

A horizontal banner with a white background. On the left and right sides are vertical panels, each containing a stylized DNA double helix with blue and green strands. The central part of the banner features a landscape illustration of rolling green hills under a light blue sky with a yellow sun. The text "Genomes to Fields" is written across the center in a large, bold, dark blue serif font.

# Genomes to Fields

## G X E 2018/19 Maize Project Proposal

ASTA G XE Organizational Meeting  
December 8<sup>th</sup>, 2016

[www.Genomes2Fields.org](http://www.Genomes2Fields.org)

# Parameters:

- ✧ Substrate for:
  - ✧ Phenotyping
  - ✧ Modeling/Genome Prediction
- ✧ Minimal barriers to sharing seed and data
- ✧ 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
  - ✧ Utilize early testers to adapt to northern sites
- ✧ Experiment should be founded in hypotheses/concepts
  - ✧ Links to previous years is helpful
- ✧ Must be possible to produce large amounts of hybrid seed reliably

# Proposal:

- ✧ PHW65 mini-NAM DH populations (400 plots/location)
  - ✧ Concepts:
    - ✧ 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)
  - ✧ Populations:
    - ✧ 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
- ✧ Continue a component of the ex-PVP Design II hybrids or NIL component for additional years (~70 plots/location)
  - ✧ Accumulate G X Y data and link previous work to new locations
- ✧ Select Yellow Stripe hybrids (30 plots/location)
  - ✧ Accumulate G X Y data and link previous work to new locations
  - ✧ Minimize extremes in flowering

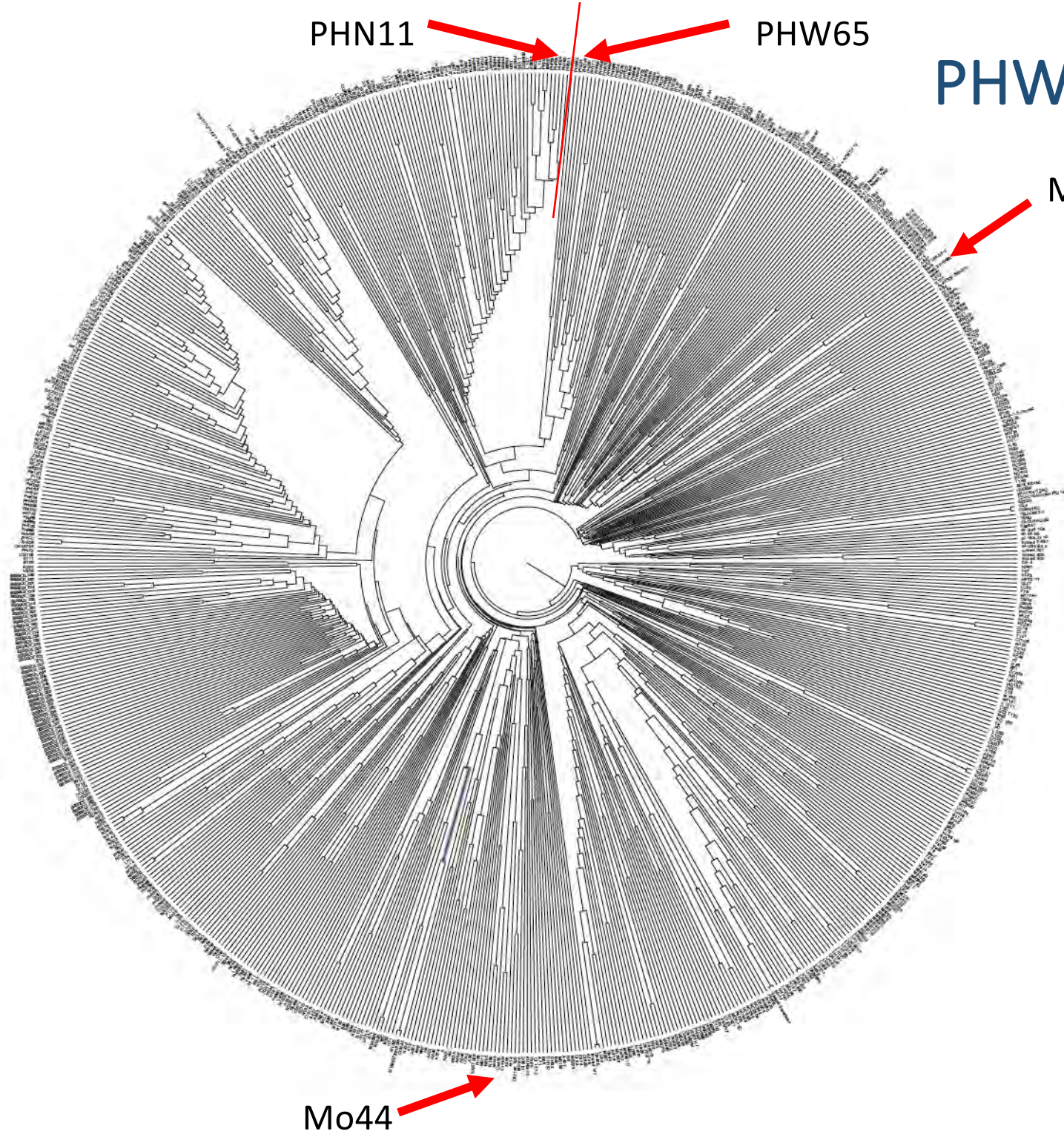
# The Challenge with Extreme Flowering



Photo from Byron Good



# PHW65 Populations



**PHW65: PH861 X PH595**

**PHN11: PH806 X PH207(2)**

**Mo44: Mo22 X Pioneer Mex Syn 17**

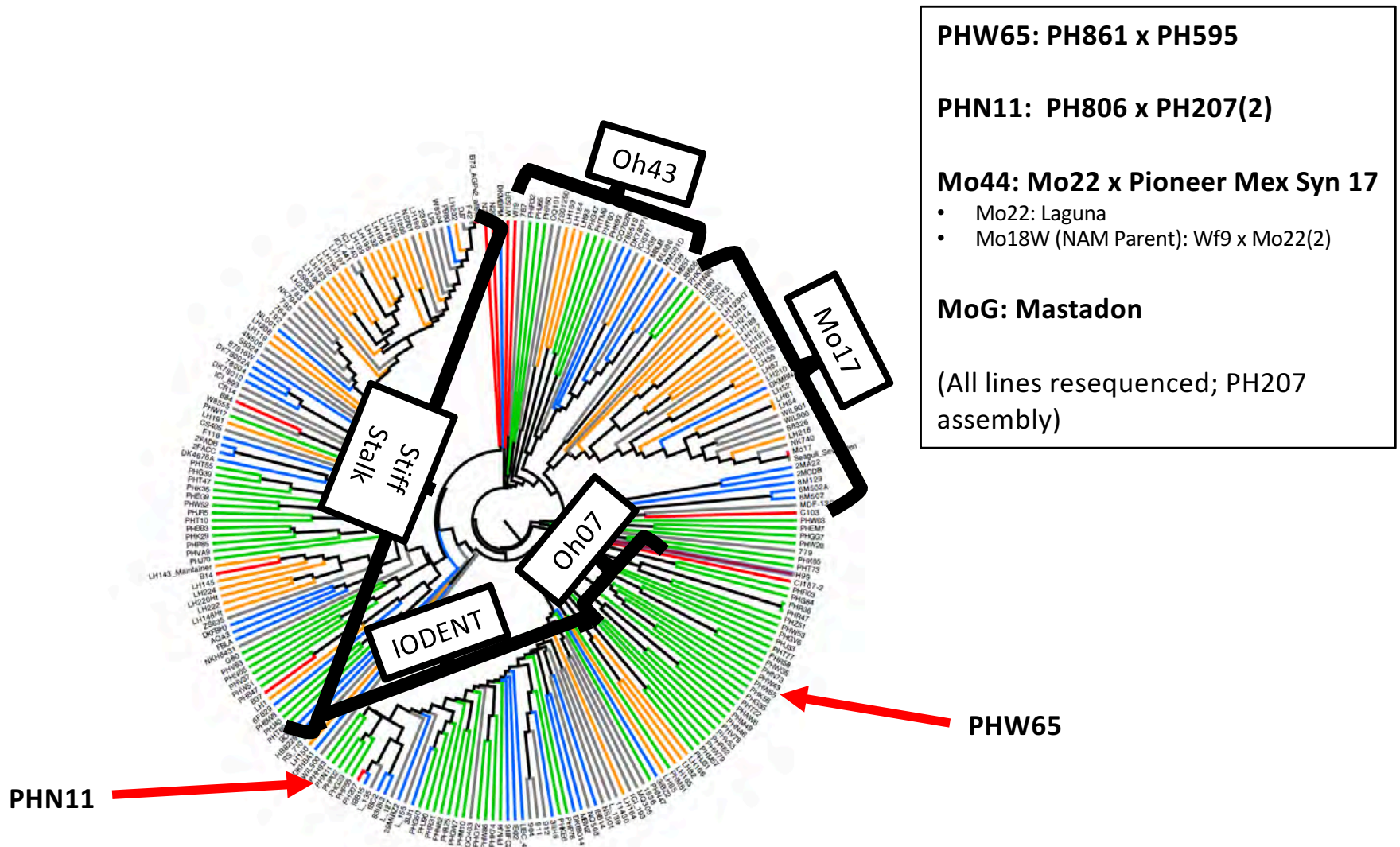
- Mo22: Laguna
- Mo18W (NAM Parent): Wf9 x Mo22(2)

**MoG: Mastadon**

(All lines resequenced; PH207 assembly)



# PHW65 Populations – ex-PVPs Comparison:



**PHW65: PH861 x PH595**

**PHN11: PH806 x PH207(2)**

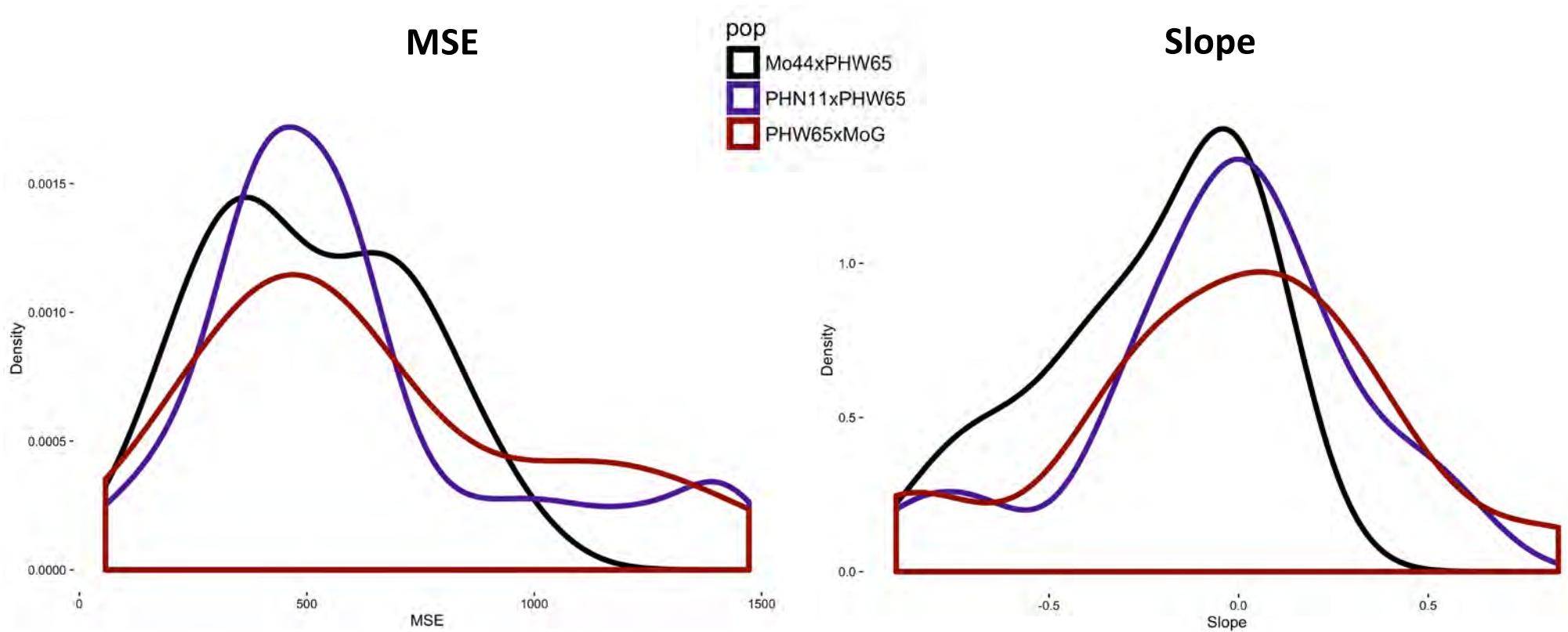
**Mo44: Mo22 x Pioneer Mex Syn 17**

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

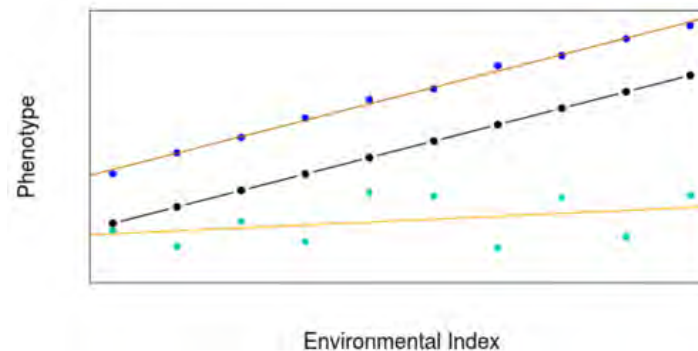
**MoG: Mastadon**

(All lines resequenced; PH207 assembly)

# 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





## Dissecting Slope and MSE across pops & testers:

Tester	Slope	MSE	No. of Env.
LH195	1.13	604	13
PB80	1.07	436	10
LH185	1.00	587	13
LH198	0.93	634	15
CG102	0.19	611	16

# Proposed Experiment:

- ✧ Tester:
  - ✧ LH195 (B37 X B73) Midwest to South
  - ✧ Early SS (TBD) for North
- ✧ 10 to 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 hybrids from three groups allows direct comparison
  - ✧ But, blocking by material will likely make a more uniform trial...
- ✧ Data
  - ✧ Regular performance data
  - ✧ Can we implement any uniform phenotyping among more sites with this?
- ✧ Continue set of common hybrids to maintain connections across years and increasing years of data on a subset of hybrids
- ✧ Analysis – NAM QTL – any details to highlight
  - ✧ Also, identify specific lines and extreme groups for further more detailed mechanistic analysis

