GWAS and genomic prediction for nitrogen use efficiency in tropical maize

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Team, partners, and support

ESALQ-USP

Tropical corn for the second growing season

8PhD Candidates
2 Undergrad Student
1 technician

Companies that we have GS projects together

EMBRAPA (*Brachiaria and Beans*)
IAC - *Coffee*
Helix Seeds – *Tropical Corn*
GDM Seeds - *Soybean*

Partners

CIMMYT
Jose Crossa

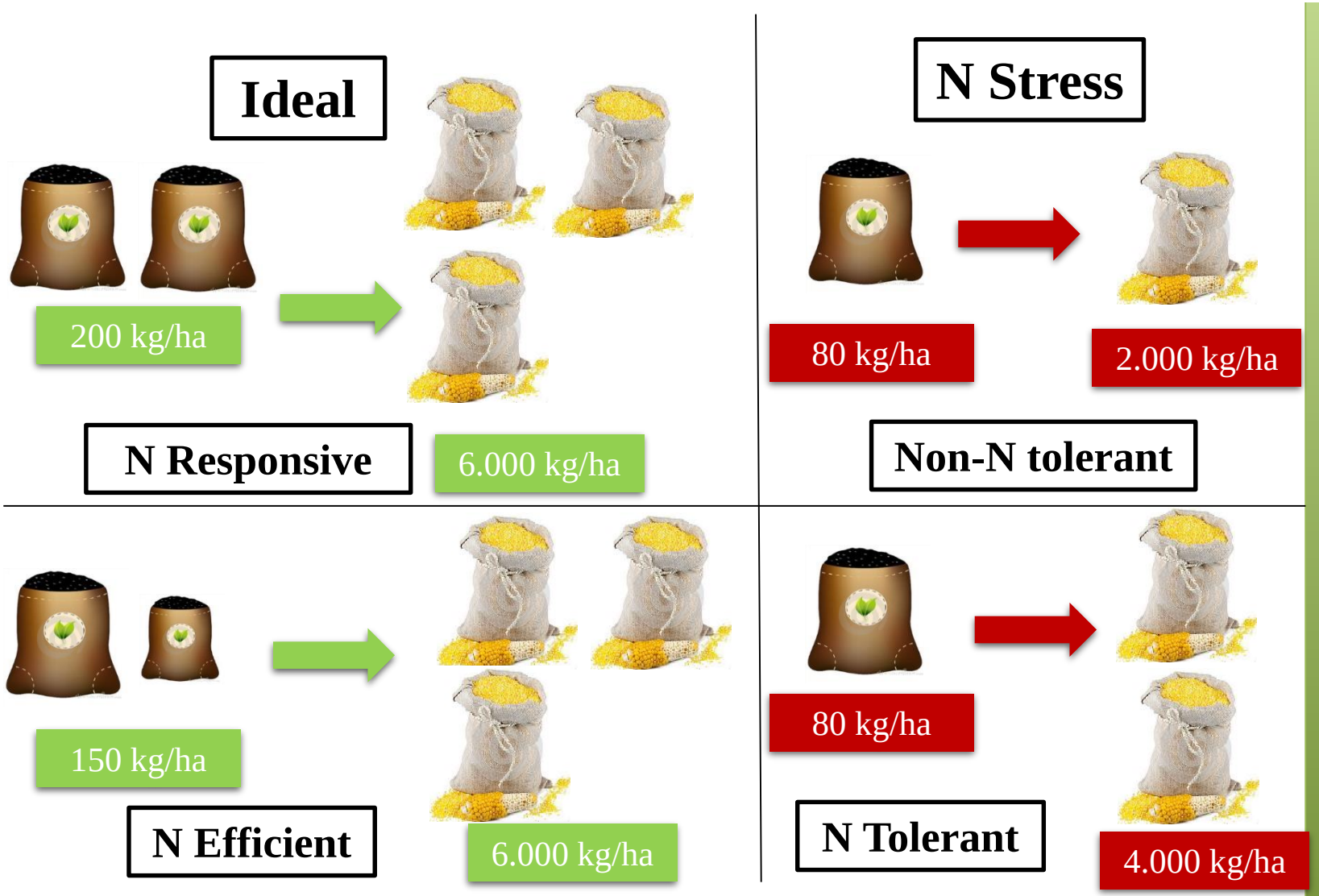
Cornell University
Jean-Luc Jannink

Iowa State University
Jianming Yu

Michigan State University
Gustavo de los Campos

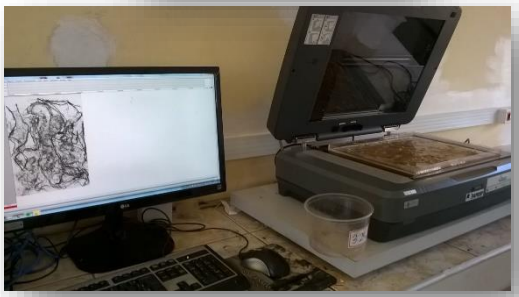
University of Wisconsin
Jeffrey Endelman

NUE *vs*. N tolerance

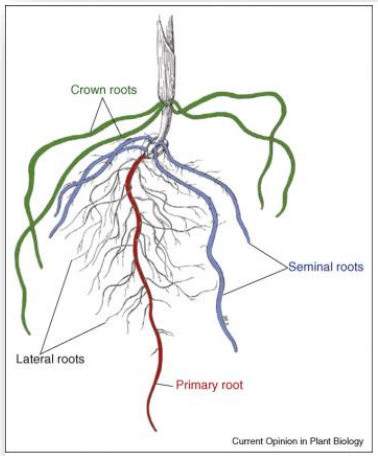


Root traits

Greenhouse



WinRHIZO



Roots

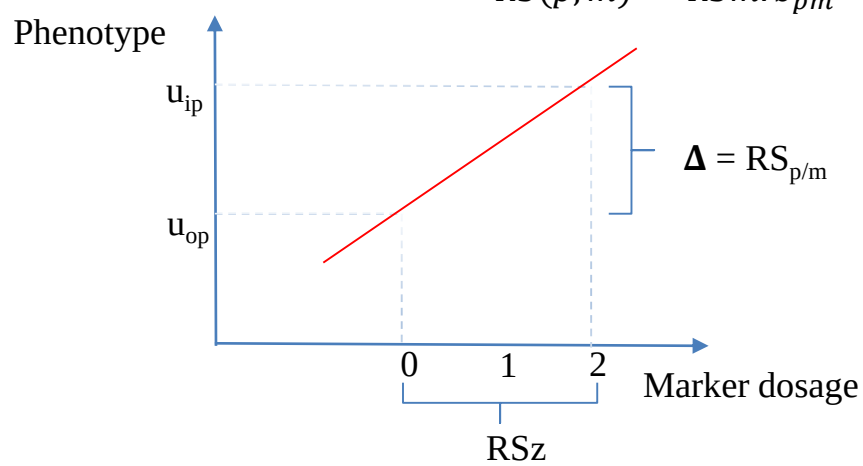
Field trial

Why Genomic Selection?

- The Breeder's equation

$$RS = \frac{i.r_a.\sigma_a}{T}$$

$$RS(p,m) = RSm.b_{pm}$$



- Predictive Ability vs. Accuracy

$$COV_{(\hat{y},y)} = COV_{(gm,g+e)} = COV_{(gm,g)} + COV_{(gm,e)} = \sigma_g^2$$

$$V_{(\hat{y})} = V_{(gm)} = \sigma_{g_m}^2 \qquad V_{(y)} = Vg + Ve = \sigma_g^2/h_g^2$$

$$r_{(\hat{y},y)} = \frac{COV_{(\hat{y},y)}}{\sigma_{\hat{y}}\ \sigma_y} = \frac{\sigma_g^2}{\sigma_{\hat{y}}\ .\sigma_g\ /h_g} = \frac{\sigma_g^2}{\sigma_{\hat{y}}\ \sigma_g}.h_g\ = r_{(\hat{y},g)}.h_g$$

$$r_{(\hat{y},g)}. = r_{(\hat{y},y)}/h_g$$

- Response to selection

$$b_{yx} = \frac{COV_{(x,y)}}{\sigma_x^2} \qquad RS(p,m) = i\frac{COV_{G(p,m)}}{\sigma_{Pm}} \qquad RS(p,m) = i\frac{r_{(p,m)}\,\sigma_{gp}\sigma_{gm}}{\sigma_{Pm}} \qquad RS(p,m) = ir_{(p,m)}\,h_m\sigma_{gP}$$

$$r_{xy} = \frac{\sigma_{xy}}{\sigma_x\ \sigma_y}$$

$$RS(p,m) = ir_{g(p,m)}\,\sigma_{gP}$$

$$RS(p,m) = \frac{ir_{g(p,m)}\,\sigma_{gP}}{T}$$

Plant Soil
https://doi.org/10.1007/s11104-017-3479-3

REGULAR ARTICLE

Association mapping for traits related to nitrogen use efficiency in tropical maize lines under field conditions

Júlia Silva Morosini · Leandro de Freitas Mendonça · Danilo Hottis Lyra · Giovanni Galli · Miriam Suzane Vidotti · Roberto Fritsche-Neto

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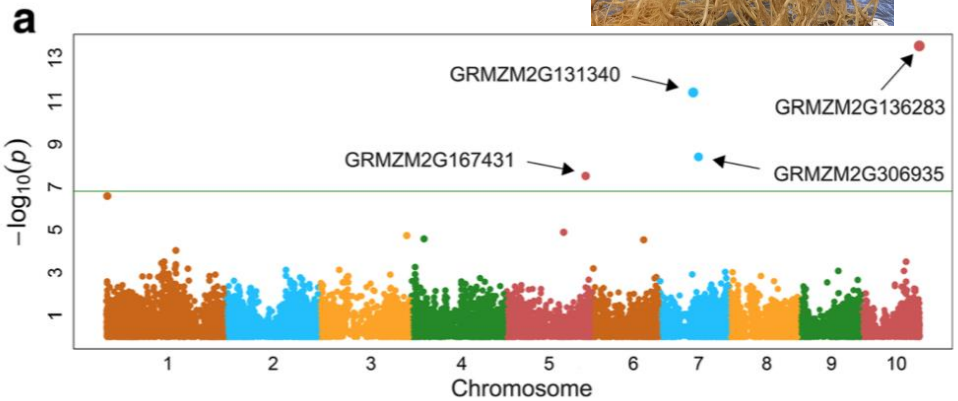
$$LNTI_{ij} = \left(1 - \frac{GY_{(LN)_{ij}}}{GY_{(IN)_{ij}}}\right) \times 100$$



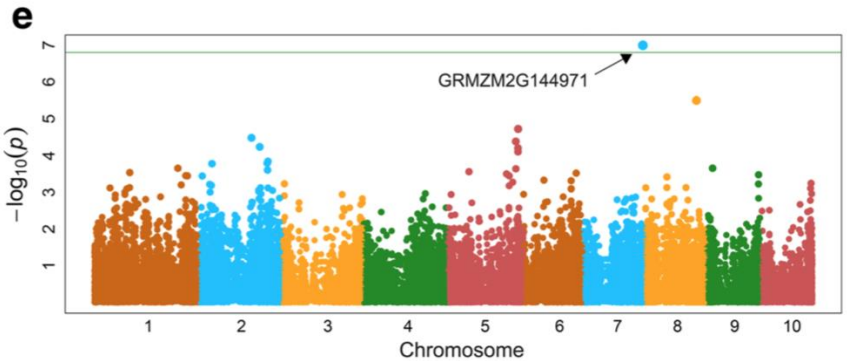


Table 2 List of SNPs significantly associated with LNTI and TRL traits by SNP-based GWAS

N°	Trait	Gene ID	Chr*	Position (bp)	*P* value	MAF[a]	ASE[b]	Annotation[c]
1	LNTI	GRMZM2G136283	10	148,504,575	2.71×10^{-14}	0.32	8.0	GMP Synthetase
2		GRMZM2G131340	7	85,581,217	4.01×10^{-12}	0.32	6.6	Transcription regulation
3		GRMZM2G306935	7	98,855,426	3.94×10^{-9}	0.22	7.1	DNA repair
4		GRMZM2G167431	5	200,437,599	3.05×10^{-8}	0.21	4.6	3-ketodihydrosphingosine redutase
5	TRL IN	AC234185.1_FG006	8	72,174,334	5.24×10^{-8}	0.36	5.7	Transcriptional factor MADS-box
6		GRMZM2G099408	4	6,448,544	1.25×10^{-7}	0.20	7.2	Transcriptional factor MADS-box
7	TRL LN	GRMZM2G144971	7	172,363,612	1.01×10^{-7}	0.11	10.3	Protein associated to microtubule

[*] Chromosome
[a] Minor allele frequency
[b] Allelic substitution effect (% for LNTI; cm for TRL)
[c] Some are putative annotations

Mol Breeding (2017) 37:80
DOI 10.1007/s11032-017-0681-1

Multi-trait genomic prediction for nitrogen response indices in tropical maize hybrids

Danilo Hottis Lyra · Leandro de Freitas Mendonça · Giovanni Galli · Filipe Couto Alves · Ítalo Stefanine Correia Granato · Roberto Fritsche-Neto

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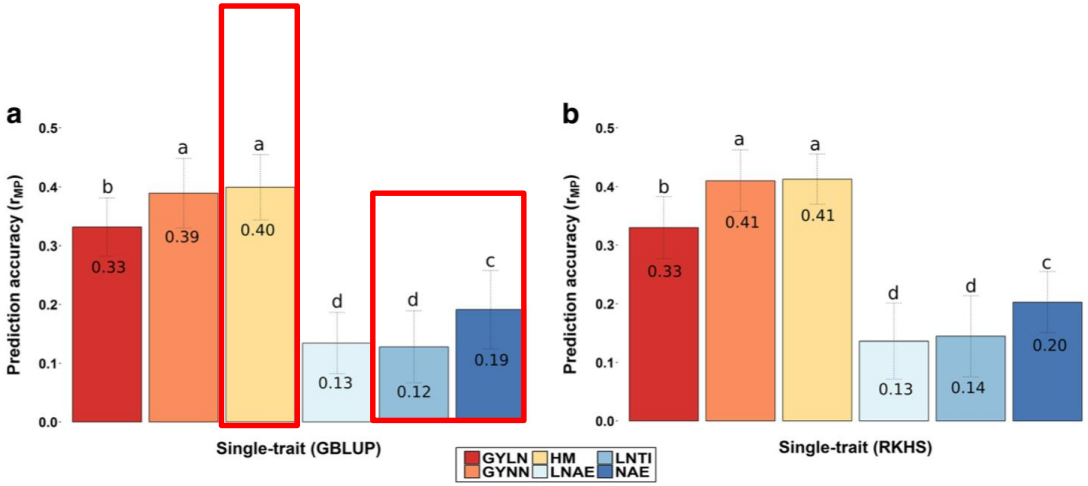
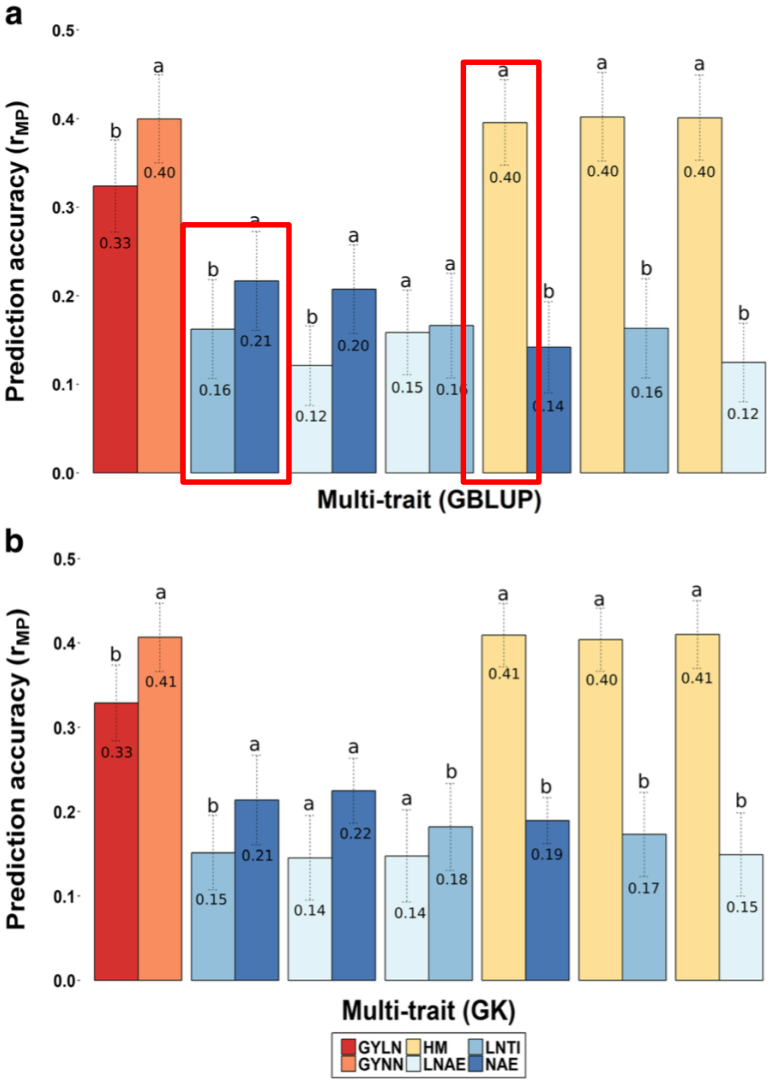




We have moved toward to

Milho Stand

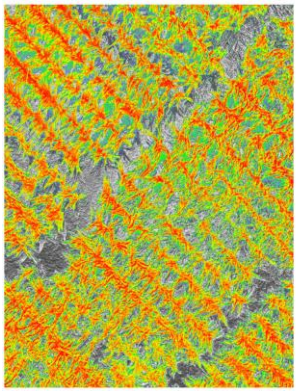
$$RS = \frac{i.r_a.\sigma_a}{T}$$

Measuring Plant Canopy Traits with UAV

UAV = Unmanned Aerial Vehicle

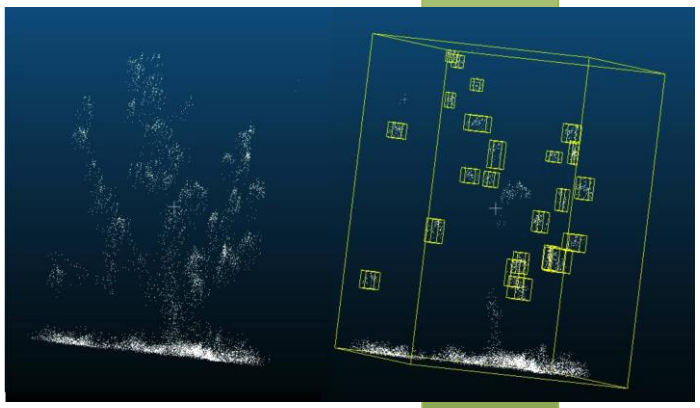
Machine	Manual
2.25 seconds per plot	5.75 seconds per plot
Requires 1 person	Requires 9 people

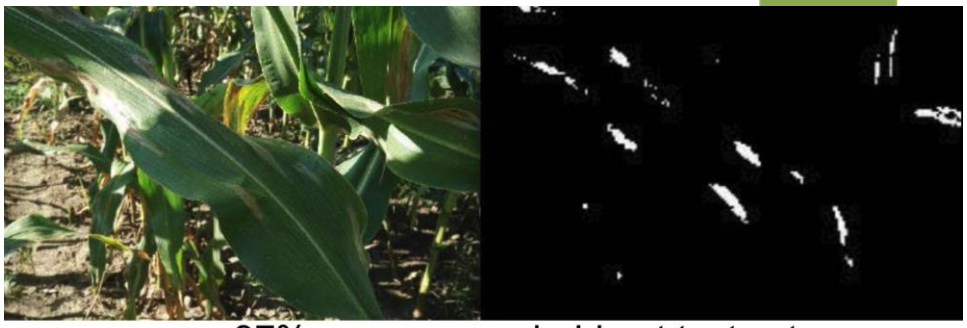
Machine Average	Manual Average
2%	5.6%
Range 0% - 5% on plot basis	Range 0% - 26% on plot basis



NDVI =

$$\frac{(NIR - red)}{(NIR + red)}$$





~97% accuracy on held out test set

Fonte: Gore (2017)

Closing remarks

- **For the future, the Breeders should know:**

- ***use this increase in quantity and type of data***
- ***working in interdisciplinary groups***
- ***a programming language***
- ***how to integrate/share data***
- ***how to differentiate Bandwagon and Frontier***
- ***Be fast - the time between ideas and publish must be little***

- **Hypotheses will not be limited by data, but by the researcher's imagination**

Thank you!

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