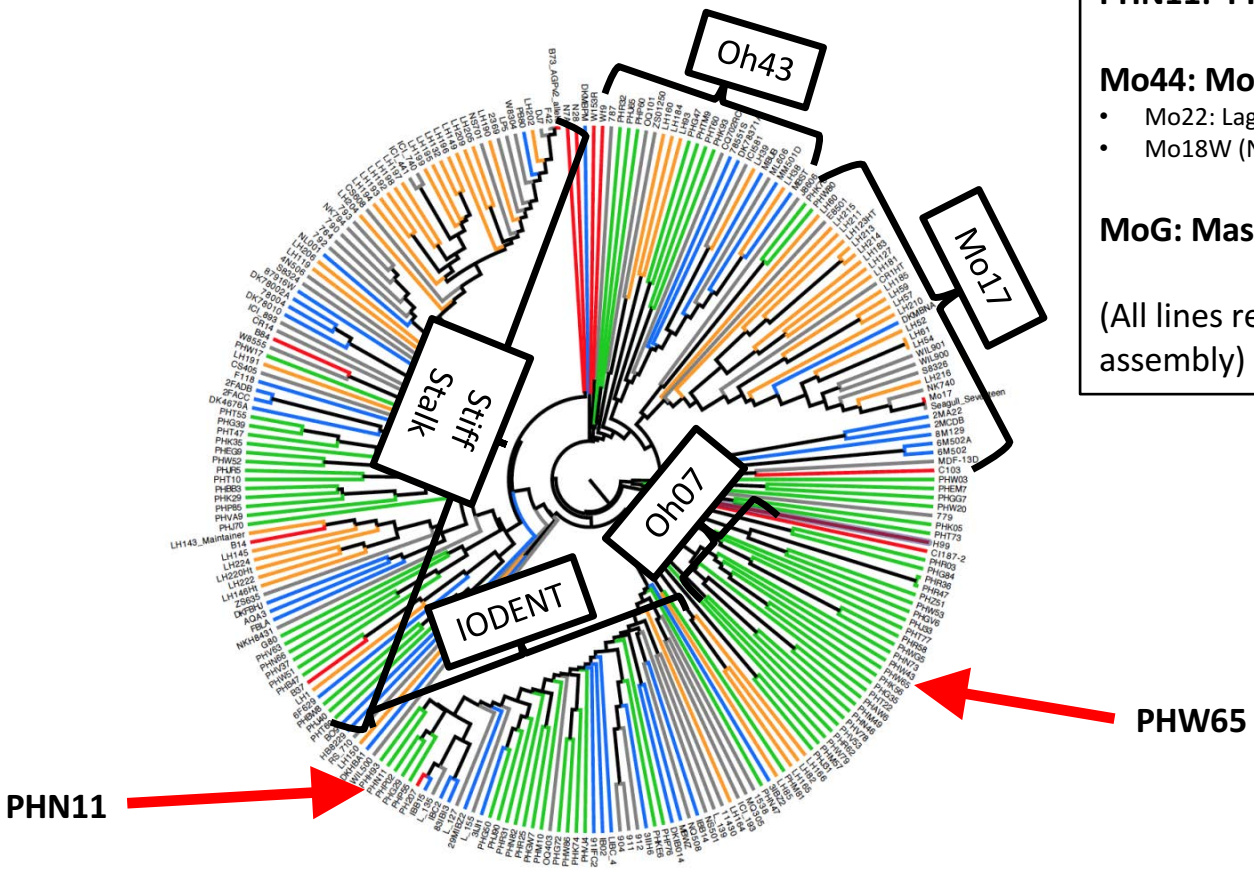
(All lines resequenced; PH207 assembly)



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