

# Choosing the Best Vegetation Index for Use in Nitrogen Use Efficiency Selection in Winter Wheat

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## INTRODUCTION

- Nitrogen use efficient (NUE) crops are needed due to environmental impacts and high nitrogen (N) costs.
- Traditional phenotyping methods for NUE are labor intensive and destructive.
- Canopy spectral reflectance (CSR) can be used as a proxy for physical sampling.
  - Data is collected in a short time period with low labor requirements.
  - Measurements are non destructive and repeatable.

## OBJECTIVES

- Examine relationship between vegetation indices and measures of plant productivity for use in NUE phenotyping.
- Test ability of vegetation indices to discriminate genotypes.

## MATERIALS

### Plant Material

Hard Winter Wheat Association Mapping Panel

- 299 genotypes
- 2 check genotypes

Located near Ithaca, NE in 2012 and 2013

- Split plot augmented design
  - Whole plot: two nitrogen treatments 44 and 88 kg ha<sup>-1</sup> residual + applied
  - Subplot: 299 genotypes arranged in incomplete blocks of 20 entries plus 2 check plots
- Two replications
- Plot size: 4 rows, 3m long with 30.5 cm spacing.

### Equipment

- A two inter-calibrated Ocean Optics USB2000+VIS-NIR spectrometer system developed by CALMIT was used to measure downwelling and upwelling radiation simultaneously.
- Spectral Resolution: 0.4 nm; 350.02 to 1011 nm.

### Measures of Plant Productivity

- Anthesis biomass: 2 x 30cm row
- Anthesis and maturity date: Julian date
- Plant height: cm
- Grain weight: g/ m<sup>2</sup>
- Grain N yield = (grain yield) x (N concentration)

## METHODS

- 2012
  - CSR measured at 4 point measurements in center two rows of plot.
  - Data recorded in first replication of trial.
- 2013
  - CSR measured by continuous scanning of center two rows of plot.
  - Data recorded in both replications of trial.

### Vegetation Indices

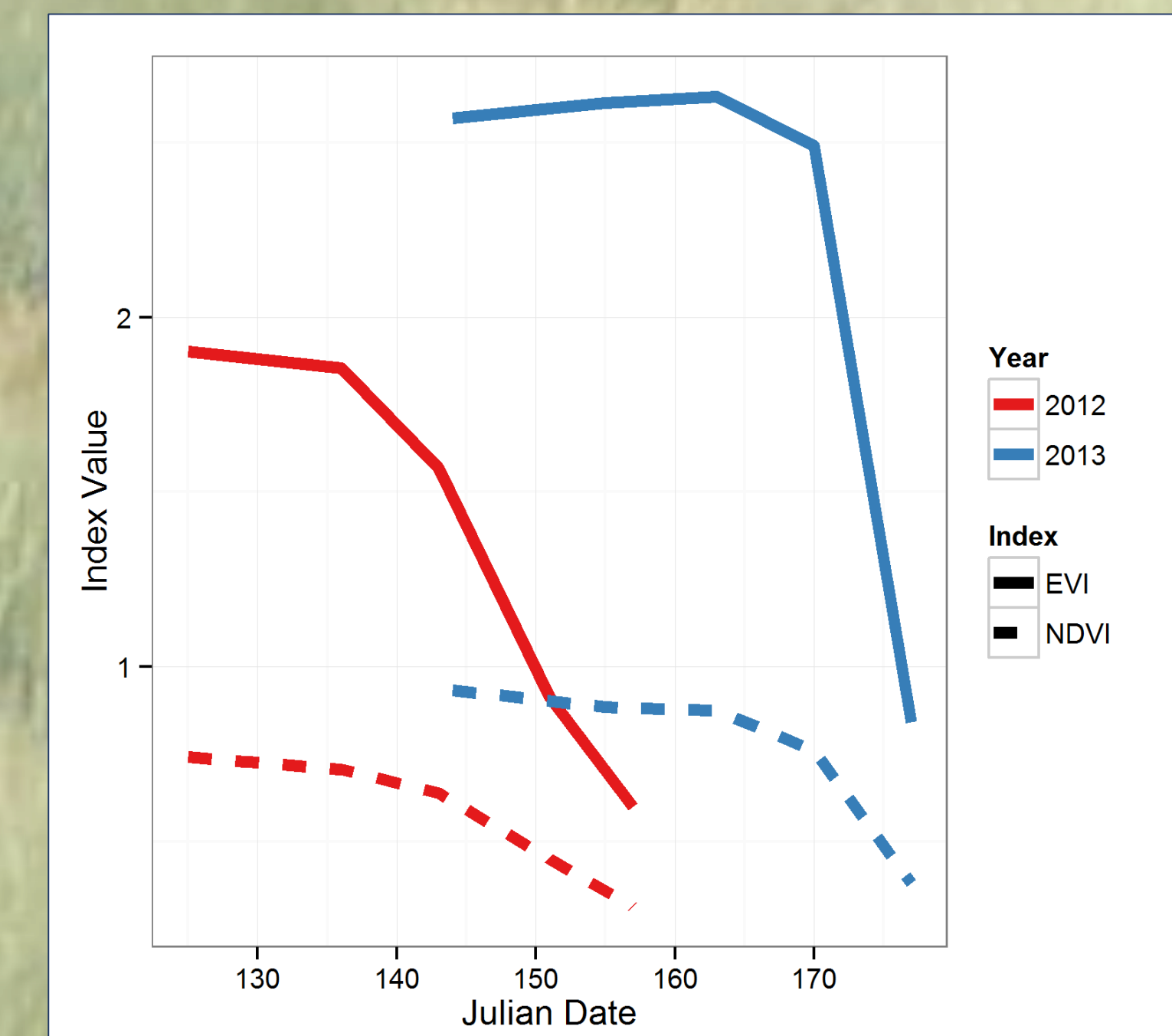
All vegetation indices calculated in T3 database (<http://triticaletoolbox.org/>) according to formula shown in Table 1.



**Table 1:** Vegetation indices used

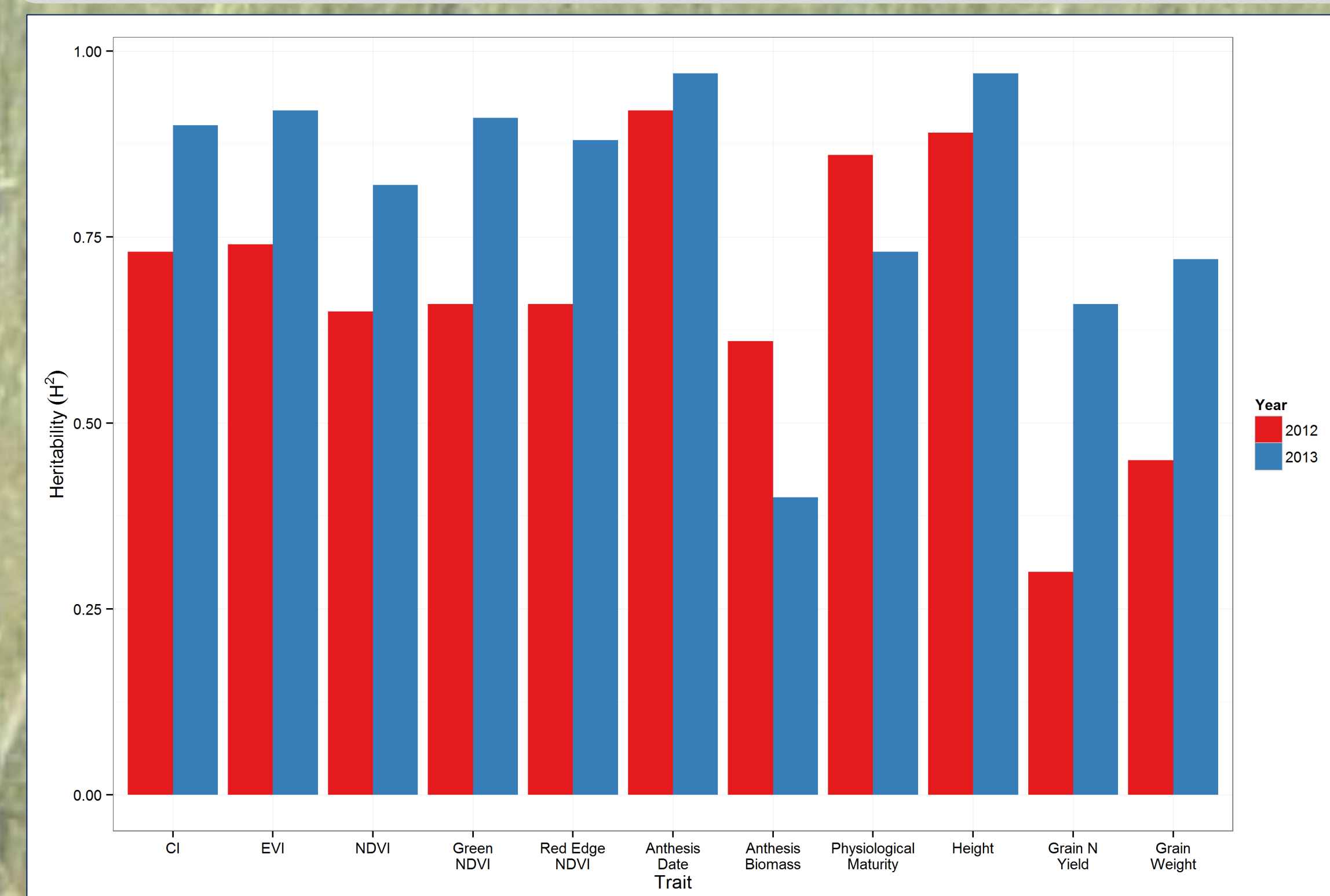
Acronym	Index	Formula	Reference
NDVI	Normalized difference vegetation index	$\frac{R_{890} - R_{670}}{R_{890} + R_{670}}$	Rouse et al. (1973)
NDVIg	Green normalized difference vegetation index	$\frac{R_{750} - R_{550}}{R_{750} + R_{550}}$	Gitelson et al. (1996)
EVI	Enhanced vegetation index	$\frac{2.5(R_{NIR} - R_{RED})}{(R_{NIR} + 6R_{RED} - 7.5R_{BLUE} + 1)}$	Huete et al. (2002)
CI	Chlorophyll index	$\left(\frac{R_{NIR}}{R_{GREEN}}\right) - 1$	Gitelson et al. (2003,2005)

**Figure 1.** EVI and NDVI season curves for check genotype Jagger in 2012 (red) and 2013 (blue).

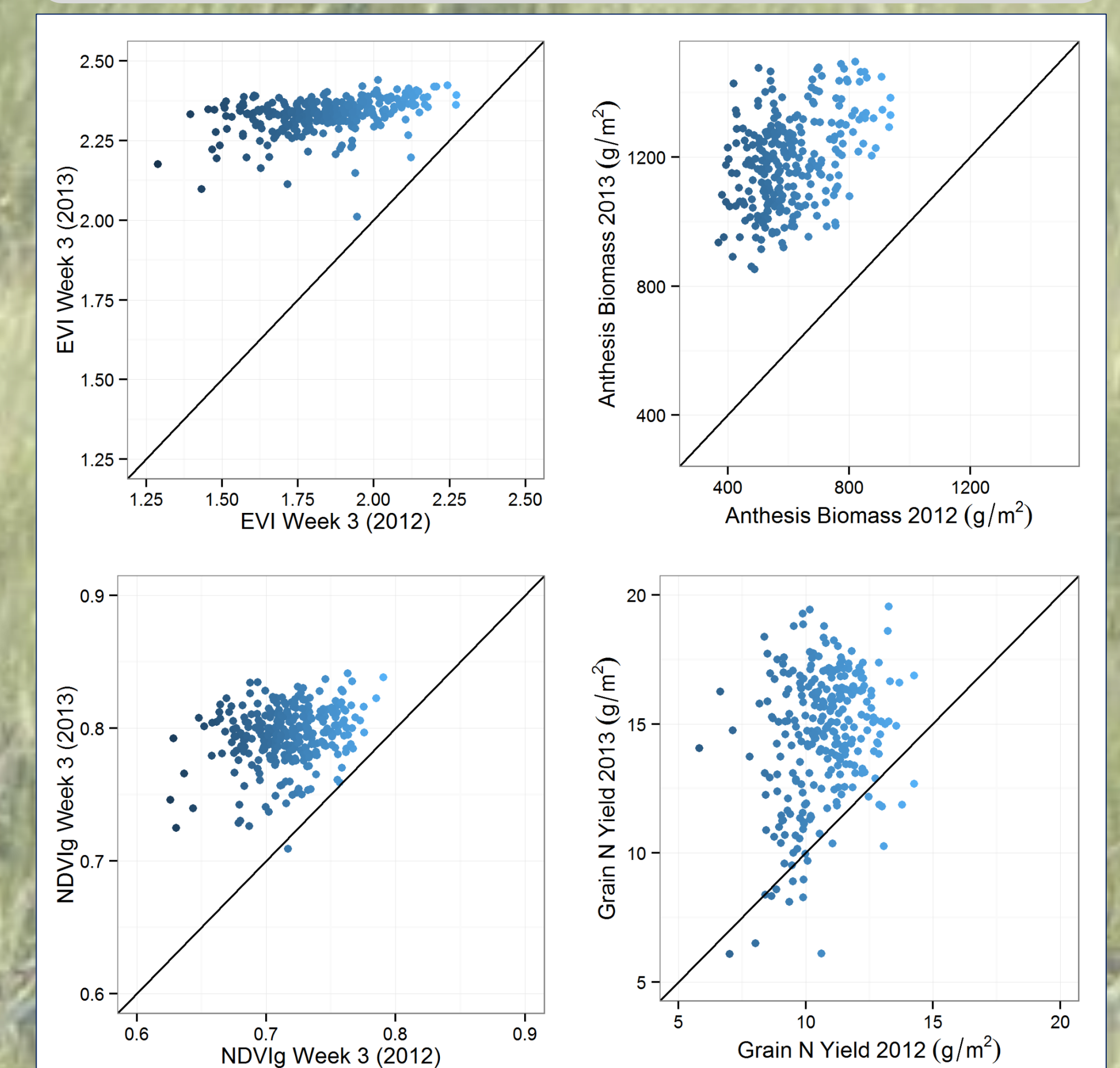


## RESULTS

**Figure 2.** Entry mean heritability of VI and plant productivity parameters in 2012 (red) and 2013 (blue).



**Figure 3.** EVI, NDVIg, Anthesis Biomass, and Grain N Yield in 2012 regressed on 2013 values.

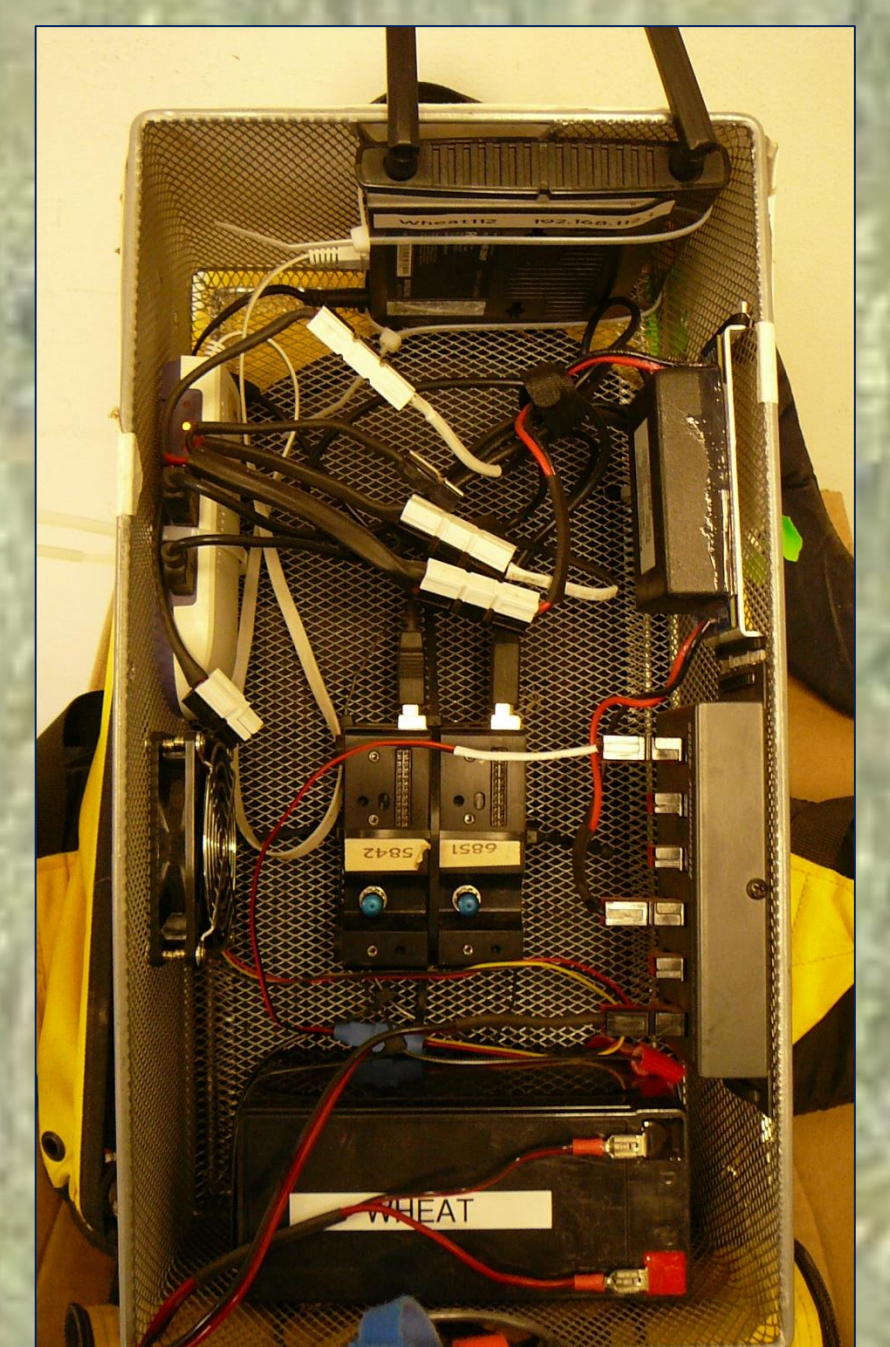


**Table 2:** Correlations of VI in 2012 and 2013 at Week 3 with plant productivity measures (N=278)

	Year	Anthesis Date	Anthesis Biomass	Plant Height	Grain N Yield	Grain Weight	Maturity Date
CI†	2012	0.591***	0.533***	0.372***	0.437***	0.480***	0.634***
EVI	2012	0.722***	0.656***	0.572***	0.344***	0.426***	0.737***
NDVI	2012	0.659***	0.611***	0.548***	0.363***	0.430***	0.681***
NDVIg	2012	0.603***	0.551***	0.429***	0.436***	0.484***	0.642***
NDVIre	2012	0.652***	0.605***	0.553***	0.361***	0.427***	0.670***
CI	2013	0.067ns	0.044ns	-0.229***	0.434***	0.481***	0.247***
EVI	2013	0.283***	0.212**	0.150**	0.127*	0.150**	0.365***
NDVI	2013	0.222**	0.132*	-0.099ns	0.287***	0.348***	0.373***
NDVIg	2013	0.060ns	0.022ns	-0.216**	0.434***	0.484***	0.257***
NDVIre	2013	0.200**	0.126*	-0.078ns	0.304***	0.357***	0.126***

## CONCLUSIONS

- The most predictive VI differed in the two years due to environmental effects.
  - Yield limiting environment (2012): EVI had the highest heritability and had high correlations with plant productivity parameters.
  - Optimal yield environment (2013): VI had highly heritability but were less sensitive to genotype differences. Alternative VI or analysis methods are needed.



†Pearson  $r^*$  =  $p < 0.05$ , \*\* =  $p < 0.01$  \*\*\* =  $p < 0.001$

