# Genomic Selection Using Maize ex-PVP Germplasm for the Prediction of N-use Traits

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#### Introduction:

- Nitrogen use efficiency (NUE) in maize (*Zea mays* L.) is an important trait to help feed the world with minimal environmental impact.
- Current breeding and biotechnological approaches have failed to develop a maize hybrid with optimal NUE.
- Genomic selection for N-use traits may speed up the breeding cycle of research programs targeting improvements in maize NUE.

### **Genomic Selection Approach:**

- **Data Analysis:** Breeding value for each hybrid (GCA's + SCA) was calculated for different phenotypic NUE traits (Figure 3) using REML<sup>a</sup>.
- **G-BLUP**<sup>b</sup>: Untested hybrids were predicted using the genetic covariance matrix of untested and tested hybrids ( $C_{UT}$ ), the phenotypic covariance matrix of tested hybrids ( $C_{TT}$ ), and the estimated breeding value. The genomic coefficient<sup>c</sup> of each inbred was computed to the  $C_{UT}$  and  $C_{TT}$  matrices.
- **Cross-Validation**<sup>d</sup>: Three cross-validation methods changing the training set (TS) composition were compared using 1,000 iterations:
  - 1. TO: hybrids in which none of their parents were included in the TS or the



#### **Objectives:**

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- Identify genomic prediction accuracy for different Nuse traits in maize using G-BLUP.
- Evaluate the impact of training population sizes and training composition for effective application of genomic prediction of NUE traits in maize breeding programs.

## **Materials and Methods:**

522 single-cross hybrids derived from 91 ex-PVP inbreds (33 SSS and 58 NSS) adapted to the U.S. Corn Belt (Figure 1) were tested in 10 environments during 2011 and 2016 (Figure 2).
On average, each SSS and NSS line was tested with 9 and 15 hybrids, respectively.

validation set (VS).

2. T1: hybrids in which one of their parents were included in the TS and VS.

3. T2: hybrids in which both of their parents were included in the TS and VS. In each cross validation method, a random subset of the T2 hybrids were used to predict either the T0, T1, or the remaining T2 hybrids.

#### **Results:**

Prediction accuracy increased 20% when the training composition changed from T0 to T1 and 17% when training composition changed from T1 to T2 hybrids when averaged across phenotypic traits and training sizes (Table 1).
Lower H<sup>2</sup> under low N compared to high N was probably due to higher soil heterogeneity (e.g. NHI<sub>LOWN</sub>).

Yield<sub>LowN</sub> and HI<sub>LowN</sub> exhibited the highest prediction accuracy under low N.
Yield<sub>HighN</sub> and Protein<sub>HighN</sub> exhibited the highest accuracy under high N.
NUE, NUPE, and NUtE were positively correlated to Yield<sub>HighN</sub> (Table 2).
GU and HI (low and high N) were positively correlated to Yield<sub>LowN</sub>.



**Figure 3.** N-use traits evaluated for genomic selection: N-Use Efficiency (NUE), Nutilization efficiency (NUtE), N-Uptake Efficiency (NUpE), and Genetic Utilization (GU). Harvest Index (HI), N-harvest index (NHI), and grain protein concentration were measured at low and high N conditions. Plant biomass (BM) and N concentration were measured at physiological maturity.

**Table 1.** Genomic prediction accuracy of T0, T1, and T2 hybrids (averaged across training set sizes). Training set was constituted from a constant number of SSS and NSS lines (16 and 30, respectively). Broad-sense heritabilities (H<sup>2</sup>) were estimated from ex-PVP maize hybrids grown across 10 environments at two levels of fertilizer N.

Trait	Т0	T1	T2	Range	<b>H</b> <sup>2‡</sup>
<b>Yield</b> <sub>LowN</sub>	0.36	0.56	0.75	0.31/0.96	0.30
<b>Yield<sub>HighN</sub></b>	0.28	0.53	0.73	0.22 / 0.93	0.60
NUE	0.11	0.31	0.43	0.07 / 0.66	0.59
NUpE	0.16	0.34	0.45	0.12 / 0.67	0.27
NUtE	-0.16	0.17	0.36	-0.17 / 0.45	0.11
GU	0.19	0.44	0.61	0.08 / 0.98	0.58
<b>Protein</b> <sub>LowN</sub>	0.16	0.37	0.69	0.15 / 0.90	0.71
<b>Protein<sub>HighN</sub></b>	0.20	0.36	0.52	0.18 / 0.71	0.78
<b>HI</b> LowN	0.44	0.61	0.73	0.32 / 0.98	0.63
<b>HI<sub>HighN</sub></b>	0.24	0.36	0.45	0.19 / 0.65	0.71
<b>NHI</b> LowN	-0.30	-0.19	-0.18	-0.23 / -0.15	0.12
<b>NHI<sub>HighN</sub></b>	0.14	0.33	0.44	0.10/0.73	0.73



**Figure 1.** Principal component analysis (PCA) of 91 ex-PVP maize lines using 26,768 SNP's. Colors represent the origin of the different lines.



**Table 2.** Phenotypic correlations between yield and N-use efficiency (NUE), N-uptake efficiency (NUpE), N-utilization efficiency (NUtE), genetic utilization (GU), and grain protein concentration, harvest index (HI), and nitrogen harvest index (NHI) at both low and high N.

					Prot	Protein		HI		NHI	
	NUE	NUpE	NUtE	GU	Low N	High N	Low N	High N	Low N	High N	
<b>Yield</b> <sub>LowN</sub>	-0.38 <sup>+</sup>	NS	NS	0.67	-0.39	NS	0.64	0.53	NS	0.53	
<b>Yield<sub>HighN</sub></b>	0.74	0.63	0.46	NS	NS	-0.38	-0.35	NS	NS	NS	
<sup>+</sup> Pearson coefficients indicate significance at $P \le 0.001$ , NS indicate non-significant correlations.											

# **Conclusions:**

Changes in prediction accuracy as a result of training population and composition was dependent on the N use trait.

Both GU and HI<sub>LowN</sub> exhibit high prediction accuracy and correlation to Yield<sub>LowN</sub>. These traits may be integrated into maize breeding <sup>+</sup>Accuracy was calculated by dividing the correlation of predicted and observed values by the square root of H<sup>2</sup>. Training set sizes were 30, 50, 70, and 90 hybrids for yield, NUE, and grain protein, and 10, 20, 30, and 40 hybrids for NUpE, NUtE, GU, HI, and NHI. Range represents lowest and highest prediction accuracy across TS sizes and composition. <sup>‡</sup> H<sup>2</sup> was estimated on a entry mean basis<sup>e</sup>.



# **Future Research:**

Integrating the genotype by environment effect into genomic selection models may improve the prediction accuracy of low heritability traits (e.g. NUtE).

#### **References:**

a) Bernardo, R., 1996 Best linear unbiased prediction of maize single-cross performance. Crop Sci. 36: 50-56.

**Figure 2.** Hybrids were evaluated at two N fertilizer rates (0 and 252 kg N ha<sup>-1</sup>) in a RCB design: (a) number of environments planted across 3 locations in Illinois, (b) Infrared image detected from an UAV camera. Dark- and light-orange represent high and low N fertilizer treatments, respectively.

programs targeting improved performance under low N conditions (Figure 4).

Similarly, NUE and NUpE are desirable traits in breeding programs developing hybrids for agricultural systems using high N fertilizer inputs. b) Henderson, C., 1973 Sire evaluation and genetic trends. J. Anim. Sci. 1973: 10-41.

c) VanRaden, P.M., 2008 Efficient methods to compute genomic predictions. J. Dairy Sci. 91: 4414-4423.

d) Technow, F., Schrag, T. A., Schipprack, W., Bauer, E., Simianer, H., Melchinger, A.E., 2014 Genome properties and prospects of genomic preidiction of hybrid performance in a breeding program of maize. Genetics. 197:1343-1355.

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