



2022/23 Experiment Plan and Open Discussion

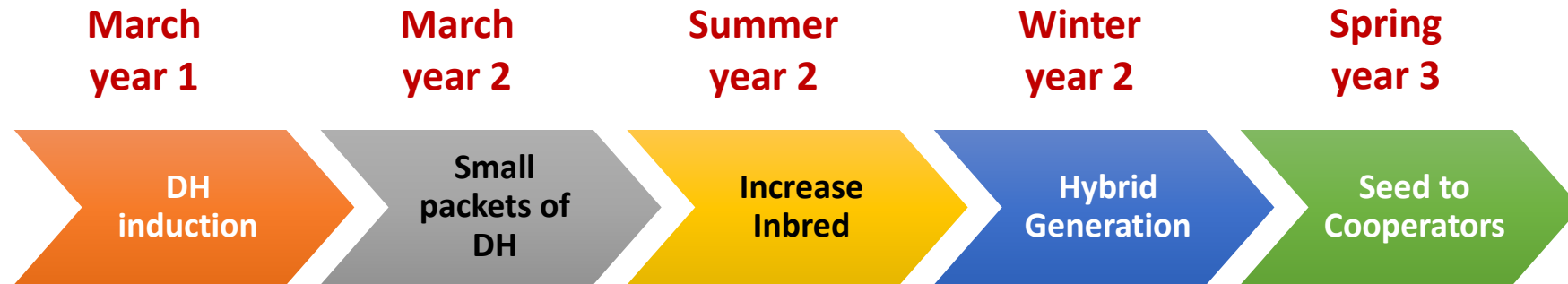
Natalia de Leon
G2F Cooperators Annual Meeting

Chicago, IL
December 10th, 2019

www.Genomes2Fields.org

Timeline for Germplasm Development:

✧ Super Fast Track:



✧ More Reasonable:

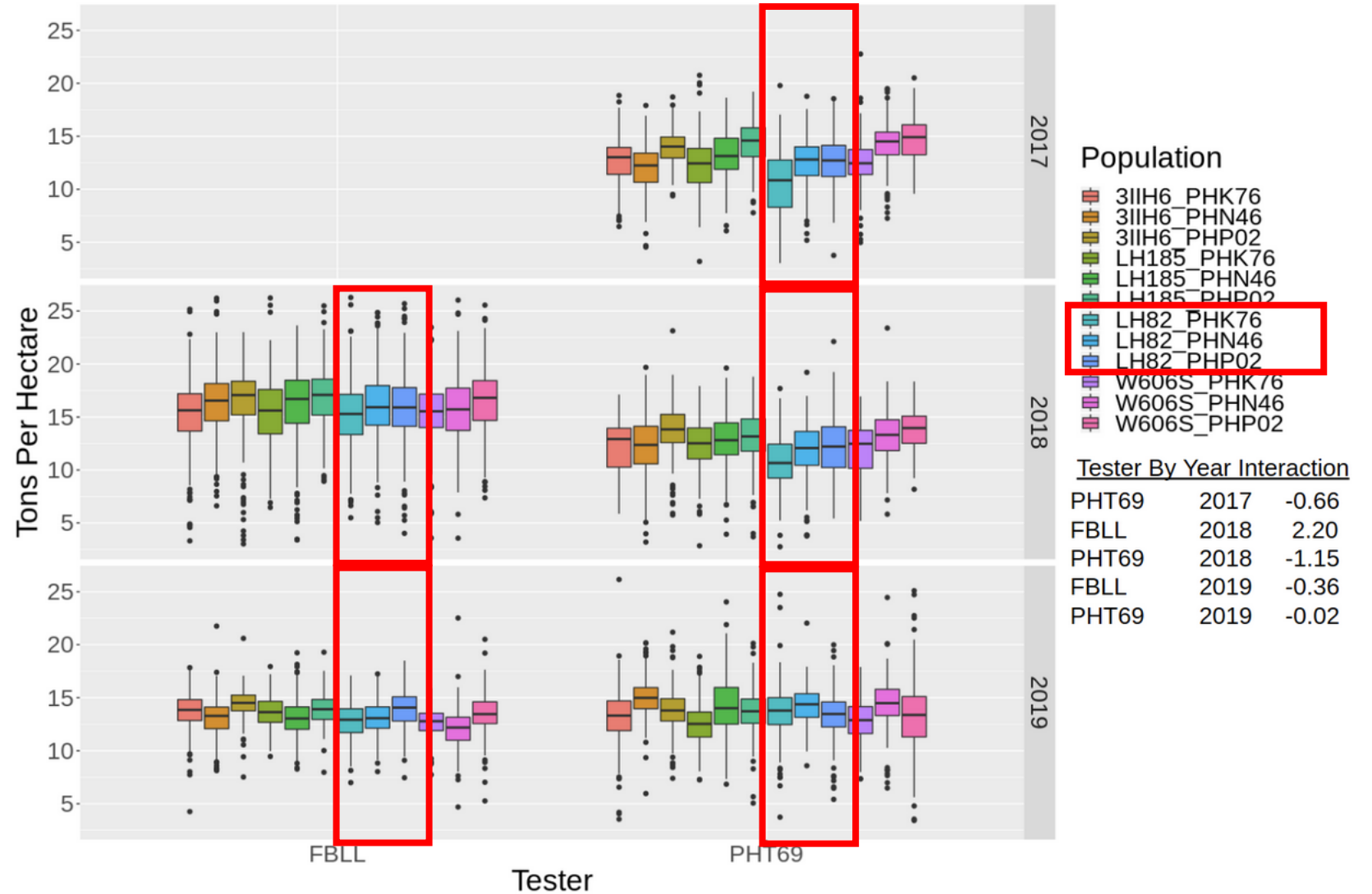


✧ Longer-term: Develop a germplasm generation infrastructure that provides useful resources to the community over time

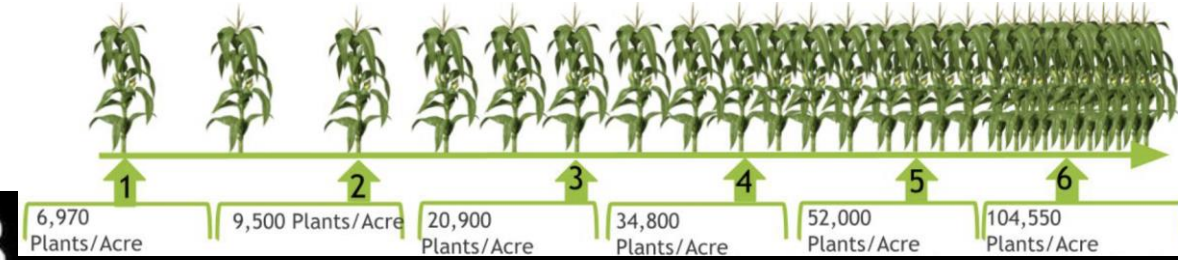
Plan for 2022-23 – alternative 1:

- ❖ Mini NAM involving LH82 crossed by PHK76, PHN46 and PHP02
- ❖ DH derived from F₂ bulk with in-kind support by AgReliant Genetics, LLC
- ❖ cross by relevant tester (e.g. PHT69 and FBLL)

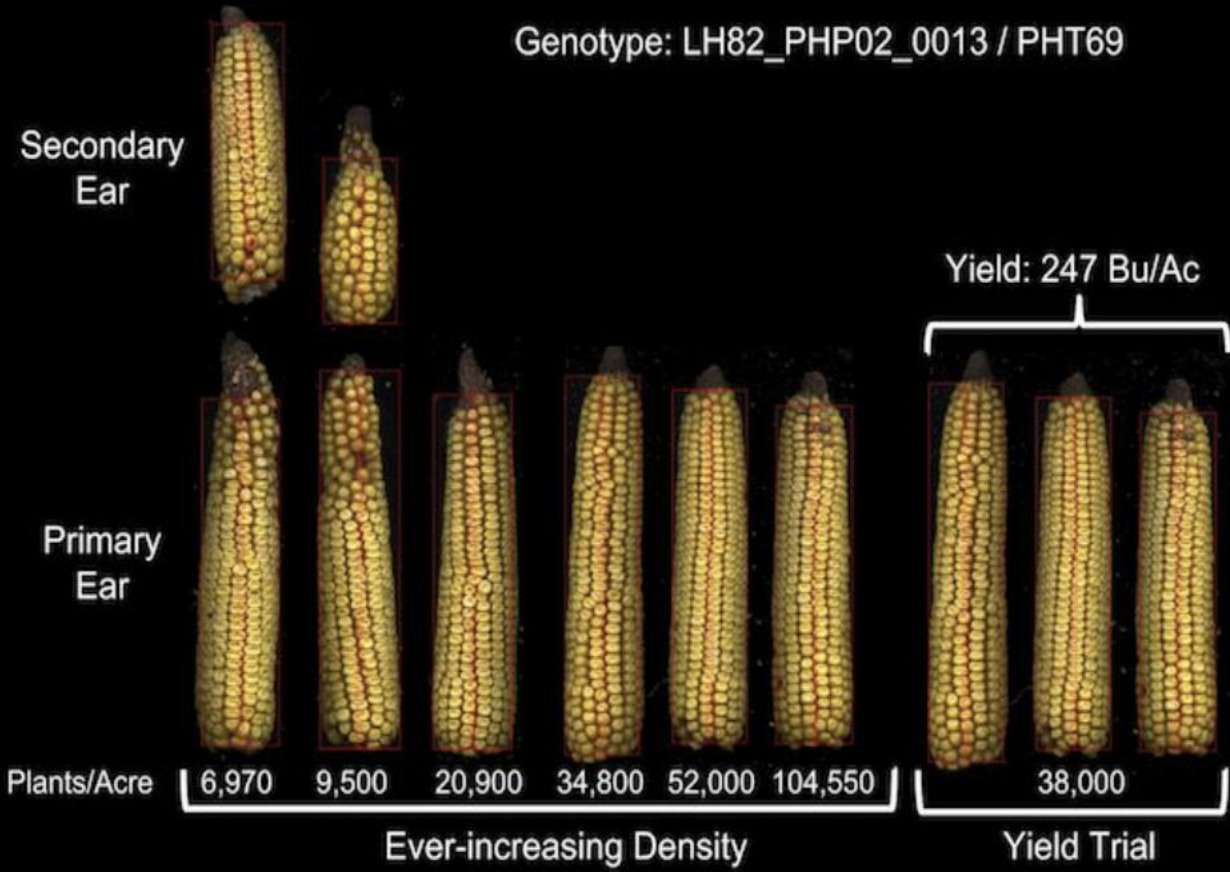
Grain Yield Year Effect



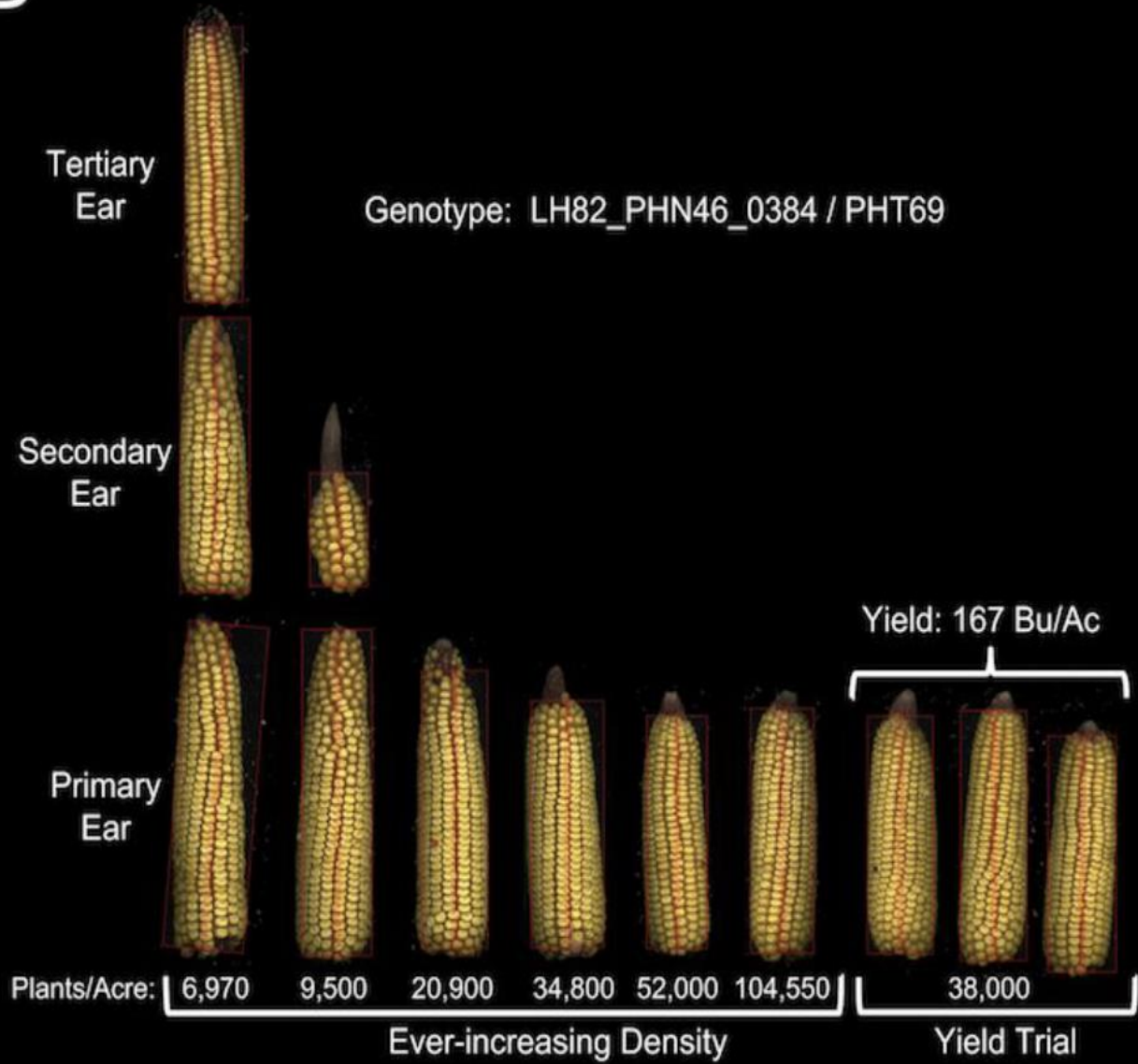
LH82 Mini NAM Example:



A



B



Plan for 2022-23 – alternative 2:

- ❖ BGEM population with PHB47 and PHZ51 (Vanous et al, 2017 - Plant Genome 11:170083 - doi: 10.3835/plantgenome2017.09.0083)
- ❖ Diverse panel of exotic derived doubled haploid lines derived from BC₁F₁
- ❖ 252 DH representing 54 different maize races

Table 1. Summary statistics of flowering and plant architecture traits for PHZ51 derived, PHB47 derived, and combined PHZ51/PHB47 derived BGEM lines.

Group†	Trait	RP‡§	Mean¶	Minimum¶	Maximum¶	Range¶	SD‡¶	h ² (SE)
PHZ51 derived BGEM Lines	GDUSHD	1481.6	1545.5	1407.6	1712.1	304.4	60.2	–
	GDUSLK	1507.7	1591.8	1426.2	1764.3	338.1	74.5	–
	ASI	-28.3	-46.3	-121.1	21.8	142.8	33.7	–
	RSHDSLK	1.0	1.0	0.9	1.0	0.1	0.02	–
	PH	181.8	182.0	143.2	246.6	103.4	16.0	–
	EH	66.4	72.1	50.3	110.9	60.6	10.2	–
	AEPH	115.6	110.0	89.8	146.3	56.5	10.1	–
REHPH	0.4	0.4	0.3	0.5	0.2	0.03	–	
PHB47 derived BGEM Lines	GDUSHD	1473.7	1528.9	1368.1	1718.7	350.6	63.6	–
	GDUSLK	1488.4	1557.8	1409.0	1719.6	310.6	61.9	–
	ASI	-14.6	-29.9	-120.4	21.1	141.5	26.4	–
	RSHDSLK	1.0	1.0	0.9	1.0	0.1	0.02	–
	PH	179.9	179.3	134.9	221.9	87.0	14.8	–
	EH	63.0	68.9	43.4	96.1	52.8	9.3	–
	AEPH	117.1	110.7	90.9	137.7	46.7	8.9	–
REHPH	0.4	0.4	0.3	0.5	0.2	0.03	–	
Combined	GDUSHD	–	1535.9	1368.1	1718.7	350.6	62.6	0.93 (0.09)
	GDUSLK	–	1572.2	1409.0	1764.3	355.3	69.4	0.94 (0.09)
	ASI	–	-36.8	-121.1	21.8	142.8	30.7	0.90 (0.09)
	RSHDSLK	–	1.0	0.9	1.0	0.1	0.02	0.90 (0.09)
	PH	–	180.4	134.9	246.6	111.7	15.3	0.90 (0.09)
	EH	–	70.2	43.4	110.9	67.5	9.8	0.88 (0.09)
	AEPH	–	110.4	89.8	146.3	56.5	9.4	0.87 (0.09)
REHPH	–	0.4	0.3	0.5	0.2	0.03	0.83 (0.09)	

† Group, PHZ51 derived BGEM Lines, corresponds to the 98 BEM lines with PHZ51 as the recurrent parent. PHB47 derived BGEM Lines corresponds to the 134 BGEM lines with PHB47 as the recurrent parent. Combined, 232 BGEM lines were used in GWAS.

‡ RP, recurrent parent; SD, standard deviation.

§ RP corresponds to groups' respective recurrent parent. Values listed are trait least-square means of recurrent parent.

¶ Values are estimated from trait BLUPs of n lines within each group. n = 98, PHZ51; n = 134, PHB47.

Plan for 2024-25:

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

- ✧ Most useful population structure (biparental, MAGIC, factorial)?
- ✧ Scale - Appropriation of Genomes to Phenomes could mean moving to 5,000 plots per location?
- ✧ Value of evaluating similar sets of materials across environments
- ✧ Research Questions?

Other Things to Consider:

- ✧ Value of evaluating similar sets of materials across environments
- ✧ Utility of managed locations
- ✧ Deploying common technologies across sites