

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/315668078>

Physiological traits to increase grain partitioning in high biomass cultivars in wheat

Conference Paper · March 2017

CITATIONS

0

READS

249

5 authors, including:



Aleyda Sierra Gonzalez
University of Nottingham

3 PUBLICATIONS 3 CITATIONS

[SEE PROFILE](#)



Alma Carolina Rivera-Amado
International Maize and Wheat Improvement Center

6 PUBLICATIONS 7 CITATIONS

[SEE PROFILE](#)



Gemma Molero
Consultative Group on International Agricultural Research

68 PUBLICATIONS 638 CITATIONS

[SEE PROFILE](#)



Matthew Reynolds
Consultative Group on International Agricultural Research

294 PUBLICATIONS 13,288 CITATIONS

[SEE PROFILE](#)

Some of the authors of this publication are also working on these related projects:



Wheat yield potential: identification of favourable ecophysiological attributes [View project](#)



AgMIP-Wheat [View project](#)

Physiological traits to increase grain partitioning in high biomass cultivars in wheat

Aleyda Sierra-Gonzalez^{1,2}, Carolina Rivera-Amado², Gemma Molero², Matthew Reynolds², John Foulkes¹

¹School of Biosciences, University of Nottingham, LE12 5RD, UK, ²CIMMYT, Int. Apdo. Postal 6-641, 06600 Mexico, DF, Mexico

Abstract

To meet global wheat demands it is important to expand our current understanding of how physiological traits are associated with genetic gains and to identify phenomic and genomic approaches to improve yield potential (Aisawi et al., 2015).

Yield is directly related to both biological yield (above-ground dry-matter per unit area; AGDM) and harvest index (grain yield/AGDM; HI), but in recent years the rate of genetic progress in HI has not increased; indeed, there is evidence for decreases in CIMMYT spring wheat modern cultivars as a result of a trade-off with increasing biomass (Aisawi et al., 2015). Therefore, it is important to identify new avenues for optimal dry matter (DM) partitioning of assimilates in order to improve grain sink strength – grain number – and HI in high biomass backgrounds as well as further identify genetic markers for these traits for application in marker-assisted selection.

A summary of the main DM partitioning data collected during 2015-16 in the CIMMYT high biomass spring wheat panel **HiBAP** (High Biomass Association Panel, 150 genotypes) is presented and discussed. The general aim is to identify combinations of novel DM partitioning traits to increase HI. Results showed a strong association amongst genotypes between grain yield and AGDM ($R^2=0.49$, $P<0.001$), a trade-off between AGDM and HI ($R^2=0.23$, $P<0.001$) and an association between enhanced HI and reduced length of internode 3 (peduncle -2) ($P<0.05$) at anthesis (GS65 +7d).

Introduction

Grain yield was historically increased with the introduction of the semi-dwarf *Rht* genes during the Green Revolution, by increasing assimilate availability to the developing spike favouring grain number per m² (GN) and harvest index (HI) (González et al., 2011; Lázaro & Abbate, 2012). Therefore, optimizing source-sink relationships before grain filling is critical for determining GN and grain yield. Increasing the amount of assimilate partitioning to the spike during the stem-elongation phase, in which the peduncle and other internodes are extending, is one opportunity to raise GN, by reducing the competition between the spike and alternative sink organs during this phase (Rivera-Amado, 2015). To achieve this, spike partitioning index (spike dry weight /AGDM at anthesis; SPI) has been identified as a trait that offers scope to enhance GN by making more of the total assimilates available to reproductive structures (Gaju et al., 2009; 2014). An alternative trait to increase GN is the fruiting efficiency (ratio of GN to spike dry weight at anthesis; FE) which is potentially additive to SPI (Ferrante et al., 2015; Foulkes et al., 2011; Lázaro & Abbate, 2012). This has been demonstrated in recent field investigations where genotypes combining high SPI with high FE were identified (Lázaro and Abbate 2012; Rivera-Amado, 2015).

Since Green Revolution HI values have increased, to ca. 0.45-0.50 in spring wheat and 0.50-0.55 in winter wheat (Foulkes et al., 2011) with a hypothetical limit of approximately 0.65 (Austin et al., 1980; Foulkes et al., 2011). Recent analysis of advanced CIMMYT spring wheat lines (Rivera-Amado et al., 2016) in the CIMCOG (Mexico Core Germplasm) panel has demonstrated that HI > 0.60 can theoretically be achieved given the ideal combination of traits including: (1) increased spike partitioning index through reduced stem structural dry matter, (2) increased fruiting efficiency, and (3) improved spike morphology (through decreased rachis specific weight and increased lemma partitioning). While stable expression of HI at values of 0.55 and above (Aisawi et al., 2015; Rivera-Amado, 2015; Shearman et al., 2005) would represent a step change in yield (given that the average expression in spring wheat is closer to

0.45), the ability to improve HI is currently restricted by a limited understanding of its genetic basis.

The aim of this project is to identify physiological traits associated with enhanced grain partitioning in high biomass backgrounds and to identify genetic markers for these traits through Genome Wide Association Study (GWAS) for application in marker-assisted selection.

Methods

A high biomass association panel (*HiBAP*) of 150 CIMMYT spring wheat genotypes was grown during the 2015-16 cycle at CIMMYT experimental station near Ciudad Obregón, NW Mexico. The panel was grown under full irrigated raised beds system, using an alpha-lattice design with four replications. The experiment was sown on the 24th November 2015 and harvested during the second week of May 2016.

Physiological traits were measured at different stages during the whole cycle, with emphasis at seven days after anthesis (GS65+7d), when a full DM partitioning analysis was carried out for the 150 genotypes (spike, leaf lamina and stem and leaf sheath DM proportions) including stem morphological related traits, such as internode lengths: internode 2 and 3 (peduncle -1 and -2, respectively). At physiological maturity, AGDM, grain yield and yield components were evaluated within a plot area of 4 m².

A similar but more detailed analysis of true-stem and leaf-sheath internode DM partitioning (peduncle, internode 2 internode 3 and internode 4+) was done in 30 genotypes *subset 1* at GS65+7d. The subset was selected to represent the full range found among the 150 genotypes for internode 2 and 3 length, spike, stem and lamina DM with a restricted range of anthesis date. From subset 1, a non-grain spike DM partitioning analysis (glume, palea, lemma, awns and rachis) was done at GS65+7d in 15 genotypes *subset 2*. The rationale for the selection of subset 2 was having a full range of dry matter partitioning for stem and leaf lamina components at GS65+7d and spike partitioning index (SPI).

Results/Discussion

DM partitioning traits at GS65+7d, fruiting efficiency and associations with key yield components traits

Wide genetic variation was found at GS65+7d for DM per shoot for each plant component: spike = 0.52-1.09 g per shoot ($P < 0.001$), stem+leaf sheath = 0.92-2.00 g per shoot ($P < 0.001$) and green lamina = 0.46-0.91 g per shoot ($P < 0.05$). Genetic variation was also found for DM partitioning indices (plant component DM as a proportion of total plant DM) calculated for each plant component: spike partitioning index (SPI) = 0.19-0.36 ($P < 0.001$), stem and leaf sheath partitioning index (StemPI) = 0.46-0.56 ($P < 0.001$) and lamina partitioning index (LamPI) = 0.18-0.28 ($P < 0.05$) (Fig. 1).

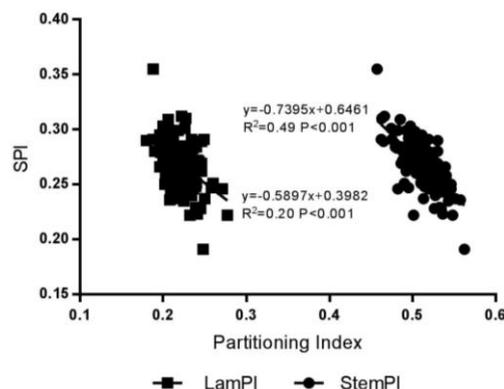
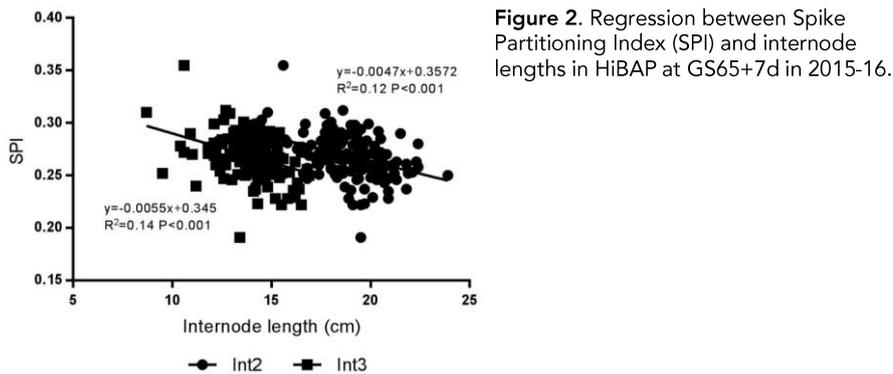


Figure 1. Regression between spike PI (SPI) and lamina PI (LamPI) and stem+leaf sheath PI (Stem PI) at GS65+7d stage in HiBAP during 2015-16.

Results showed a negative linear association between SPI and StemPI, indicating that a high DM partitioning to the spike was strongly associated with reduced DM partitioning to the stem at GS65+7d; there was also a weaker but significant negative relation between SPI and LamPI. Stem morphological traits showed that internode 3 length at GS65+7d ranged from 8.7-17.3 cm ($P < 0.001$) and internode 2 length from 14.2-23.9 cm ($P < 0.001$). A negative linear association was found between SPI and internode 2 length ($R^2=0.12$, $P < 0.001$) and internode 3 length ($R^2 = 0.14$, $P < 0.001$; Fig. 2). These preliminary results suggest that genotypes with a longer internode 2 and 3 compete more with the spike for assimilate at GS65+7d and could be related to reduced GN and HI within HiBAP genotypes.



A more detailed internode DM partitioning analysis was done on 30 genotypes (*subset 1*). Genetic variation among genotypes was found for true stem (TS) and leaf sheath (LS) DM partitioning indices at each internode (internode PI) with a positive association between GN and true-stem internode 2 PI ($R^2 = 0.20$, $P < 0.05$; Fig.3).

For the 15 genotypes of HiBAP (*subset 2*), the DM partitioned to the different spike structural components was determined at GS65+7d showing that dry matter was allocated according to the following pattern: lemma > awns > glumes > rachis > palea. Genetic variation was found for all spike component partitioning indices (spike component DM/total spike DM excluding grain) and there was a positive association between DM per spike and each of rachis PI ($R^2=0.176$, $P < 0.01$) and palea PI ($R^2=0.113$, $P < 0.05$). However, there were no statistically significant associations between spike DM partitioned to each component (glumes, lemma, palea, awns, rachis PIs) and FE (data not shown).

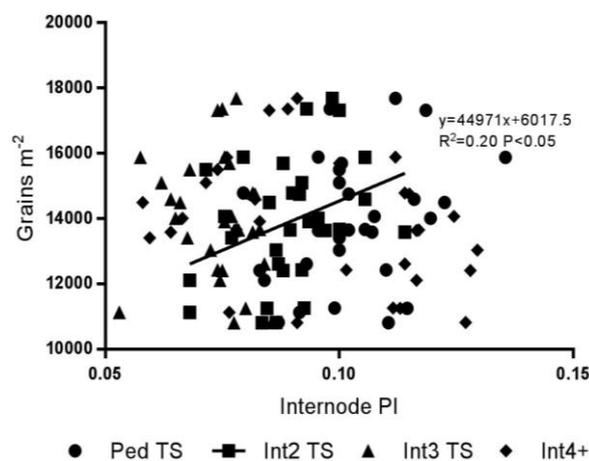


Figure 3. Regression of grains m^{-2} vs true stem internode PIs at GS65+7 days in HiBAP experiment 2015-6.

Physiological maturity traits: grain yield and its components

Overall, grain yield ranged amongst HiBAP genotypes from 487 to 797 g m⁻² ($P < 0.001$) and GN from 10,815-17,689 ($P < 0.001$). A positive linear association was found between grain yield and GN ($R^2=0.21$, $P < 0.001$; Fig. 4a), as well as a weaker association between grain yield and HI ($R^2=0.05$, $P < 0.05$; Fig 4b). There was a strong association between grain yield and AGDM ($R^2=0.49$, $P < 0.001$; Fig 4c), but also a trade-off between AGDM and HI ($R^2=0.23$, $P < 0.001$; Fig 4d). Moreover, a trend for a trade-off was found between FE and SPI ($R^2=0.10$, $P < 0.05$), indicating higher SPI was associated with more chaff per grain.

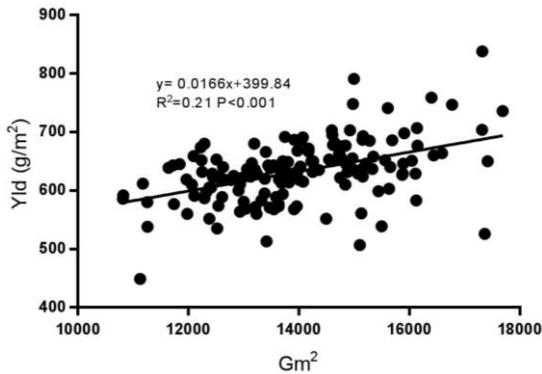


Figure 4a. Regression between grain yield and grains per meter square at PM in HiBAP 2015-6.

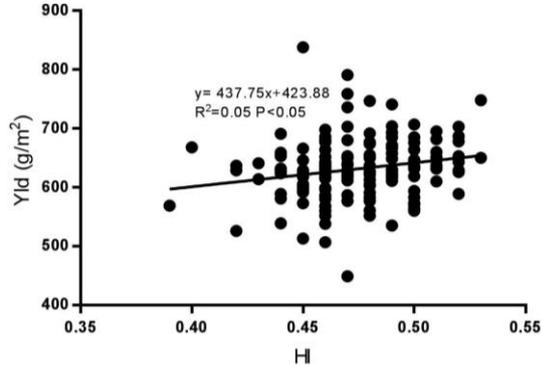


Figure 4b. Regression between grain yield and HI at physiological maturity in HiBAP 2015-6.

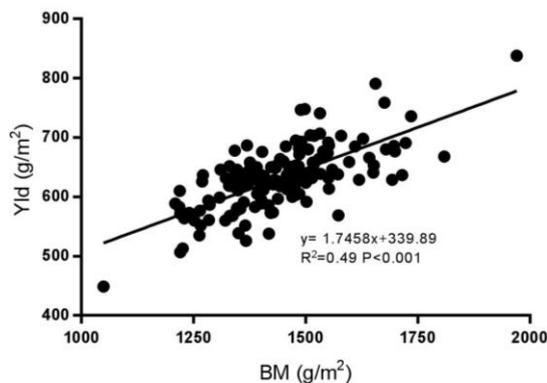


Figure 4c. Regression between yield and biomass at physiological maturity in HiBAP 2015-6.

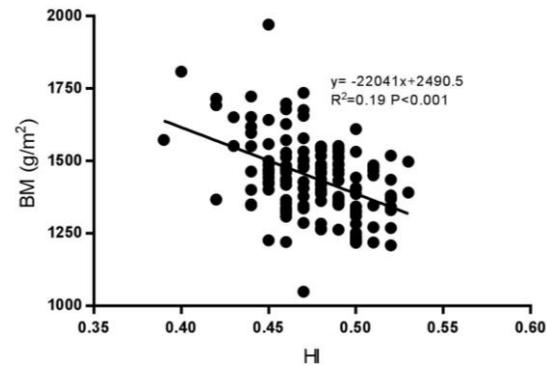


Figure 4d. Regression between biomass (AGDM) and HI at physiological maturity in HiBAP 2015-6.

Overall summary: spring wheat HiBAP field cycle 2015-16

In Table 2 a summary of the genetic ranges for key traits measured at GS65+7d and physiological maturity is shown, as well as correlations with grain yield), harvest index and grain number per meter square. Results showed that fruiting efficiency was positively correlated with HI ($r = 0.37$, $P < 0.001$) and GN ($r = 0.41$, $P < 0.001$). Spike partitioning index was also positively correlated with HI ($r = 0.22$, $P < 0.01$) and with GN ($r = 0.17$, $P < 0.05$). There were also negative correlations between internode 3 length and HI ($r = -0.22$, $P < 0.01$) and GN ($r = 0.27$, $P < 0.001$).

Table 2. Genetic ranges for DM partitioning traits at GS65+7d and correlations with grain yield (GY), harvest index (HI) and grain number per meter square (GN) for HiBAP in 2015-16.

Traits	Range (Min-Max)	Prob.	Correlation (r)			
			GY	HI	GN	
Yield (g m ⁻²)	449.3-837.8	***	-	0.20*	0.46***	
Harvest Index	0.39-0.53	***	0.20*	-	0.14ns	
Grains m ⁻²	10,815-17,689	***	0.46***	0.14ns	-	
Fruiting Eff. (grains g ⁻¹)	41.0-97.6	***	-0.03ns	0.37***	0.41***	
DM g m ⁻²	GS65 + 7 d	604.78	***	0.08ns	-0.21**	0.02ns
	Physiol. mat.	1049-1971	***	0.70***	-0.44***	0.26***
Length (cm)	Internode 2	14.2-23.9	***	0.07ns	0.06ns	-0.11ns
	Internode 3	8.7-17.3	***	-0.03ns	-0.22**	-0.27***
DM g shoot ⁻¹	Stem	0.92-2.00	***	0.20*	-0.34***	-0.26***
	Spike	0.52-1.09	***	0.17*	-0.18*	-0.14ns
	Lamina	0.46-0.91	**	0.18*	-0.35***	-0.24**
Part. Index GS65+7d	Stem	0.46-0.56	***	0.10ns	-0.19*	-0.15ns
	Spike	0.19-0.36	***	-0.04ns	0.22**	0.17*
	Lamina	0.18-0.28	*	-0.07ns	-0.05ns	-0.03ns

Next steps:

- ☞ Data from a second year of the HiBAP experiment are needed to confirm results obtained in the cycle 2015-16, as well as to be able to run a more detailed analysis to test specific hypotheses within subsets of genotypes 1 and 2 in 2016-17.
- ☞ Using SNPs (Single Nucleotide Polymorphism) a Genome Wide Association Study (GWAS) will be done in the HiBAP experiment to identify marker-trait associations for the key DM partitioning traits determining SPI and FE to increase HI in high biomass backgrounds.
- ☞ For a winter wheat Savannah x Rialto DH population, a DM partitioning data set has been collected in a field experiment at Nottingham 2015-16, UK (data not shown in this paper). The experiment will be repeated in 2016-17 and a QTL (Quantitative Trait Loci) analysis will be run to determine the chromosomal locations for DM partitioning traits.
- ☞ Associations between phenotypic and genomic data will be quantified in the spring and winter panel/population to review the possibility of having common selection criteria for raising HI in high biomass backgrounds in spring and winter wheat breeding programs.

Acknowledgments

We thank CONACYT, MasAgro and The University of Nottingham for funding the PhD studentship of Aleyda Sierra-Gonzalez. We are grateful to Dr Francisco Piñera-Chavez for his advice and the CIMMYT Wheat Physiology team for their help with the collection of field data in the HiBAP experiment.

References

- Aisawi, K. A. B., Reynolds, M. P., Singh, R. P., & Foulkes, M. J. (2015a). The physiological basis of the genetic progress in yield potential of CIMMYT spring wheat cultivars from 1966 to 2009. *Crop Science*, 55(4), 1749–1764. <http://doi.org/10.2135/cropsci2014.09.0601>
- Aisawi, K. A. B., Reynolds, M. P., Singh, R. P., & Foulkes, M. J. (2015b). The Physiological Basis of the Genetic Progress in Yield Potential of CIMMYT Spring Wheat Cultivars

- from 1966 to 2009. *Crop Science*, 55(4), 1749.
<http://doi.org/10.2135/cropsci2014.09.0601>
- Austin, R. B., Bingham, J., Blackwell, R. D., Evans, L. T., Ford, M. a., Morgan, C. L., & Taylor, M. (1980). Genetic improvements in winter wheat yields since 1900 and associated physiological changes. *The Journal of Agricultural Science*, 94, 675.
<http://doi.org/10.1017/S0021859600028665>
- Ferrante, A., Savin, R., & Slafer, G. a. (2015). Relationship between fruiting efficiency and grain weight in durum wheat. *Field Crops Research*, 177, 109–116.
<http://doi.org/10.1016/j.fcr.2015.03.009>
- Foulkes, M. J., Slafer, G. a., Davies, W. J., Berry, P. M., Sylvester-Bradley, R., Martre, P., ... Reynolds, M. P. (2011). Raising yield potential of wheat. III. Optimizing partitioning to grain while maintaining lodging resistance. *Journal of Experimental Botany*, 62(2), 469–486. <http://doi.org/10.1093/jxb/erq300>
- Gaju, O., Allard, V., Martre, P., Le Gouis, J., Moreau, D., Bogard, M., ... Foulkes, M. J. (2014). Nitrogen partitioning and remobilization in relation to leaf senescence, grain yield and grain nitrogen concentration in wheat cultivars. *Field Crops Research*, 155, 213–223. <http://doi.org/10.1016/j.fcr.2013.09.003>
- Gaju, O., Reynolds, M. P., Sparkes, D. L., & Foulkes, M. J. (2009). Relationships between large-spike phenotype, grain number, and yield potential in spring wheat. *Crop Science*, 49(3), 961–973. <http://doi.org/10.2135/cropsci2008.05.0285>
- González, F. G., Miralles, D. J., & Slafer, G. a. (2011). Wheat floret survival as related to pre-anthesis spike growth. *Journal of Experimental Botany*, 62, 4889–4901.
<http://doi.org/10.1093/jxb/err182>
- Lázaro, L., & Abbate, P. E. (2012). Cultivar effects on relationship between grain number and photothermal quotient or spike dry weight in wheat. *The Journal of Agricultural Science*, 150(4), 442–459. <http://doi.org/10.1017/S0021859611000736>
- Rivera-Amadao, C., Trujillo-Negrellos, E., Sylvester-Bradley, R., , Molero, G., Sierra-Gonzalez, A., Reynolds, M.P., Foulkes, M. J. (2016). Achieving increases in spike growth, fruiting efficiency and harvest index in high biomass wheat cultivars. *Conference Paper: 2nd International TRIGO (Wheat) Yield Potential*, (Workshop March 2016).
- Rivera-Amado, A. C. (2015). Identifying physiological traits to optimize assimilate partitioning and spike fertility for yield potential in wheat (*Triticum aestivum* L.) genotypes. *PhD Thesis, University of Nottingham School of Biosciences, Sutton Bonnington Campus, Leicestershire, UK*, (September).
- Shearman, V. J., Scott, R. K., & Foulkes, M. J. (2005). Crop Physiology and Metabolism. Physiological Processes Associated with Wheat Yield Progress in the UK. *Crop Science*, 185, 175–185. <http://doi.org/10.2135/cropsci2005.0175>