

# AP02 - Exploring genetic diversity for harvest index and identifying improved selection approaches

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# RESEARCH TARGETS

The overarching goal of this project is to identify genetic resources with **promising expression of HI** and related traits and development of **improved screening protocols**

- i. Screen a diverse set of genetic resources for **good expression of HI**, Fruiting efficiency, Spike Partitioning index and length of stem internodes 2 and 3 (N-IWYP700)
- ii. Study of **phenological patterns** to identify promising new sources of diversity for pre-breeding
- iii. Identify lines with particular constellations of ***Ppd*, *Vrn*, *Eps*, and *Rht* alleles** that are associated with favorable expression of HI levels (IWYP25) and **molecular markers** associated with HI and partitioning traits (N-IWYP700, IWYP64).



# MAIN PANELS STUDIED

## High Biomass Association Mapping Panel, HiBAP (150)



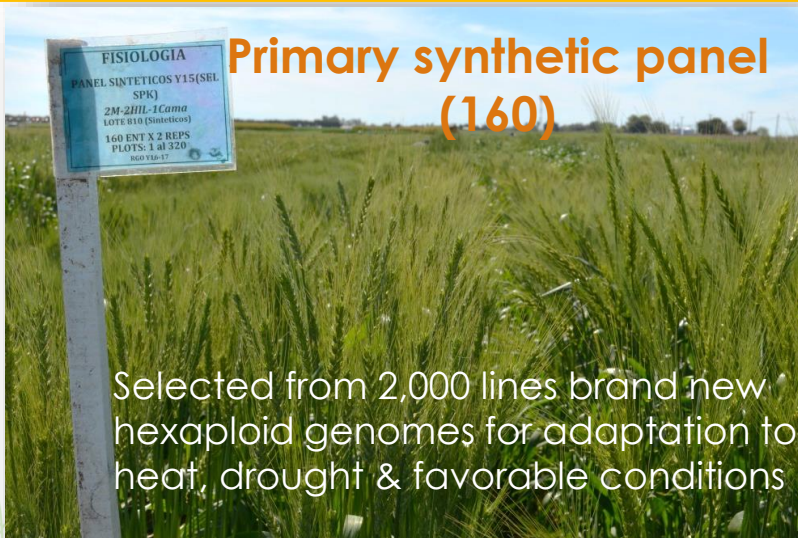
Favorable expression of biomass RUE based on systematic screening of genetic resources under fully irrigated conditions

## Bread Wheat Diversity Panel (390)



Assembled after screening ~70,000 lines for heat and drought adaption

## Primary synthetic panel (160)



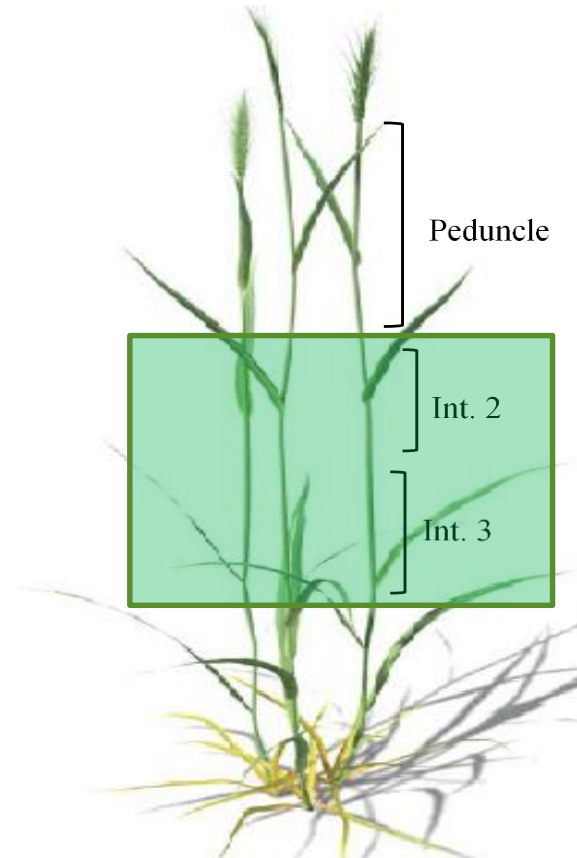
Selected from 2,000 lines brand new hexaploid genomes for adaptation to heat, drought & favorable conditions

## Durum Wheat diversity Panel (225)

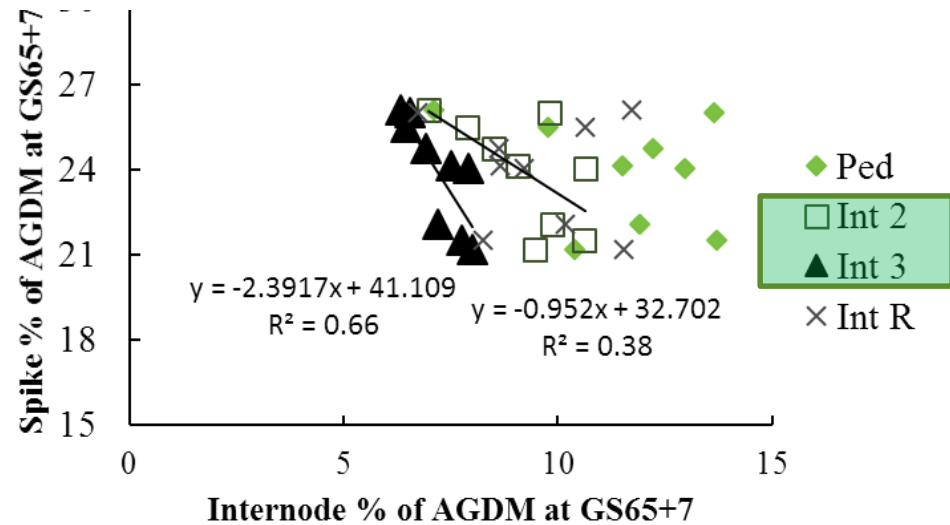
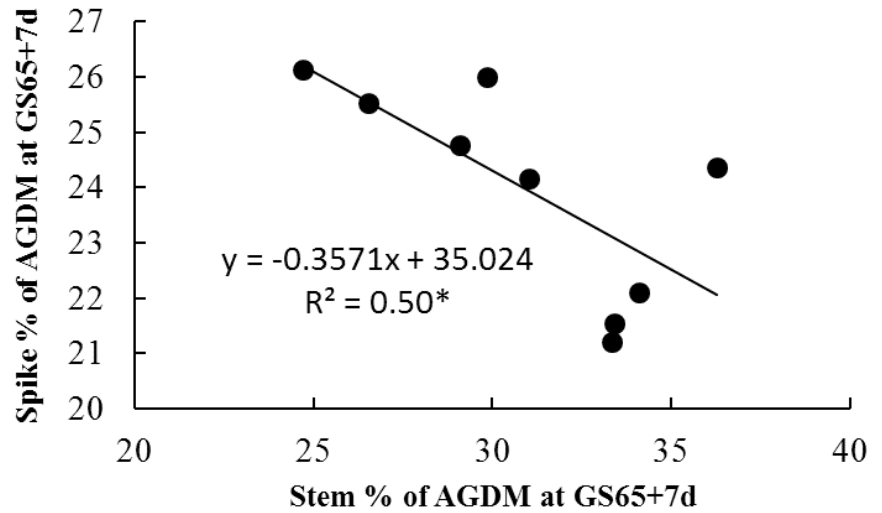


Assembled after screening ~70,000 lines for heat and drought adaption

i. Screen a diverse set of genetic resources for good expression of HI, Fruiting efficiency, Spike Partitioning index and length of stem internodes 2 and 3



**Negative associations with spike growth**



# i. Screen a diverse set of genetic resources for good expression of HI, Fruiting efficiency, Spike Partitioning index and length of stem internodes 2 and 3

Phenotypic screening of elite genetic resources to identify diversity for HI and related traits

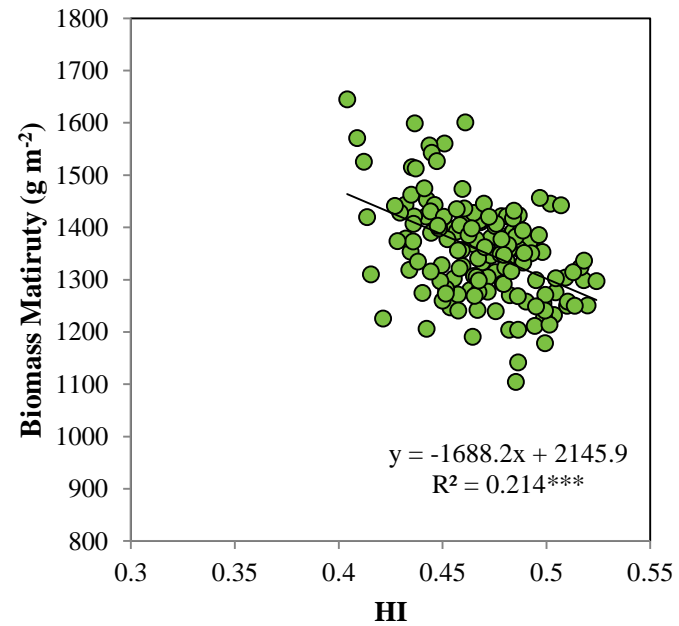
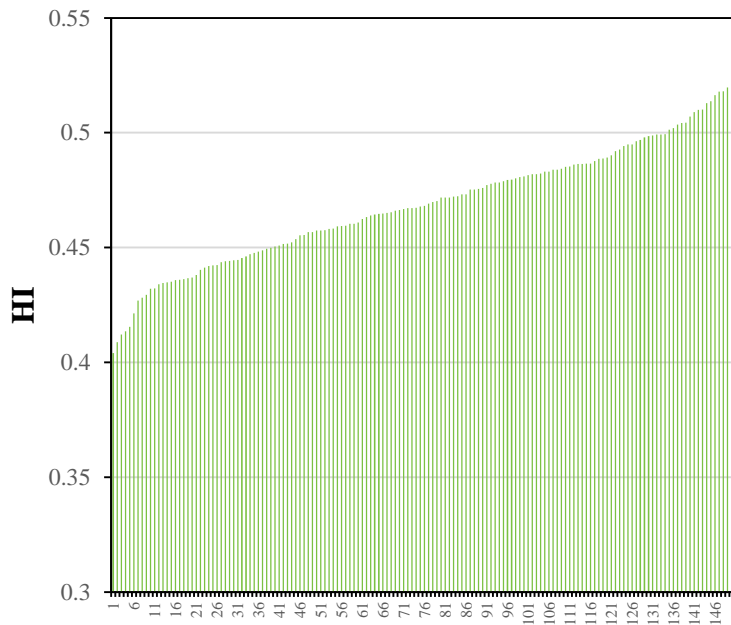
<b>HiBAP</b> (n=150) 2 years
<b>SynPan</b> (n=160) 2 years
<b>BWDiv</b> (n=370) 2 years
<b>DWDiv</b> (n=225)



> 2,000 lines from different panels have been phenotyped for harvest index and other partitioning traits since 2016

# Large genetic variation in HI in elite population; trade off with biomass

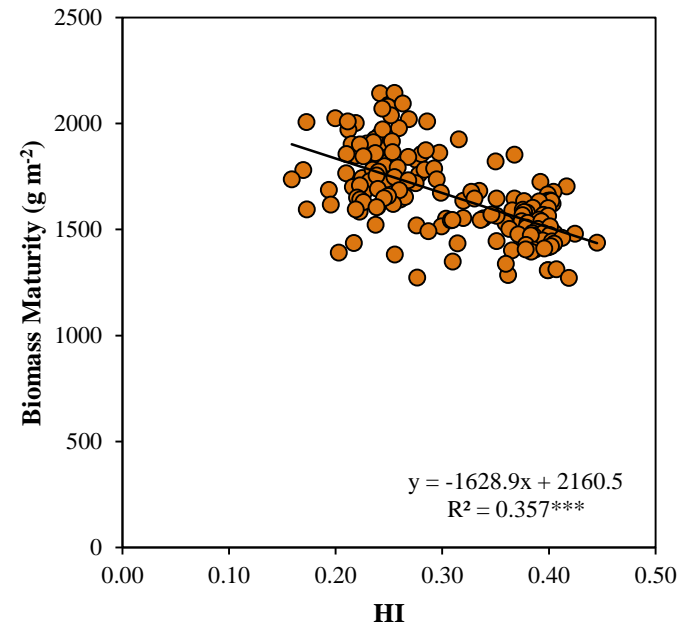
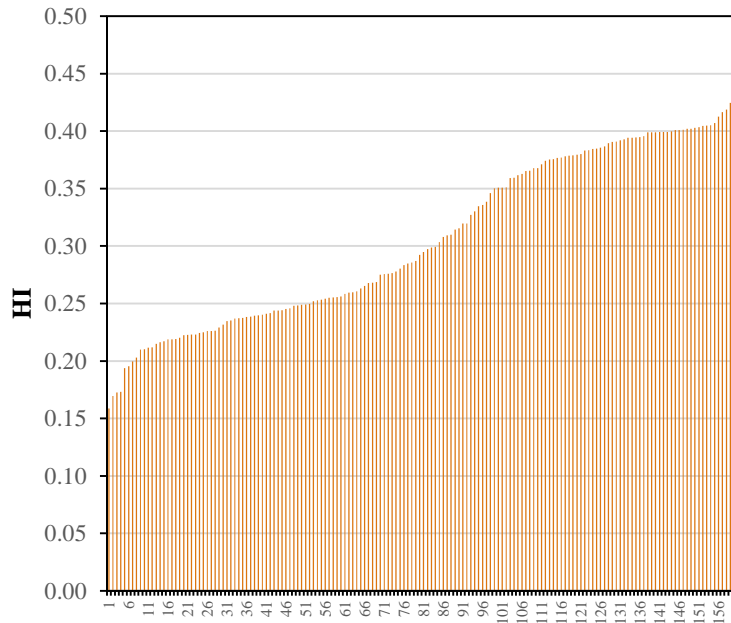
HiBAP, 2 years



HiBAP, Combined analysis 2015-2016 & 2016-2017

# Large genetic variation in HI in Primary Synthetics; trade off with biomass

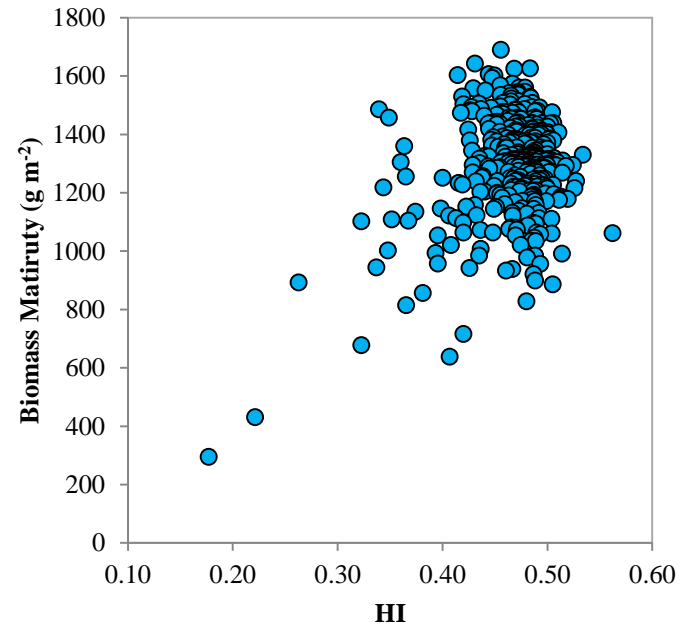
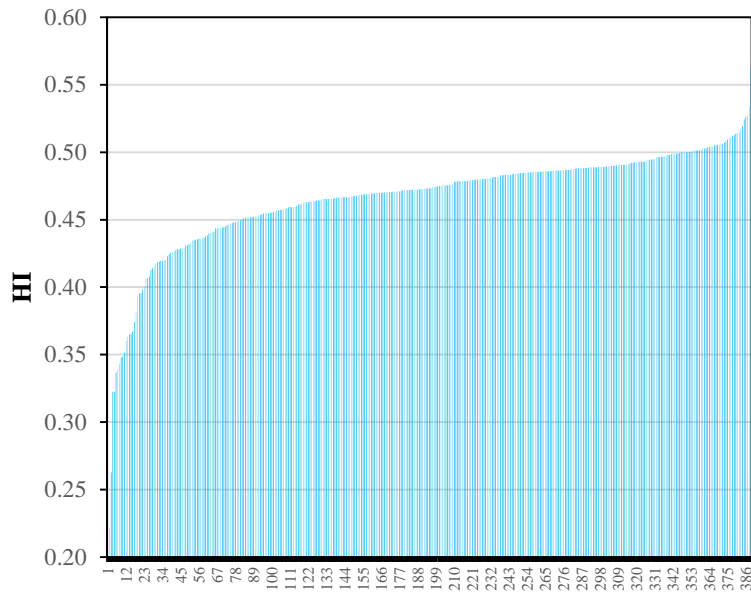
SynPan, 2 years



SynPan, Combined analysis 2015-2016 & 2016-2017

# Large genetic variation in HI in BW diversity Panel; **no** trade off with biomass

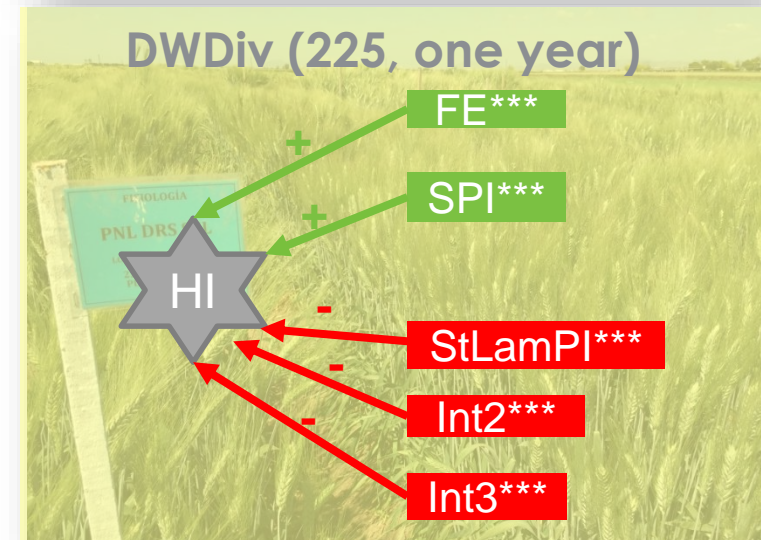
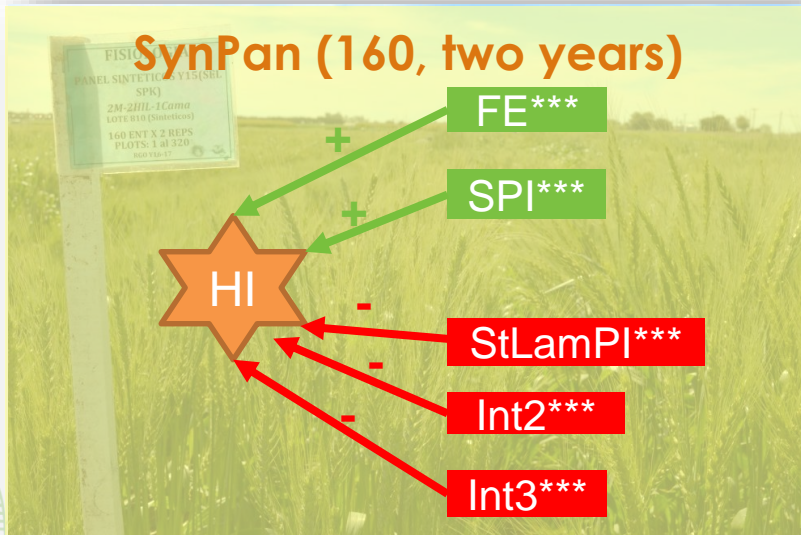
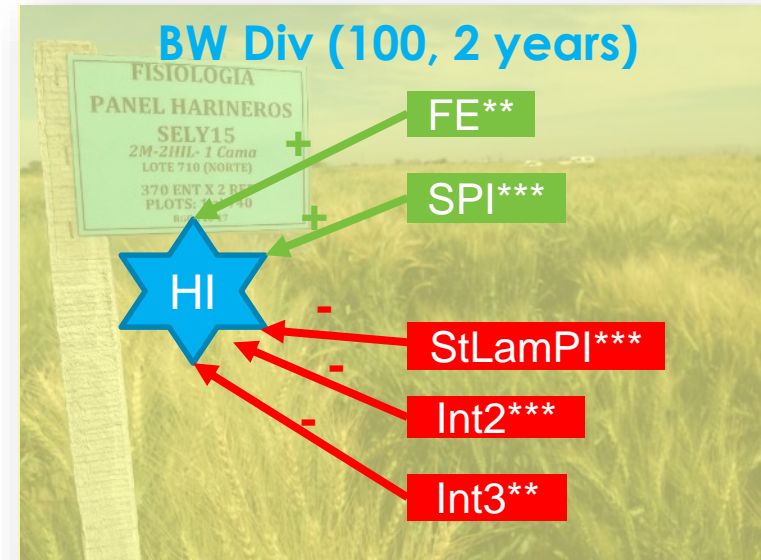
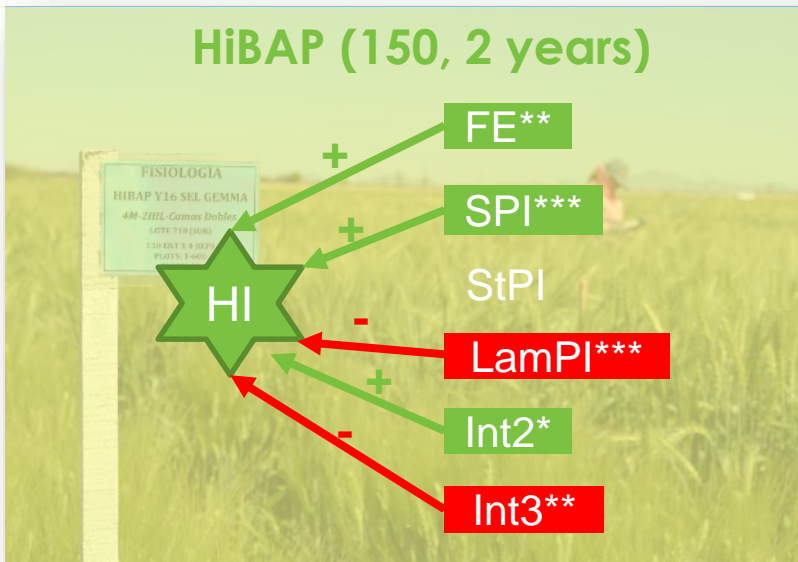
BWDiv, 2 years



BWDiv, Combined analysis 2015-2016 & 2016-2017, 390



Fruiting efficiency (# grains/spike dry wt), and Spike partitioning index (SPI) correlate with HI; Investment in Lamina and Internodes 2&3 negatively correlated



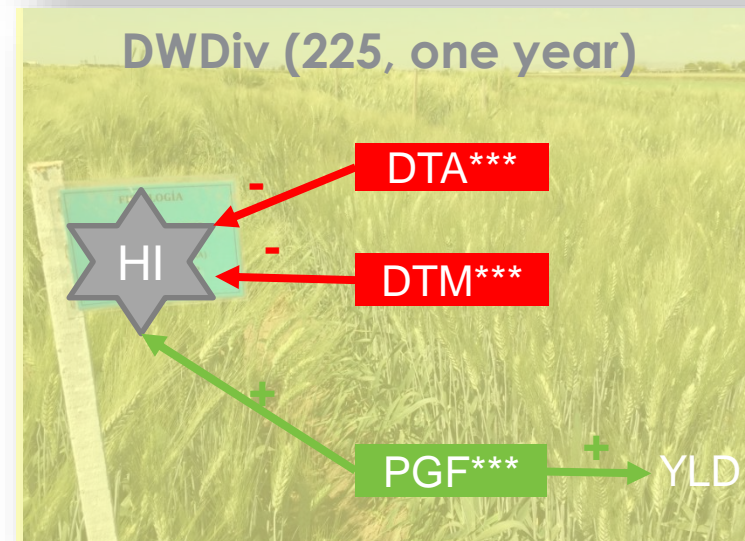
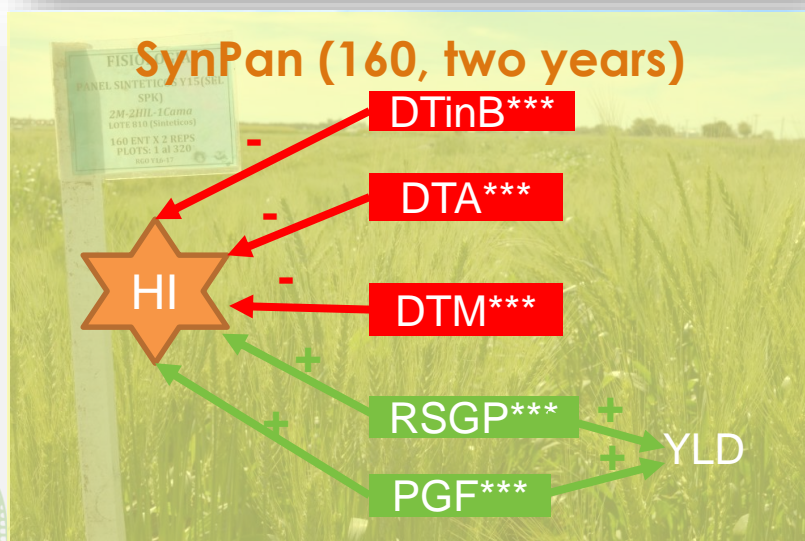
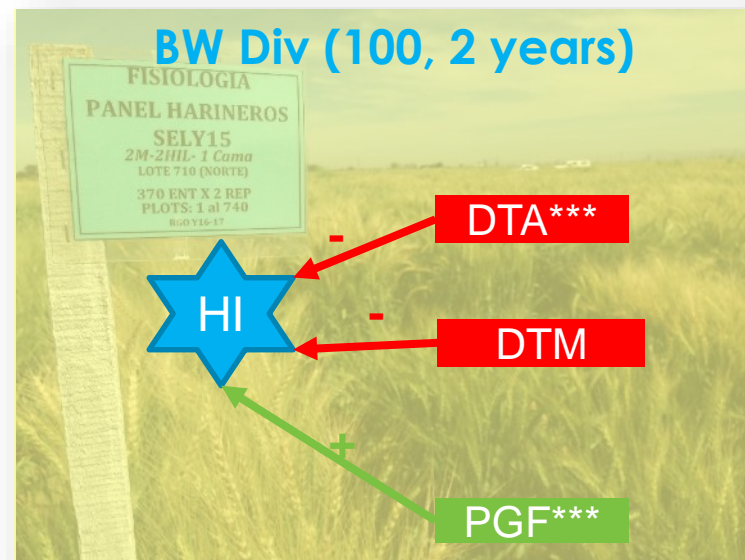
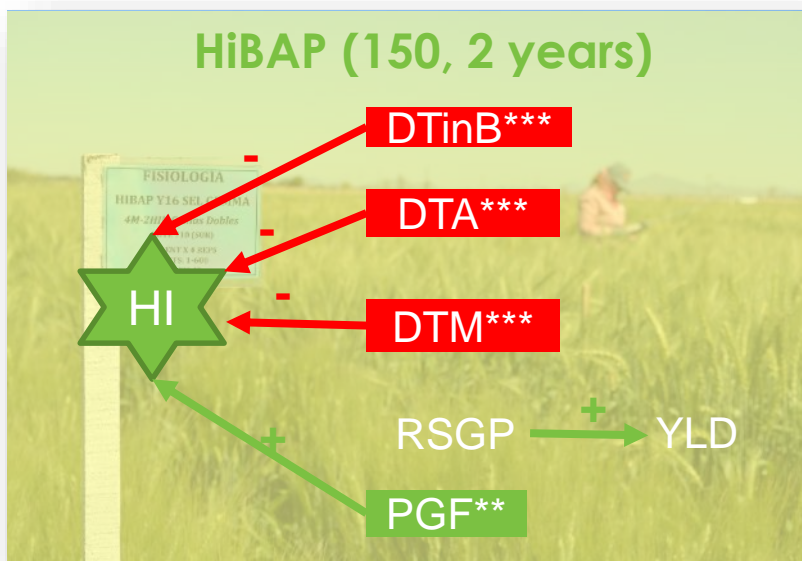
## ii. Study of phenological patterns to identify promising new sources of diversity for pre-breeding

Flowering time and phenological patterns including relative duration of:

- Rapid spike growth phase (RSGP): from initiation of booting to anthesis
- Grainfilling phase (PGF): from anthesis to physiological maturity



# Duration of grain filling period correlates with HI

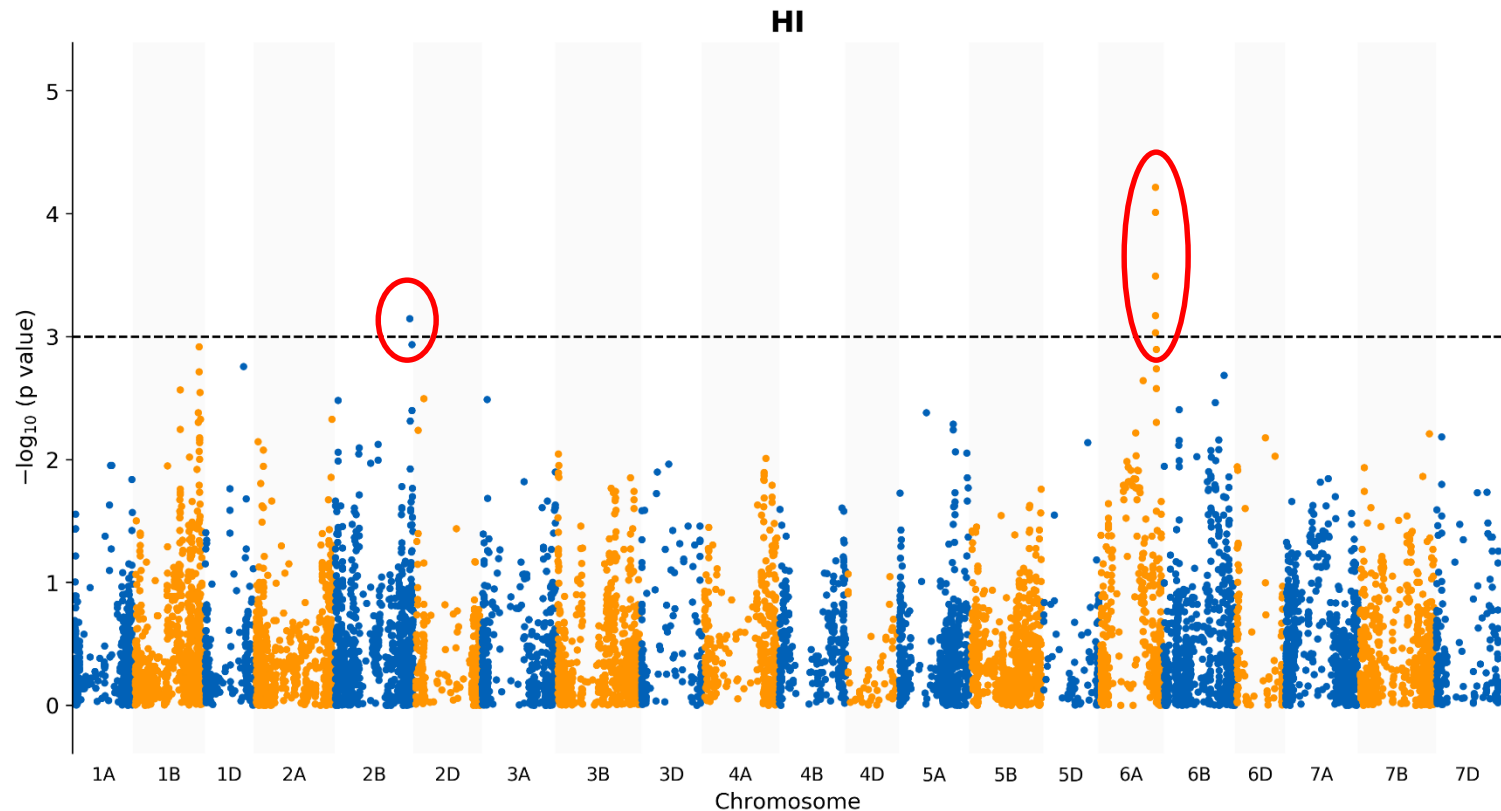


### iii. Identify lines with particular constellations of *Ppd*, *Vrn*, *Eps*, and *Rht* alleles that are associated with favorable expression of HI levels (IWYP25)

The Major genes and its alleles scored on the panels

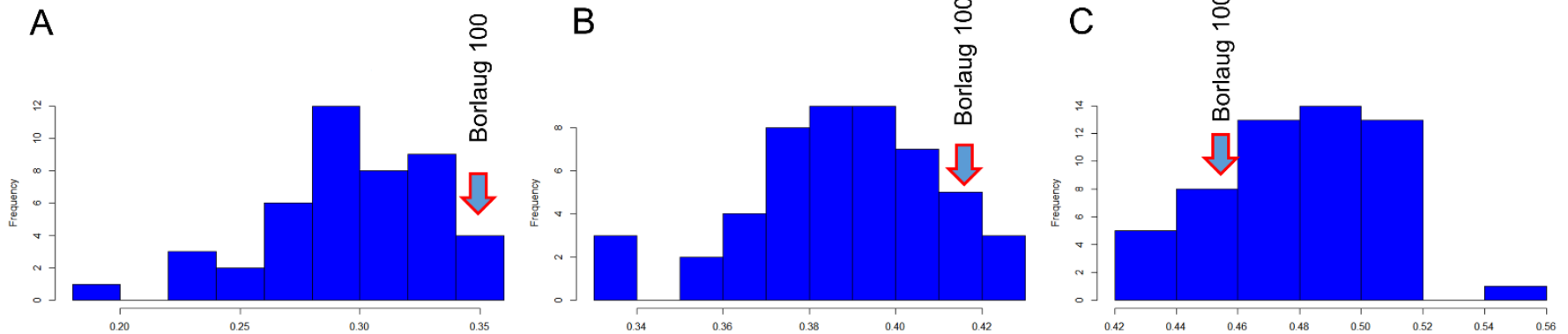
Gene/Allele	Marker	Description
Rht-B1	Rht-B1_SNP	C:C - Rht-B1a; T:T - Rht-B1b
Ppd-A1	GS105-1117ID	Ins: wildtype; Del: Ppd-A1 (GS105)
Ppd-A1	Cdex5-6ID	wt: Ppd-A1 (CD) sensitive-null
Ppd-B1	TaPpdBJ003	null: Ppd-Bb; A:A - Ppd-B1a(3x)
TaPpdDD001	TaPpdDD001	-: - : Ppd-D1a; Ins: Ppd-D1b
Ppd-D1	TaPpdDI001	Ins:Ppd-D1 (M) sensitive
Vrn-A1_9K0001	Vrn-A1_9K0001	G:G- Vrn-A1a; A:A- vrn-A1
Vrn-A1	Exon7_C/T_Vrn-A1	T:T (vrn-A1 (ex7) Veery allele
Vrn-B1a	Vrn-B1a	Vrn-B1a. Vrn-B1b, Vrn-B1c. vrn-B1
Vrn-D1-D1a_A	Vrn-D1-D1a_A	C:C: Vrn-D1a; G:G: vrn-D1
Vrn-D3	Vrn-D3F6/R8	Vrn-D3a, vrn-D3
TaFT3	TaFT3-B1_Kasp1	VIC: Rialto type
TaFT3-D1	FT3-Exon4_A/G	G:G: Rialto type, A:A: Spark type
Eps-D1	TaBradi2g14790	Ins: Rialto type, Del: Savannah type
Eps-D1	TaMOT1-D1	Ins: Rialto type, Del: Savannah type
TaTOE1-B	TaTOE1-B1_KASP1	Fam: Avalon type, VIC: Cadenza type, NA: Rialto

### iii. Identify molecular markers associated with HI and partitioning traits (IWYP64)



Trait	SNP_ID	Chromosome	Position_(bp)	p-Value	Effect
HI	AX-94728242	2B	7.64E+08	0.00072	0.08
	AX-94546552	6A	5.58E+08	0.00006	0.12

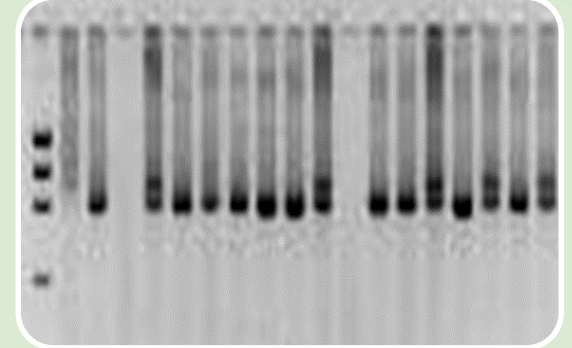
# HI of WYCYT international nurseries + its parents (A) 1<sup>st</sup> WYCYT (2) 2<sup>nd</sup> WYCYT and (3) 3<sup>rd</sup> WYCYT



Sukumaran et al, unpublished data



# Outputs



## i. Phenotyping

- >2,000 lines screened (**N-IWYP700**)
- Identification of outstanding lines
  - Mol. Markers identified for HI (2), FE (3), LamPI (3), SPI (2), StPI(4), Int3L (2) (**IWYP64 & N-IWYP700**)
- Strategic crosses (**IWYP-HUB**)

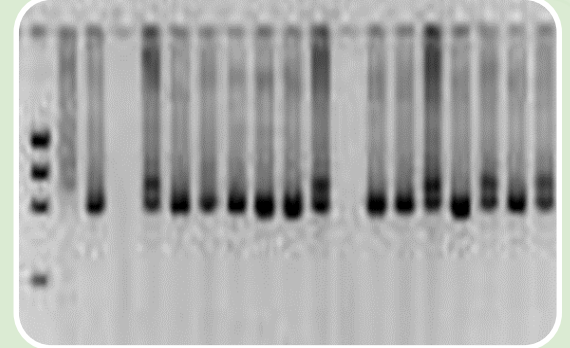
## ii. Pheno patterns

- > 2,000 lines screened ((**IWYP64, IWYP60**)
- Mol. Markers DTA (5), RSGP (4), PGF (4) (**IWYP64**)
- Strategic crosses (**IWYP-HUB**)

## iii. Genetic analysis

- Linked with IWYP25 for mayor genes
- Linked with N-IWYP700/IWYP64

# Next steps



## i. Phenotyping

- ~1,800 lines screened for HI: HiBAP II, New SynPan, hybrids, Canopy Aus (**AP05IWYP**), etc.
- Identification of new outstanding lines
- New Strategic crosses Y18-19 (**IWYP-HUB**)

## ii. Pheno patterns

- New Panel: HiBAP II, New SynPan, hybrids, Canopy Aus, etc.
- Identification of new outstanding lines
- New Strategic crosses Y18-19 (**IWYP-HUB**)

## iii. Genetic analysis

- Novel mayor genes combinations for maximum HI
- Identify other sources of variation for HI and partitioning traits



# Acknowledgements

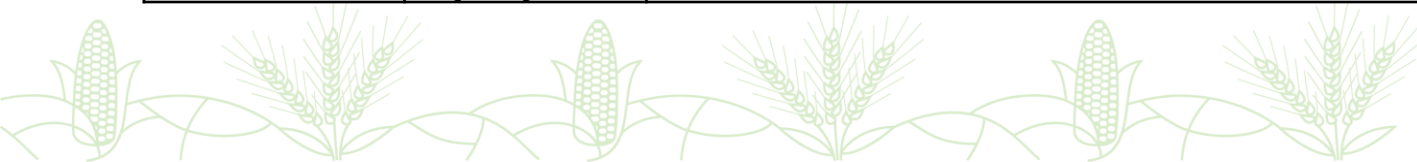


- • What are the research target(s)
- • Brief summary of the technical approaches taken (or incorporate where sensible)
- • Results to date, expected further results
- • How these results and research outputs should be applied and delivered for practical impact
- • Status - e.g., have any of the discoveries/outputs been transferred to the IWYP Hub, taken up by private industry, used in other projects, etc.
- • Next steps
- This should give you an idea of what we are looking for, i.e., less of a seminar/learning conference and more of a results driven team workshop focused on implementation to get practical results turned into delivered and applied products.



# Large genetic variation in HI and partitioning traits

		HI	Int2	Int3	StLamPI	SPI	FE
<b>HiBAP</b> <b>(n=150)</b> <b>2 years</b>	Mean	0.47	19.3	13.7	0.730	0.269	58.6
	<i>r</i> (YLD)	<b>0.40</b>	0.05	-0.08	<b>0.17</b>	<b>-0.18</b>	<b>0.31</b>
	<i>r</i> (BM)	<b>-0.46</b>	-0.10	0.14	<b>0.28</b>	<b>-0.30</b>	-0.05
<b>SynPan</b> <b>(n=160)</b> <b>2 years</b>	Mean	0.31	21.0	15.9	0.774	0.226	30.2
	<i>r</i> (YLD)	<b>0.88</b>	<b>-0.59</b>	<b>-0.72</b>	<b>-0.56</b>	<b>0.56</b>	<b>0.77</b>
	<i>r</i> (BM)	<b>-0.60</b>	<b>0.30</b>	<b>0.51</b>	<b>0.33</b>	<b>-0.33</b>	<b>-0.54</b>
<b>BWDiv</b> <b>(n=370)</b> <b>2 years</b>	Mean	0.47	20.2	14.1	0.756	0.244	47.3
	<i>r</i> (YLD)	<b>0.68</b>	<b>-0.31</b>	<b>-0.20</b>	<b>-0.33</b>	<b>0.33</b>	<b>-0.19</b>
	<i>r</i> (BM)	<b>0.33</b>	<b>-0.16</b>	-0.04	<b>-0.15</b>	<b>0.15</b>	<b>-0.16</b>
<b>DWDiv</b> <b>(n=225)</b>	Mean	0.45	17.4	13.2	0.735	0.265	38.6
	<i>r</i> (YLD)	<b>0.75</b>	<b>-0.45</b>	<b>-0.35</b>	<b>-0.40</b>	<b>0.40</b>	<b>0.28</b>
	<i>r</i> (BM)	0.04	-0.05	0.01	0.01	-0.01	0.01



# Phenological patterns from HiBAP studied during 2015-2016 and 2016-2017

		<b>DTInB</b>	<b>DTA</b>	<b>DTM</b>	<b>RSGP</b>	<b>PGF</b>
<b>HiBAP (n=150) 2 years</b>	Mean	61	76	115	13.7	33.4
	P-Value (G)	<b>0.00</b>	<b>0.00</b>	<b>0.00</b>	<b>0.00</b>	<b>0.00</b>
	<i>r</i> (YLD)	<b>-0.20</b>	-0.15	-0.15	<b>0.19</b>	0.10
	<i>r</i> (BM)	0.11	0.24	0.23	<b>0.17</b>	-0.15
	<i>r</i> (HI)	<b>-0.32</b>	<b>-0.43</b>	<b>-0.44</b>	-0.05	<b>0.27</b>
	<i>r</i> (TGW)	<b>-0.17</b>	<b>-0.17</b>	<b>-0.27</b>	0.09	-0.01
	<i>r</i> (GNO)	-0.05	-0.01	0.10	0.06	0.14
	<i>r</i> (FE)	0.14	0.14	<b>0.20</b>	-0.07	-0.01
	<i>r</i> (SPI)	<b>-0.50</b>	<b>-0.50</b>	<b>-0.50</b>	<b>0.20</b>	<b>0.33</b>
	<i>r</i> (StemPI)	0.00	-0.04	0.02	-0.07	0.09
	<i>r</i> (LamPI)	<b>0.40</b>	<b>0.43</b>	<b>0.37</b>	-0.16	<b>-0.31</b>



# Fruiting efficiency (# grains/spike dry wt), and Spike partitioning index (SPI) correlate with yield; Investment in Internodes 2&3 negatively correlated

Synthetic Panel

