

Precision phenotyping: promising physiological traits that can be used in strategic crossing

Gemma Molero

Wheat Physiology, Global Wheat Program

Conceptual Model of Yield Potential

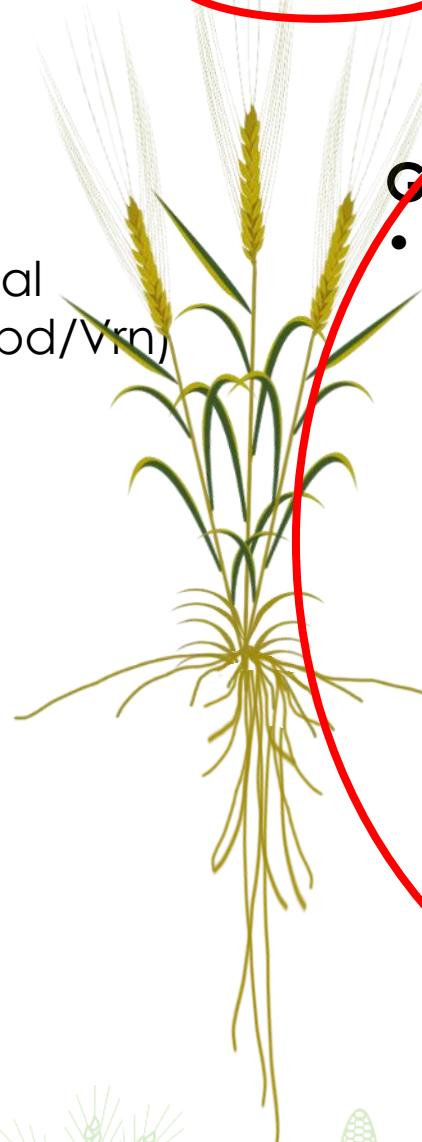
$$\text{YIELD} = \text{LI} \times \text{RUE} \times \text{HI}$$

Pre-grainfill (HI):

- Spike Fertility
 - grain no./weight potential
 - phenological pattern (Ppd/Vrn)
 - Avoid floret abortion (?)
- Lodging resistance
- Abort weak tillers

Grain-filling (HI/RUE):

- Partitioning to grain (HI)
- Adequate roots for resource capture (HI/RUE)



BIOMASS

Grain-filling (RUE/LI):

- Canopy photosynthesis (RUE/LI)
 - light distribution
 - N partitioning
 - spike photosynthesis
 - stay green

Pre-grainfill (RUE/LI):

- Light interception (LI)
- CO₂ fixation (RUE)
 - Rubisco

Exploring genetic diversity for biomass and traits related to canopy photosynthesis

The overarching goal is to **introduce sources of alleles** for high final biomass and other photosynthetic related traits into elite genetic backgrounds

- i. Screen a diverse set of genetic resources for good expression of **final biomass**
- ii. Characterize lines for expression of **LI and RUE** at specific **growth stages**
- iii. Evaluate lines for **canopy architecture** traits that permit a more vertically uniform photosynthetic rate down the leaf canopy
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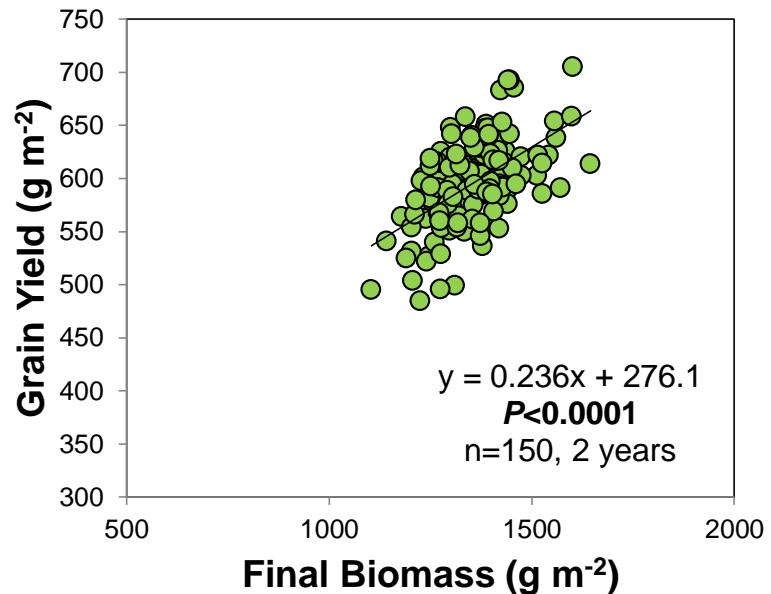
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i. Screen a diverse set of genetic resources for good expression of final biomass

Final Biomass is highly correlated with grain yield under favorable conditions



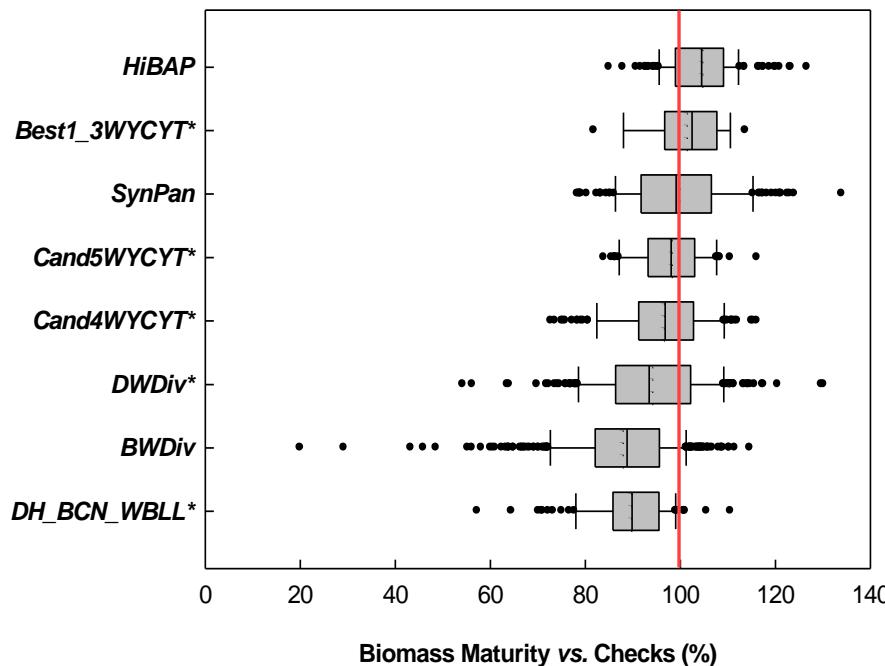
i. Screen a diverse set of genetic resources for good expression of final biomass

~1,500 lines directly evaluated for final biomass every year

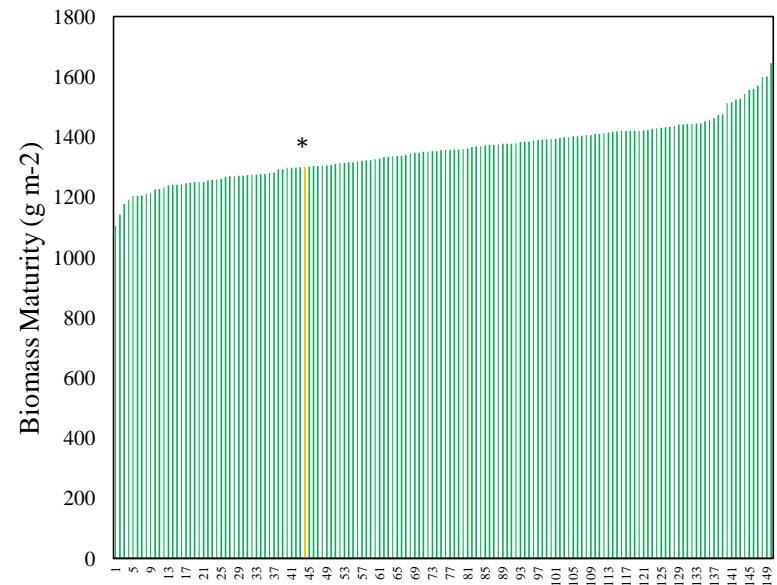


Large phenotypic variation in Biomass

Lines showing up to **34%**
higher biomass in comparison
with elite checks
(Sokoll& Borlaug 100)



HiBAP: High Biomass Panel
created where **69% of the**
lines showed higher biomass
than the best check



Combined analysis 2015-2016 & 2016-2017

Highest biomass lines have synthetic and landrace material in their pedigrees

	%BM vs. best checks	Heritability	P value (Gen)
<i>HiBAP</i>			
C80.1/3*QT4118//KAUZ/RAYON/3/2*TRCH/7/CMH79A.955/4/AGA/3/4*SN64/CNO67//I NIA66/5/NAC/6/RIALTO CHEWINK #1	127		
KACHU #1/4/CROC_1/AE.SQUARROSA (205)//BORL95/3/2*MILAN/5/KACHU	123		
C80.1/3*QT4118//KAUZ/RAYON/3/2*TRCH/7/CMH79A.955/4/AGA/3/4*SN64/CNO67//I NIA66/5/NAC/6/RIALTO DPW 621-50 -India	121	0.414	0.000
BCN/WBLL1//PUB94.15.1.12/WBLL1	120		
WBLL4//OAX93.24.35/WBLL1/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2	119		
MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/PUB94.15.1.12/WBLL1	118		
<i>SynPAN</i>			
68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (778) ALTAR 84/AE.SQUARROSA (895)	134		
CETA/AE.SQUARROSA (796)	124		
CETA/AE.SQUARROSA (273)	123		
68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (778) CROC_1/AE.SQUARROSA (466)	123	0.656	0.000
GARZA/BOY//AE.SQUARROSA (350)	121		
68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (788)	120		
<i>BWDiv</i>			
VORB//PARUS/PASTOR	115		
MEX94.2.19/PUB94.15.1.12	112	0.731	0.000
<i>DWDiv</i>			
GIZA 8 (Durum) - Saudi Arabia	130		
COULTER (Durum) - Canada	130	0.782	0.000
D86135/2*ACO89 (Durum) -Mexico	121		

Orange: primary synthetics or synthetics derived lines

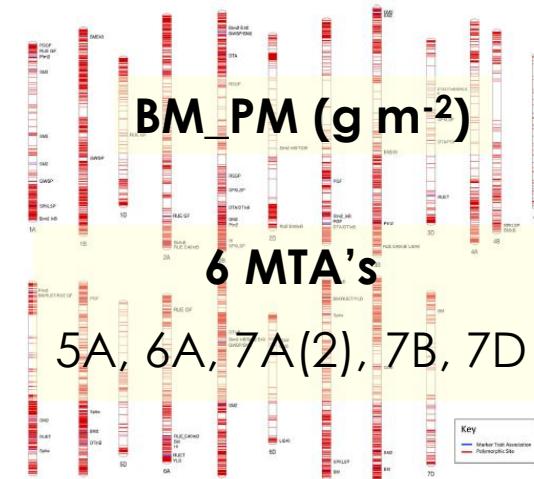
Green: landraces or landraces derived lines

Yellow: lines with synthetic and landrace background in their pedigree.



Highest biomass lines have synthetic and landrace material in their pedigrees

HiBAP, n=150, 2 years, Y15-16&Y16-17



Type	YLD	DTA	TGW	HI	Height	BM_PM
Elite	597 ^A	76 ^B	42.6 ^C	0.473 ^A	98.5 ^D	1346 ^B
Landrace derivatives	592 ^A	79^A	45.7^B	0.450^C	103.3^A	1394^A
Synthetic derivatives	594 ^A	76 ^B	45.6^B	0.463^B	100.5^C	1358 ^{AB}
Synthetic+Landrace derivative	593 ^A	76 ^B	48.2^A	0.459^B	101.7^B	1389^A



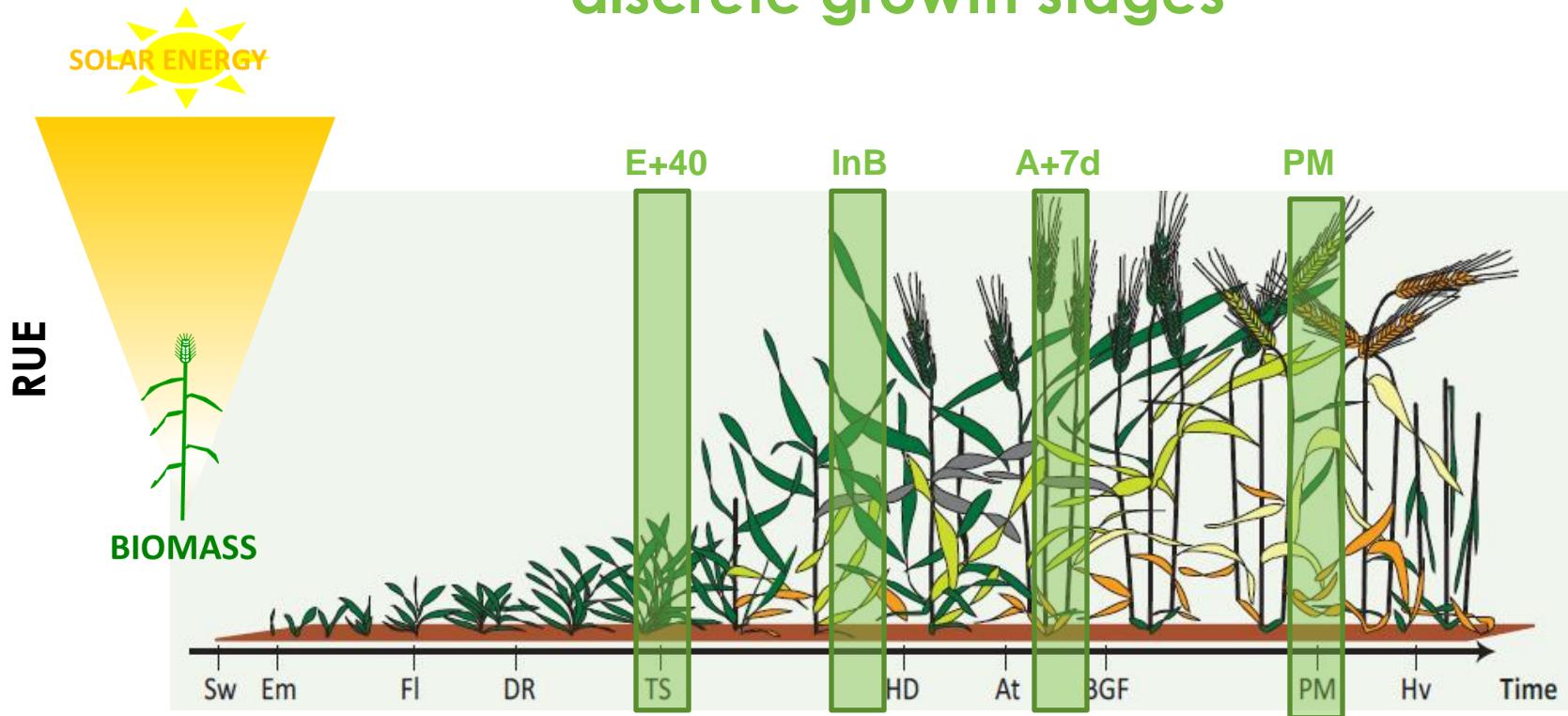
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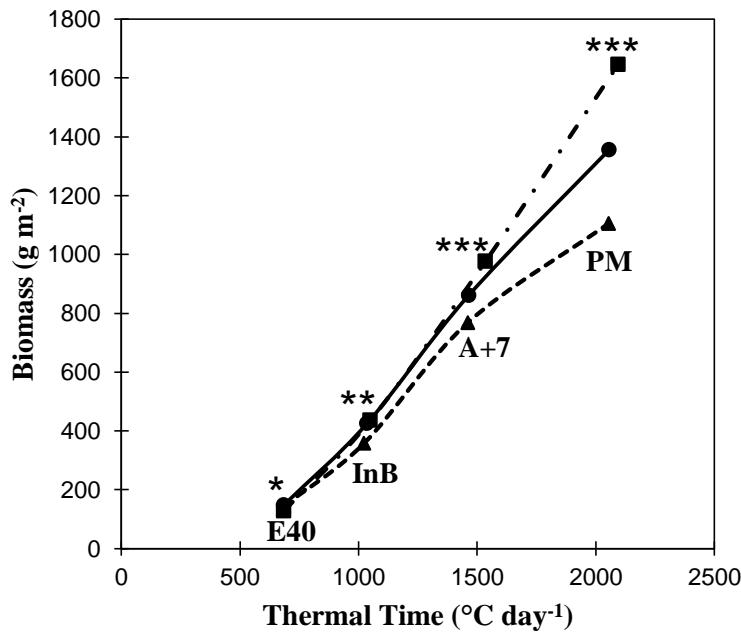
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ii. Characterize lines for expression of LI and RUE at discrete growth stages

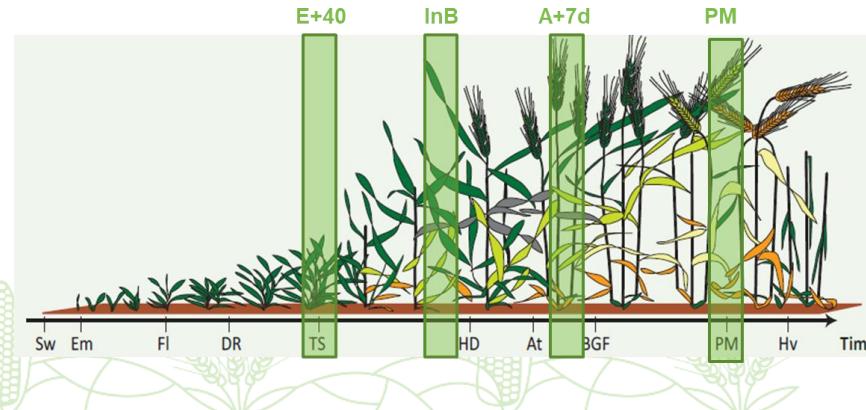


ii. Characterize lines for expression of LI and RUE at discrete growth stages

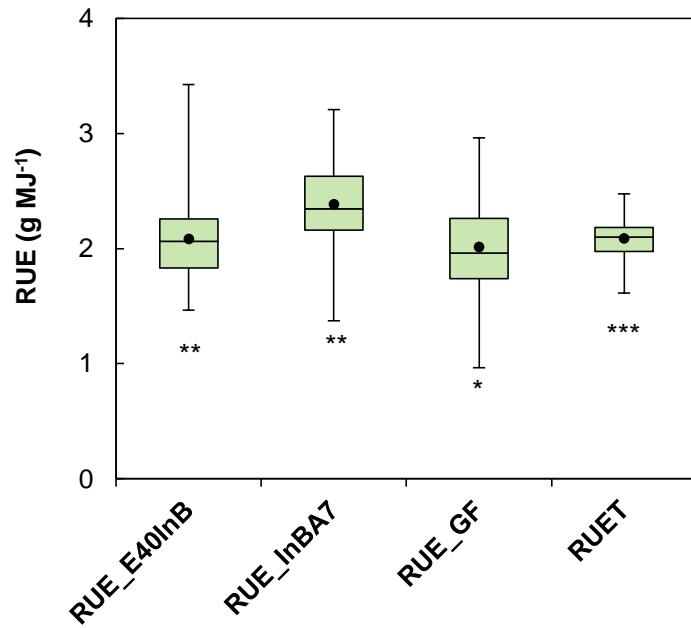
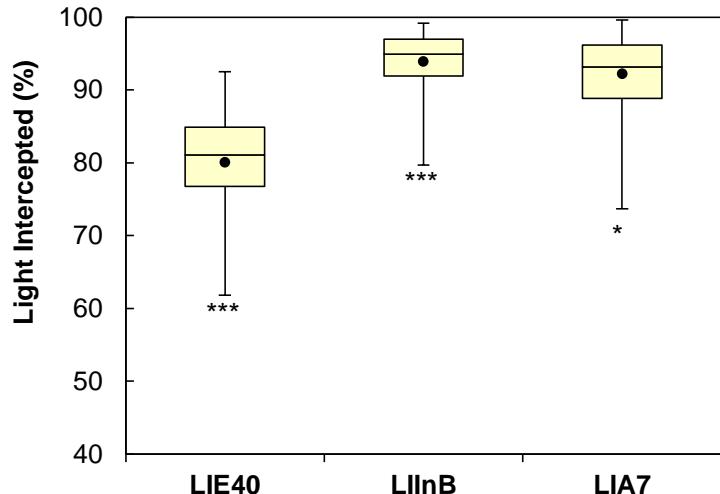


HiBAP, n=150, 2 years

	BME40	BMInB	BMA7	BMPM
Heritability (h^2)	0.240	0.342	0.498	0.414
Correl with Yield	-0.014	-0.119	0.097	0.561
Correl with BM_PM	0.153	0.303	0.25	1



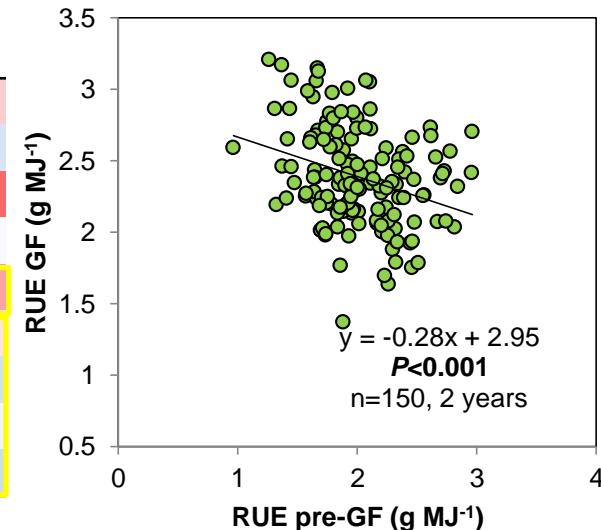
ii. Characterize lines for expression of LI and RUE at discrete growth stages



ii. Characterize lines with high biomass for expression of LI and RUE at discrete growth stages

HiBAP, 2 years

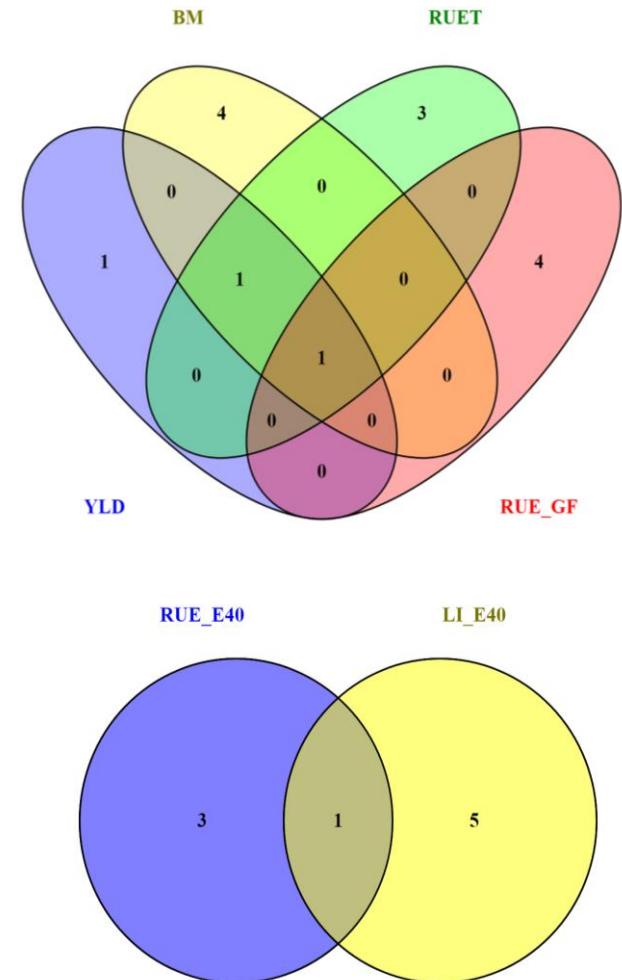
	RUE E40InB	RUE InBA7	RUE GF	RUE Total	LI E40	LI InB	LI A7
YLD	0.145	0.113	0.533	0.609	0.008	-0.019	-0.046
Height	0.061	0.044	0.139	0.265	0.27	0.253	0.254
HI	0.006	0.119	-0.219	-0.160	-0.062	-0.374	-0.378
TGW	0.162	0.028	0.274	0.453	0.292	0.019	0.118
GM2	-0.008	0.070	0.068	-0.024	-0.278	-0.093	-0.195
BME40	0.159	-0.038	-0.108	-0.008	0.355	-0.059	0.019
BMIInB	0.268	-0.204	-0.078	-0.005	0.347	0.374	0.27
BMA7	0.427	0.721	-0.248	0.378	0.167	0.003	0.15
BMPM	0.143	0.027	0.742	0.773	0.101	0.331	0.291



Identification of MTAs related with biomass, LI and RUE

HiBAP, n=150, 2 years

Trait	Number of MTAs	Chromosomes
Agronomic		
Grain Yield (kg ha^{-1})	3	5A, 6A, 7A
Plants m^{-2}	4	1A, 2B, 3B, 5A
Stems m^{-2} E40	2	2B, 6B
Stems m^{-2} lnB	4	1A, 2D, 3A, 6B
Source		
BM_E40 (g m^{-2})	2	1B, 3B
BM_lnB (g m^{-2})	3	2A, 4B, 7A
BM_PM (g m^{-2})	6	5A, 6A, 7A(2), 7B, 7D
RUE_E40lnB (g MJ^{-1})	4	2A, 2D, 3B, 6A
RUE_GF (g MJ^{-1})	5	1A, 1D, 2A, 5A, 6A
RUET (g MJ^{-1})	5	3D, 5A(2), 6A, 7A
LI_E40 (%)‡	6	1B, 3B(3), 5A, 6D



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iii. Evaluate lines for canopy architecture traits that permit a more vertically uniform photosynthetic rate down the leaf canopy



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Flats

	YLD g/m ²	BM g/m ²	HI	TGW	GM2	SM2	Height cm	DTA
Erect	471	1029	.44	25.3	19170	400	87	75
Floppy	442	972	.45	30.4	14960	302	94	72
%E vs F	6.6	5.8	-2.3	-16.7	28.1	33	-7.5	4.2

Beds

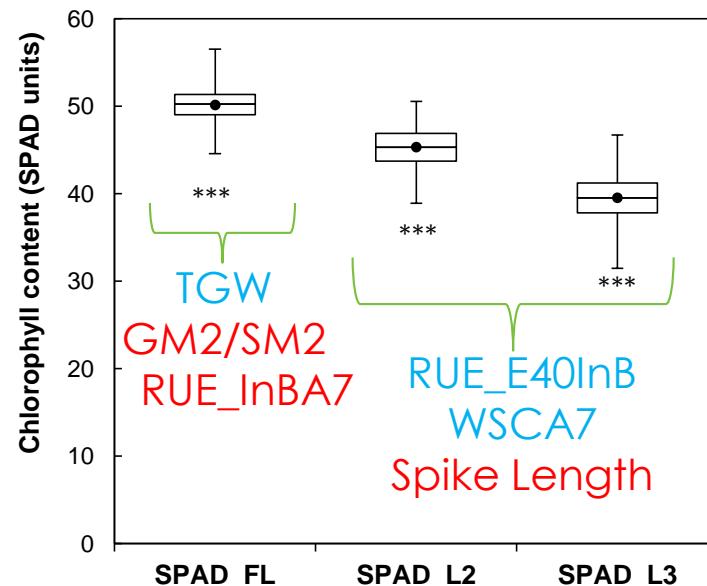
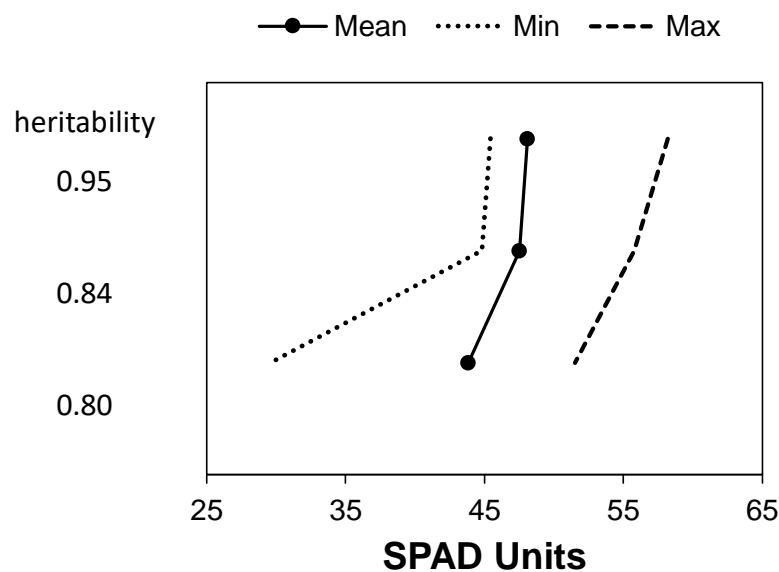
	YLD g/m ²	BM g/m ²	HI	TGW	GM2	SM2	Height cm	DTA
Erect	482	1463	.33	36.2	13410	310	88	75
Floppy	490	1469	.34	36.3	13500	301	93	76
%E vs F	-1.6	-0.5	-3.0	-0.3	-0.7	3.0	-5.4	-1.3

R. Richards, unpublished data



iii. Evaluate lines for canopy architecture traits that permit a more vertically uniform photosynthetic rate down the leaf canopy

Use of spectral reflectance at leaf level
SPAD-502 (650 nm, 940 nm)



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iv. Screen lines for flag leaf and spike photosynthesis



Initiation of booting



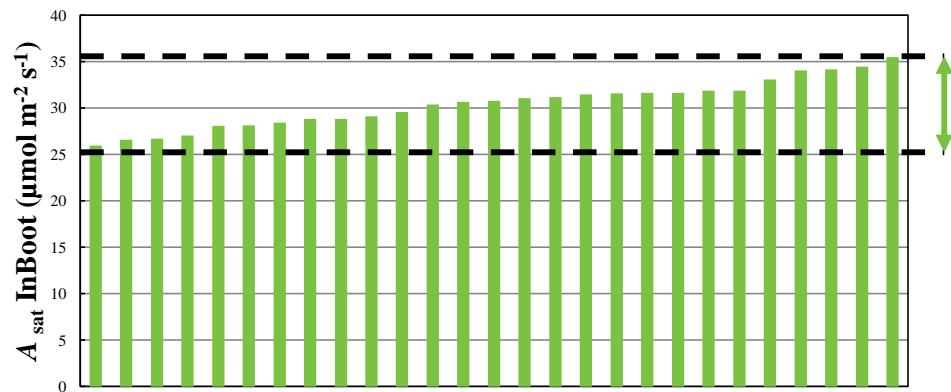
Anthesis+7d



iv. Screen lines for flag leaf and spike photosynthesis

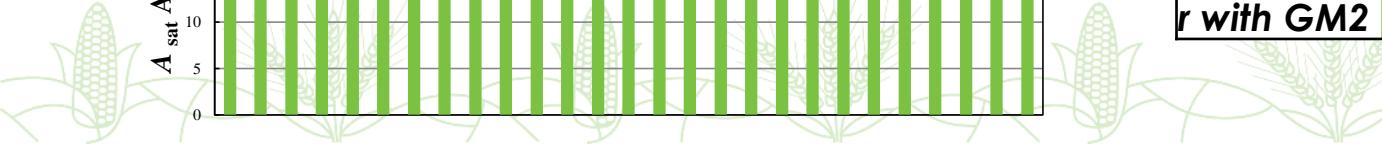


CIMCOG I, 27 Elite Lines (2 years)

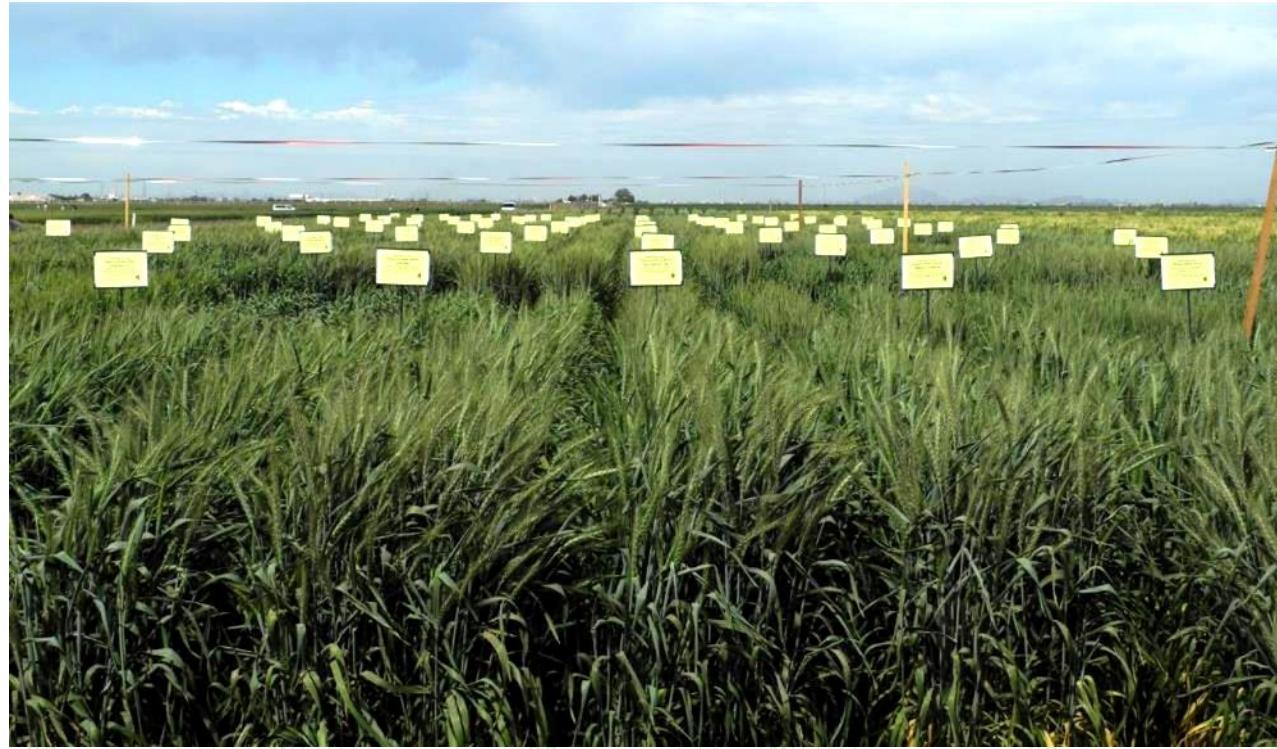


PSTails, 80 Lines (2 years)

	Photo $\mu\text{mol CO}_2\ \text{m}^{-2}\ \text{s}^{-1}$	Cond $\text{mol H}_2\text{O}\ \text{m}^{-2}\ \text{s}^{-1}$
H ²	0.378	0.446
Min	17.6	0.181
Mean	27.6	0.441
Max	32.0	0.618
G	0.014	0.004
G x Y	0.000	0.000
Y	0.266	0.082
r with YLD	0.54	0.45
r with TGW	0.18	0.01
r with HI	0.39	0.37
r with BM	0.48	0.40
r with GM2	0.45	0.48



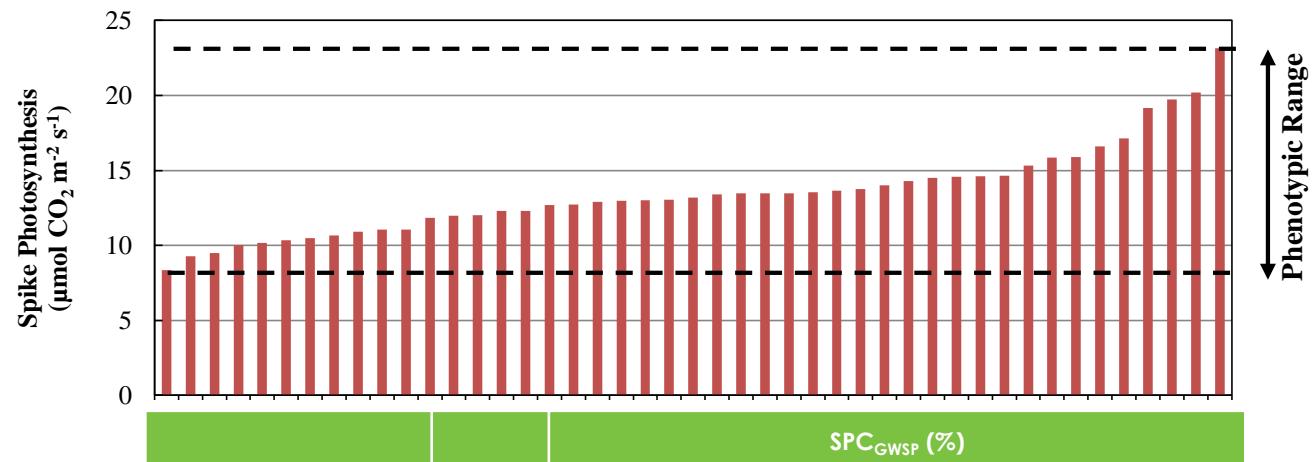
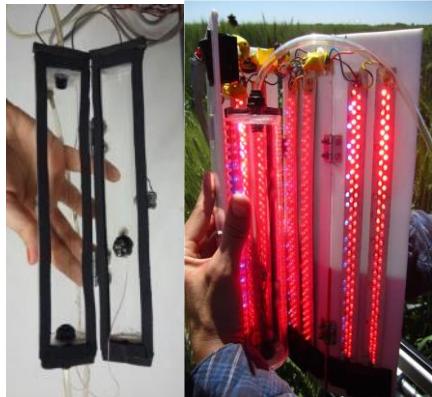
iv. Screen lines for flag leaf and spike photosynthesis



Elite spring
bread wheat
spikes
intercept up
to 45% of
sun light

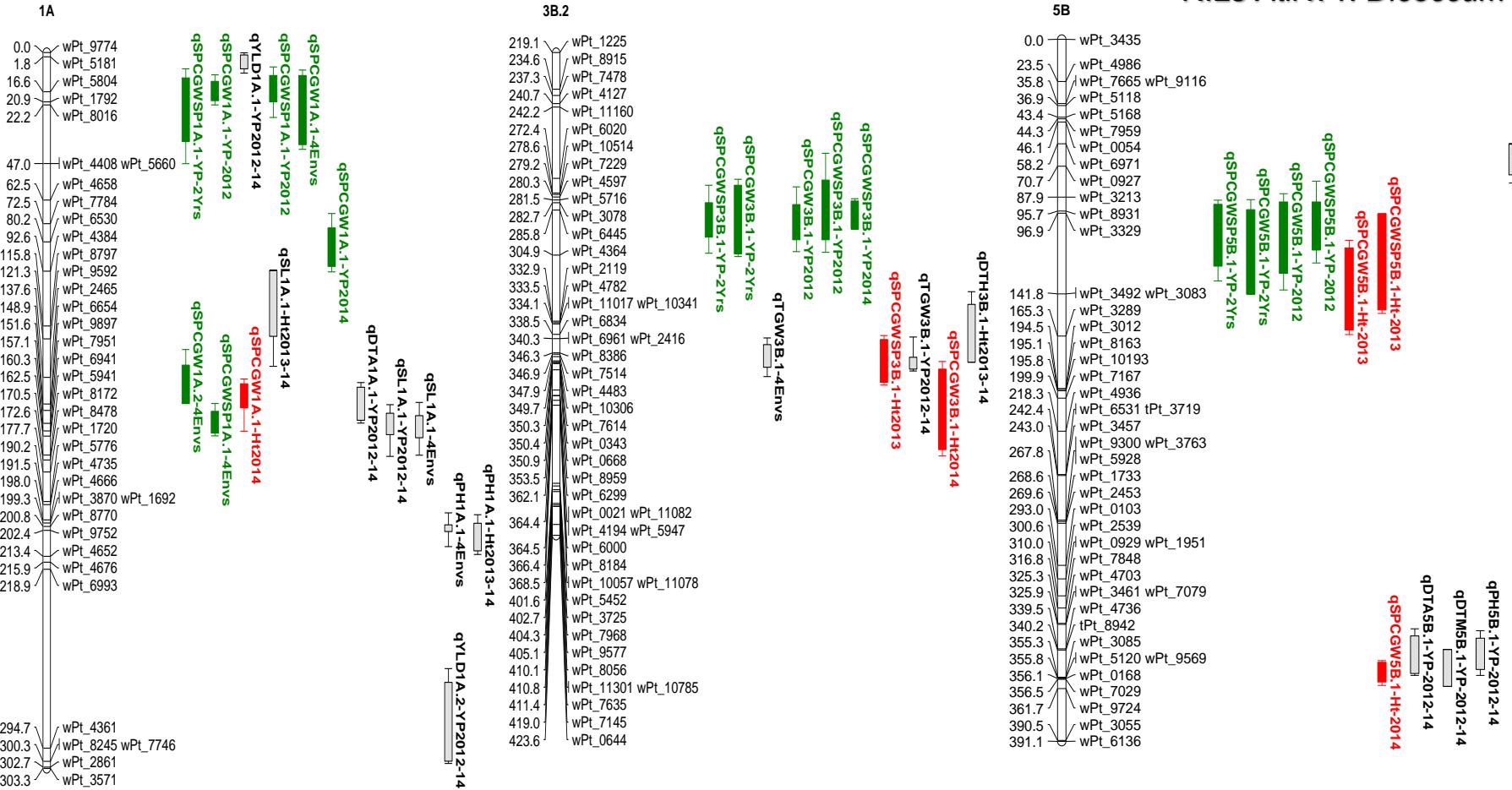


Phenotypic selection for Spike Photosynthesis

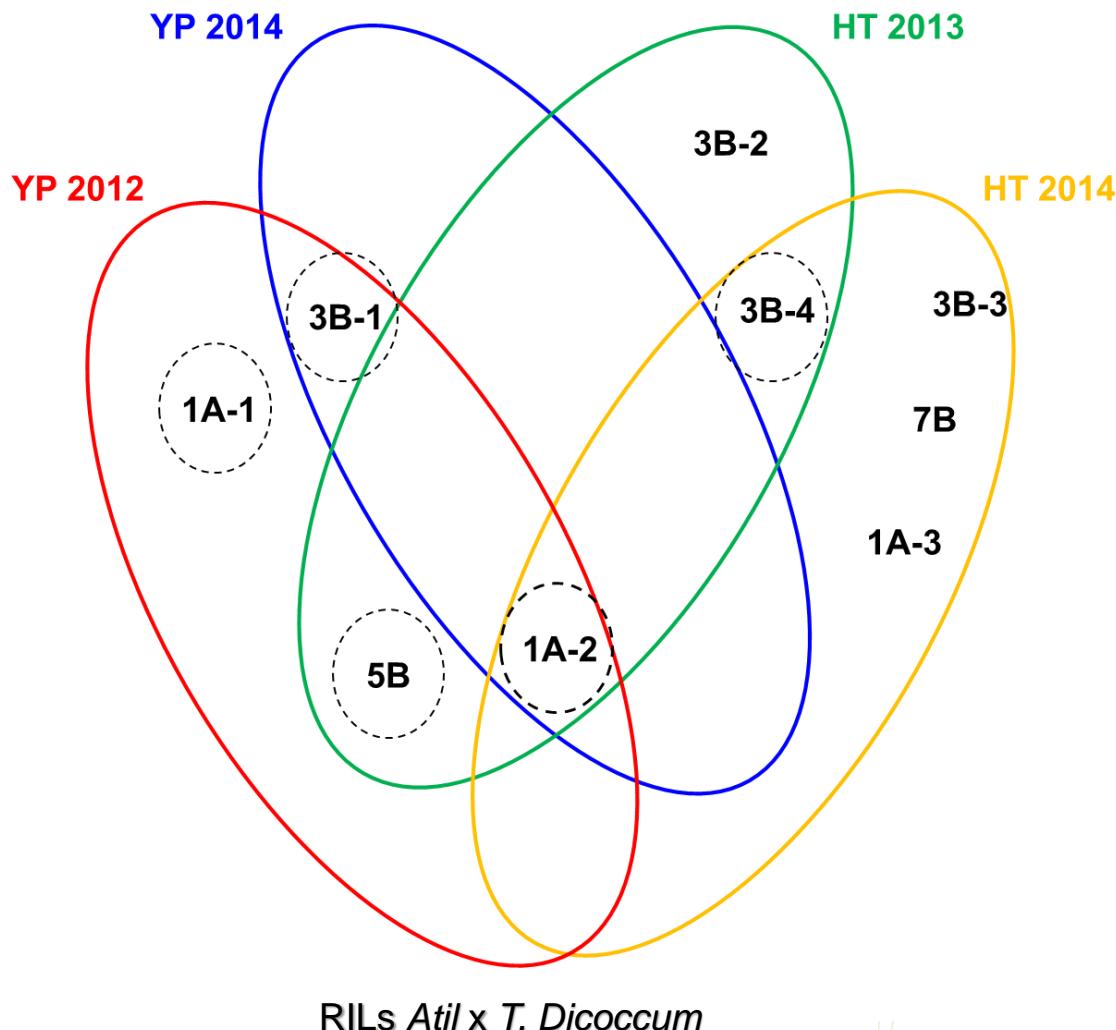


Identification of QTLs for Spike Photosynthesis

RILs *Atil* x *T. Dicoccum*



Consistent QTLs for YP and Heat



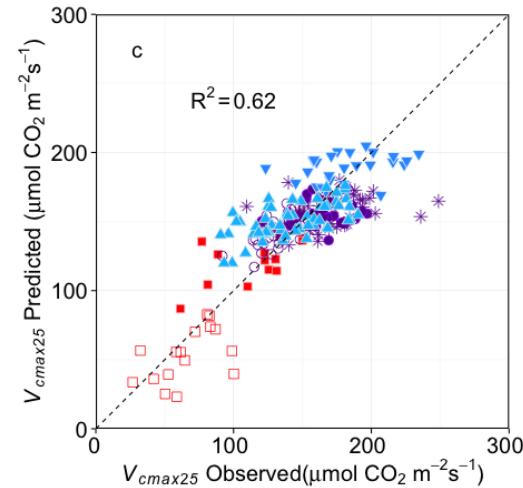
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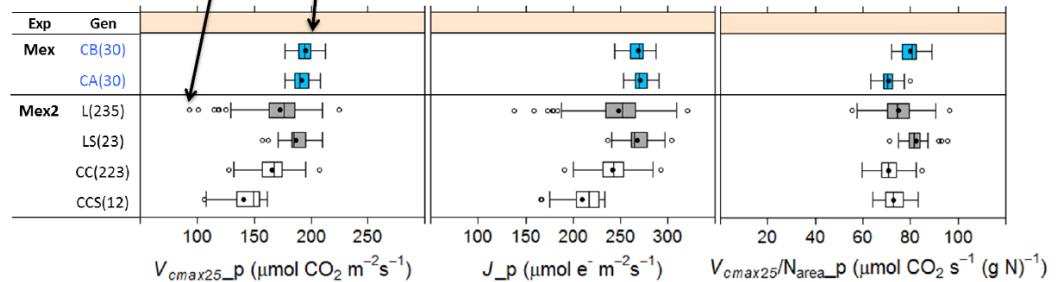
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iv. Evaluate diverse genotypes for Rubisco capacity and efficiency using high-throughput tools



Bigger variation for Landraces than elite wheat genotypes



Silva-Perez, Molero et al., 2018, JXB

iv. Evaluate diverse genotypes for Rubisco capacity and efficiency using high-throughput tools

Use of spectral reflectance at leaf level



FieldSpec3 (350-2500nm)

	YLD	TGW	HI	BM	GM2
Vcmax25	ns	<0.01	ns	<0.05	<0.05
Vcmax25/Narea	ns	ns	ns	ns	ns
J	ns	<0.01	ns	<0.05	<0.01
J/Narea	ns	ns	ns	ns	ns
LMA_O	ns	ns	<0.001	ns	<0.01
Nmass_O	ns	<0.01	ns	ns	<0.01
SPAD_Calc	ns	<0.001	ns	<0.05	<0.01

HiBAP, 2 years



Silva-Perez, Molero et al., 2018, JXB

Conceptual Model of Yield Potential

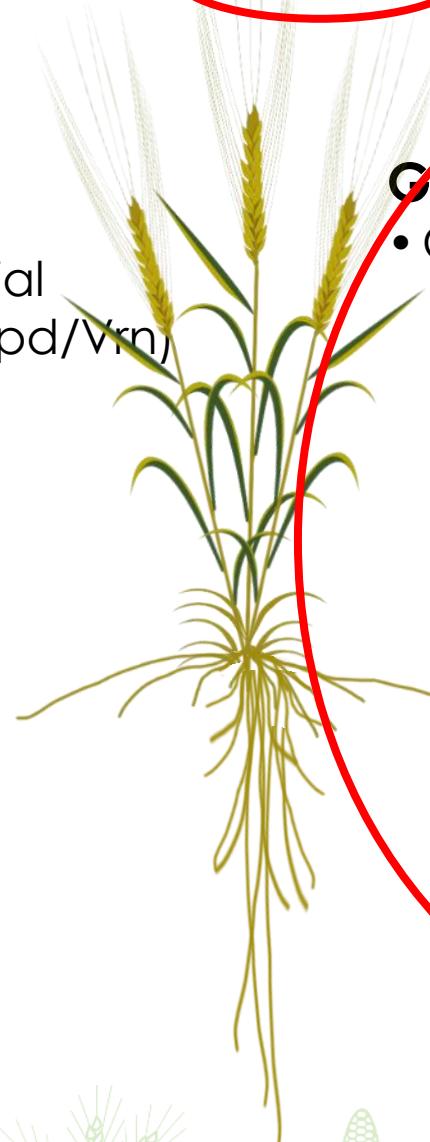
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Pre-grainfill (RUE/LI):

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- CO₂ fixation (RUE)
 - Rubisco

Use of phenotypic data in physiological Pre-Breeding

- ✓ Genetic Variation
- ✓ Good heritability estimates
- ✓ Correlated with YLD/Biomass
(not necessarily)



Use of phenotypic data in physiological Pre-Breeding

Trait	P (GEN)	h^2	r YLD	r BM
A _{sat} lnB Flag leaf	***	0.65	0.227	0.245
A _{sat} A+7 Flag leaf	***	0.38	0.540	0.450
A _{sat} A+7 Spike [†]	**	0.72	0.287	0.354
Spike Photo contribution	***	0.66	-0.204	-0.133
RUEpre-gf	***	0.54	0.28	0.602
RUEgf	**	0.62	0.587	0.803
Biomass at lnB	***	0.90	0.085	0.391
Biomass at A+7	***	0.54	0.003	0.340
Biomass at PM	***	0.74	0.709	-



Strategic crossing



Strategic crossing

Physiology crossing block for drought used to direct crosses

	Drought yield g/m ²	Biomass anthesis g/m ²	Canopy temperature depression		Carbon isotope discrim. ‰	Stem carbohydr. transloc. % stem DW	Water extraction (30-120cm) % of avail.	Spectral reflectance	
			vegetat.	grainfill				RARSa (Chla) (au)	Water Index (WI) (au)
JUN/GEN	338	424	19.2		21.8	-23.1	13.3	84	0.63
CROC/AE.SQ.(224)//OPATA	278	510	19.8		22.6	-22.5	19.1	79	0.64
BABAX	354	647	19.3		22.2	-22.8	13.9	83	0.57
KLEIN CACIQUE	247	638	20.1		23.3	-22.6	3.4	82	0.53
TIE CHUAN 1	211	407	20.2		22.5	-22.3	14.7	78	0.65
ATTILA	307	536	19.7		22.3	-22.9	16.1	82	0.58
WEEBILL1	348	513	19.3	21.7	-22.5	17.5	17.5	83	0.63
Correlation with yield			0.21	-0.74	-0.60	-0.64	0.32	-0.62	-0.02
									0.27

Jun/Gen X Croc/Ae.Sq//Opata

Traits considered for 2019 related with Biomass for increasing Yield Potential

- Biomass/day
- Yield/day
- Biomass
- Leaf photosynthesis
- Spike photosynthesis
- Stomatal conductance, Ci
- Fluorescence
- V_{cmax} (Rubisco)
- RUEpre-gf, RUEgf, RUE_Total
- BMInB, BM A+7
- Canopy architecture (erect)



International yield trials data

4th WCYT (2016/17)

	Clusters based on G x E for yield					
Cluster of sites	C1	C2	C3	C4	C5	Combined
Best PT line (t/ha)	4.96 ^{ns}	5.45*	7.41*	5.89 ^{ns}	8.05*	5.44*
Borlaug (t/ha)	5.29	4.46	5.45	5.65	7.28	5.09
% over Borlaug	-6.2%	22.3%	36.0%	4.2%	10.6%	6.9%*



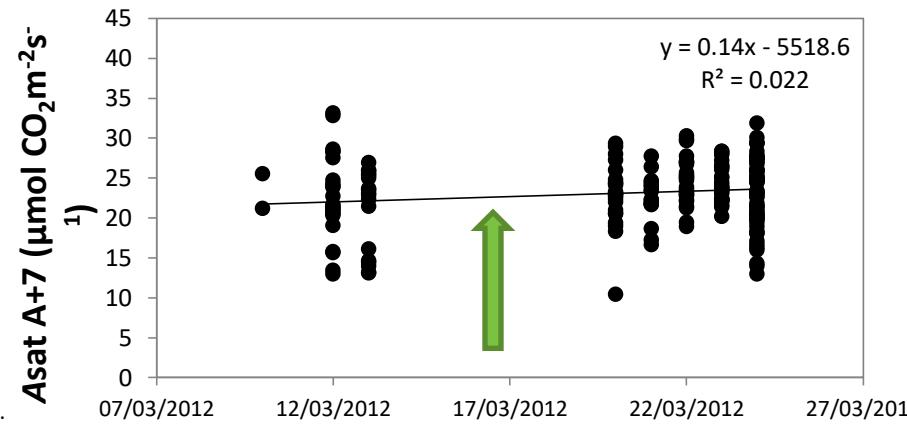
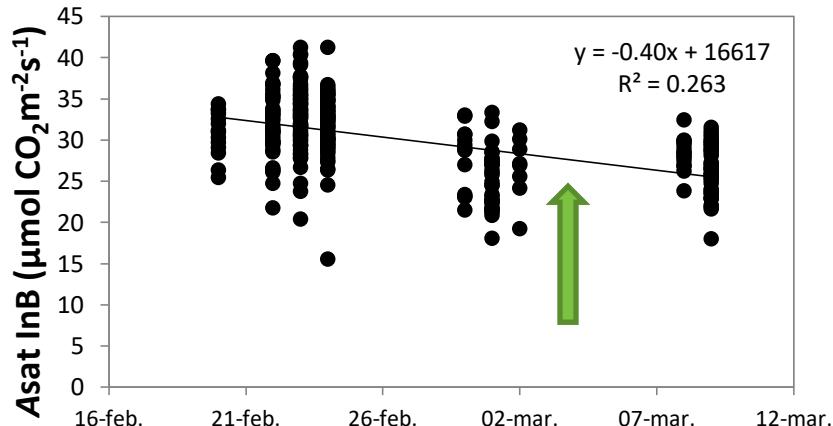
Thanks!



iv. Screen lines for flag leaf and spike photosynthesis



Year 1



Year 2

