

1 Relationships between physiological traits, grain number and yield  
2 potential in a wheat DH population of large spike phenotype  
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5 Oorbessy Gaju <sup>a</sup>, Matthew P. Reynolds <sup>b</sup>, Debbie L. Sparkes<sup>a</sup>, Sean Mayes<sup>a</sup>, Gracia Ribas-  
6 Vargas<sup>a</sup>, Jose Crossa <sup>b</sup>, and M. John Foulkes <sup>a,\*</sup>  
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8 <sup>a</sup> *Division of Plant and Crop Sciences, School of Biosciences, University of Nottingham,*  
9 *Leicestershire, LE12 5RD, UK*

10 <sup>b</sup> *CIMMYT International Maize and Wheat Improvement Center (CIMMYT), Km. 45,*  
11 *Carretera Mexico, El Batan, Texcoco, Mexico*  
12  
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14  
15

16 \* Corresponding author at: *Division of Plant and Crop Sciences, School of Biosciences,*  
17 *University of Nottingham, Leicestershire, LE12 5RD, UK.*

18 Tel.: +44 1159 516024; fax: + 44 1159 516060 .

19 E-mail address: [John.Foulkes@nottingham.ac.uk](mailto:John.Foulkes@nottingham.ac.uk) (M. John Foulkes)  
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23 **Abstract**

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25 Our objective was to investigate the relationships between spike traits, grain number and yield  
26 potential and their physiological basis in a doubled-haploid (DH) population derived from a  
27 cross between a CIMMYT spring wheat (*Triticum aestivum* L.) advanced line of large-spike  
28 phenotype (LSP2; *+Tin1* tiller inhibition gene) and the UK winter wheat cultivar Rialto (R; -  
29 *Tin1*) of conventional spike phenotype. Field experiments were carried out in high radiation,  
30 irrigated conditions in NW Mexico in two seasons. Comparing the two groups of *+Tin1* and -  
31 *Tin1* DH lines, results showed the presence of the *+Tin1* allele for tiller inhibition increased  
32 spike partitioning index (spike DM / above-ground DM at GS61+5d ;SPI) from 0.32 to 0.34  
33 (+6.3%) ( $P < 0.01$ ) and grains spike<sup>-1</sup> by 5.1 (+13.9%) ( $P < 0.001$ ), but reduced spikes m<sup>-2</sup> by  
34 20.7 (-5.7%) ( $P < 0.01$ ). Overall a significant increase in grains m<sup>-2</sup> of 865 (+6.6%) was observed  
35 in *+Tin1* DH lines compared to *-Tin1* DH lines ( $P < 0.05$ ), but the effect on grain yield was not  
36 statistically significant. Spike partitioning index was positively correlated with spike biomass  
37 per unit area amongst the 57 DH lines ( $r = 0.58$ ,  $P < 0.001$ ). There was a negative correlation  
38 between SPI and the spike partitioning index (grains per gram spike DM at GS61+5d; FE) ( $r = -$   
39  $0.59$ ,  $P < 0.01$ ); and for future application of large-spike phenotype it will be important to  
40 minimise this trade-off between SPI and FE. Our results indicated that introgressing the *+Tin1*  
41 allele into modern wheat germplasm may offer scope to increase grains spike<sup>-1</sup> and grains m<sup>-2</sup> in  
42 irrigated, high radiation environments.

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55 **Key words:** Spike fertility, assimilate partitioning, tiller inhibition, awns, wheat breeding

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## 57 **1. Introduction**

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59 Wheat (*Triticum aestivum* L.) is globally one of the three most important cereal crops  
60 grown on more than 214 million hectares of land with an average grain yield of 2.83 t ha<sup>-1</sup>  
61 (FAOSTAT, 2011). Since global demand for wheat is predicted to increase at a faster rate  
62 (Rosegrant & Agcaoili 2010) than the current annual genetic gains of ca. 1% (Shearman *et*  
63 *al.*, 2005; Fischer, 2007; Miralles and Slafer, 2007; Zhou *et al.*, 2007, Clarke *et al.*, 2012),  
64 improvement in genetic yield potential will need to be accelerated. Genetic gains have  
65 historically been achieved by improvements in grain number per square metre (GN), with  
66 little change in individual grain weight (Foulkes *et al.*, 2009, 2011; Reynolds *et al.*, 2009,  
67 2012). Semi-dwarf cultivars introduced in the 1960s and 1970s contributed large increases in  
68 GN associated with more fertile florets per spike as a consequence of increased assimilate  
69 partitioning to the spike during the pre-flowering period (Fischer, 1983). Since then, there  
70 have been continued improvements in both GN and HI in breeding programs worldwide  
71 (Reynolds *et al.*, 1999; Foulkes *et al.*, 2009; Peltonen-Sainio *et al.* 2009; Reynolds *et al.*,  
72 2011, 2012; Clarke *et al.*, 2012).

73 Wheat is generally reported to be a sink-limited crop under favourable conditions with  
74 grain growth limited by the storage capacity of the grains for assimilate during the grain  
75 filling period (Borghetti *et al.*, 1986; Savin and Slafer, 1991; Fischer *et al.*, 1998; Austin, 1999;  
76 Borras *et al.*, 2004; Acreche and Slafer, 2009; Foulkes *et al.* 2011).. Therefore strategies to  
77 improve spike fertility are one of the most important avenues in the genetic improvement of  
78 yield potential (Slafer and Savin 1994; Reynolds *et al.*, 2005, Fischer, 2007; Miralles and  
79 Slafer, 2007; Foulkes *et al.*, 2011; Reynolds *et al.* 2012). In this respect, there is recent  
80 evidence from a study in spring wheat in the CIMMYT program in NW Mexico that novel  
81 large-spike phenotype (LSP) traits (e.g. high assimilate partitioning to spike, long rachis, high  
82 spikelet number per spike, high fertile florets per spikelet) may offer scope for increasing  
83 spike fertility and GN in future years (Gaju *et al.*, 2009).

84 Large-spike “Gigas” phenotypes, having up to 30 spikelets, 9 grains per spikelet and  
85 individual grain weight of 63 mg, were characterised by Atsmon and Jacobs (1977),  
86 exhibiting tiller inhibition attributed to a single recessive gene *Tin1* on chromosome 1AS  
87 (Richards, 1988; Spielmeyer and Richards, 2004). In Australia under terminal drought,  
88 averaging effects in four pairs of near-isogenic lines, the *Tin1* gene increased grains per spike  
89 (+9%), but decreased spikes per square meter (-11%) and grain weight (-2%); with overall a

90 neutral effect on grain yield (Duggan *et al.*, 2005). Elsewhere in Eastern Europe, crosses with  
91 wheats having novel tetrastichon spike morphology succeeded in boosting number of  
92 spikelets per spike (+10%), grains per spikelet (+9%) and GN (+18%) compared to the parent  
93 with normal spikes, although GN and individual grain weight were negatively correlated  
94 (Dencic, 1994). Motzo *et al.* (2004), examining the progeny of bread wheat genotypes Kite  
95 and Janz containing the *Tin1* gene crossed with the durum wheat (*Triticum turgidum* subsp.  
96 *durum*) cultivars Simeto and Valbelice, observed that the *Tin1* gene increased HI from 0.31 in  
97 freely tillering plants to 0.35 in uni- and bi-culm plants. Low tillering was associated with  
98 greater grain yields per spike, mainly resulting from greater spikelet fertility (up to 3.5 grains  
99 per fertile spikelet) and a lower incidence of sterile spikelets. In general, it can be concluded  
100 that restricted tillering to boost spike size in many cases worldwide did not increase grains  
101 per unit area due to a large degree of plasticity amongst yield components. So for future  
102 application of large-spike phenotype in breeding programs, it may be important to identify  
103 large-spike phenotypes associated with only moderate reductions in tillering capacity.

104         Restructured hexaploid wheat plant types exploiting heterosis were developed at  
105 CIMMYT during the 1990s, through a wide-crossing program involving *Agropyron*  
106 *elongatum* L., *Triticum polonicum* L. and *Triticum aestivum* L. var. Morocco wheat (Rajaram  
107 and Reynolds, 2001). These novel wheats, when grown as spaced plants, have intermediate  
108 tillering capacity (up to 10 tillers), long spikes (30 cm) and high spike fertility (up to 200  
109 grains per spike). CIMMYT has developed new advanced lines derived from crosses with  
110 these novel wheats which have more grains per spike compared to modern CIMMYT releases  
111 when grown as spaced plants. Previously, we examined the CIMMYT wheat advanced line of  
112 large-spike phenotype (LSP2, +*Tin1*) compared with the check cultivar, Bacanora (-*Tin1*), in  
113 high radiation, irrigated field conditions in NW Mexico (Gaju *et al.*, 2009). Results showed  
114 for LSP2 spikelets per spike (+4%), grains per spike (+5%) and individual grain weight  
115 (+10%) were increased compared to Bacanora, but grain yield was reduced (-8%) due to  
116 fewer spikes per square metre (-26%). In the present paper, we present the results of the field  
117 analysis of effects of the presence/absence of +*Tin1* in a doubled-haploid (DH) population  
118 derived from a cross between LSP2 and Rialto. Rialto is a UK winter wheat cultivar released  
119 in 1995 and was selected as a parental line due to its high expression of both sink-type (grains  
120 per spike) and source-type (radiation-use efficiency and stem carbohydrate reserves) traits  
121 amongst UK cultivars (Shearman *et al.*, 2005). A degrading treatment (removal of 50% of  
122 the spikelets per spike) was carried out at GS61+14d) to assesses whether grain growth

123 amongst the *+Tin1* and *-Tin1* lines was limited by grain source or grain sink size. Grain  
124 growth responses to degrading (where assimilate supply per grain is increased by 100%) of  
125 ca. 0-10% are indicative of sink limitation of grain growth, whereas those of ca. 10-20% are  
126 indicative of co-limitation of grain growth by sink during the earlier phase of grain fill and  
127 source during the latter phase of grain fill (Acreche and Slafer, 2009).

128 The objectives of the present study were to examine the association of  
129 presence/absence of the *Tin1* gene with grains per m<sup>2</sup>, grain yield and associated  
130 physiological traits and its physiological basis in a wheat LSP2 x Rialto DH population  
131 segregating for the *Tin1* gene.

132

## 133 **2. Materials and Methods**

134

### 135 *2.1 Plant material*

136

137 The CIMMYT spring wheat LSP2 for  
138 CMH79A.955/4/AGA/3/4\*SN64/CNO67//INIA66/5/NAC was crossed with the UK winter  
139 wheat cultivar Rialto to generate a doubled-haploid (DH) population, using the maize  
140 pollination technique (Laurie and Bennett, 1986). A total of 138 lines were developed.  
141 However, only 57 DH lines were used in the present experiments carried out in Ciudad  
142 Obregon, NW Mexico. The LSP2 advanced line contains the dominant spring wheat *Vrn-A1*  
143 allele for vernalization response on chromosome 5A, whereas the winter wheat Rialto  
144 contains the recessive *vrn-A1* allele; similarly LSP2 contains the dominant *Ppd-D1a* allele for  
145 photoperiod insensitivity on chromosome 2D, whereas Rialto contains the recessive *Ppd-D1b*  
146 allele for photoperiod sensitivity. The progeny thus segregated for winter/spring vernalization  
147 and photoperiod sensitivity/insensitivity characteristics. The DH populations were initially  
148 grown as spike rows in a glasshouse under natural photoperiod at CIMMYT, El Batan,  
149 Mexico City in 2001-2 and 2002-3 and 57 of the LSP2 x Rialto (R) DH lines were selected  
150 for field analysis on the basis of acceptable flowering dates, i.e. those lines exhibiting  
151 photoperiod insensitivity and nil or low vernalization requirements.

152 The LSP2 (*+Tin1*) x Rialto (R) (*-Tin1*) population was segregating for the *Tin1* gene;  
153 and the 57 lines of this population were genotyped for three SSR markers in the vicinity of  
154 the gene on the short arm of chromosome 1 (Gdm33, W49 and Wms136). The 57 lines  
155 examined in the present study were also genotyped for the *Rht-B1a* (*tall*) and *Rht-B1b* (*semi-*

156 *dwarf*) gene for gibberellic acid-insensitivity and plant height using a perfect marker (Ellis *et*  
157 *al.*, 2002); LSP2 (*Rht-B1b* for semi-dwarf allele) and Rialto (*Rht-B1a* for tall allele). Both  
158 parental lines possessed the *Rht-D1b* semi-dwarf allele of the *Rht-D1* gene. The 57 DH lines  
159 were also segregating for the presence and absence of awns (LSP2 awned and Rialto  
160 unawned).

161

## 162 2.2 Site and experimental treatments

163

164 The experiments were located at CIMMYT experimental station near Ciudad Obregon,  
165 North West Mexico located at 27° 20' N, 109° 54' W, 38 m above sea level in the state of  
166 Sonora. The soil type at the experimental station is a coarse sandy clay, mixed montmorillonitic  
167 type calciorthid, low in organic matter and slightly alkaline (pH 7.7) in nature (Sayre *et al.*,  
168 1997). One experiment was carried out examining 57 DH lines from the LSP2 x R DH  
169 population in each of 2004-5 in 2005-6. The experimental design was an alpha-lattice with  
170 two replicates. Plot size was 5 x 1.6 m on raised beds (2 beds per plot; 2 rows per bed). The  
171 width of the bed was 80 cm, with 30 cm between rows. In the experiment in 2004-5 the LSP2  
172 parental line was not included but in 2005-6 it was. The UK winter wheat Rialto parent was  
173 not included in the field experiments since it is photoperiod sensitive (*Ppd-D1b*) and has a  
174 vernalization requirement (*Vrn-A1*) and is unadapted to the growing conditions in NW  
175 Mexico. In addition, in 2005-6, a subset of eight DH lines from the LSP2 x R population was  
176 sown in a third experiment in four replicates using a randomised block design. Plot size was 5  
177 x 1.6 m on raised beds (2 beds per plot; 2 rows per bed) with duplicate plots, one designated  
178 for growth analysis and the other for machine-harvested yield. The subset of eight DH lines  
179 was selected to represent two groups of *+Tin1* and *-Tin1* lines which were overall balanced  
180 for anthesis date and plant height, and with the eight individual DH lines representing  
181 restricted ranges for anthesis date and plant height.

182

## 183 2.3 Plot management

184

185 The experiments were sown on 24 November 2004 and 22 November 2005 with 80 g  
186 seed per plot (approximately 300 seeds m<sup>-2</sup>). In each experiment, plots were irrigated using a  
187 gravity-based system with flood irrigations four to six times during the crop cycle at 3- to 4-  
188 week intervals to supply adequate moisture to avoid water stress during the growing season.

189 In each season, 150 kg ha<sup>-1</sup> nitrogen fertilizer as urea was applied in a two-split program; the  
190 first half was applied to the seed bed during land preparation shortly before planting and the  
191 other at the time of the first irrigation close to the onset of stem elongation. Fifty kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>  
192 was applied during land preparation to the seed bed. One hundred and forty g ha<sup>-1</sup> Pirimicarb (2-  
193 dimethylamino-5,6-dimethylpyrimidin-4-yl-dimethyl-carbamate) was applied to control aphids  
194 during vegetative development. Herbicides and fungicides were applied as necessary to  
195 minimise weeds and diseases. No plant growth regulator was applied.

196

## 197 *2.4 Crop measurements*

198

199 Dates of flowering (GS61) (Tottman and Broad, 1987) and physiological maturity  
200 (when 50% of the shoots had no flag leaf or spike green area and less than 10% of the stem  
201 remained green) were recorded for each plot in all years.

202

### 203 *2.4.1 Measurements at GS61+5d in LSP2 x R (57 lines) experiments*

204 Plant material was sampled on the actual calendar date that the lines reached the stage  
205 (i.e. genotypes were sampled on different dates). In 2005, growth of the above-ground plant  
206 material was analyzed in two 50 cm length rows of the bed (= 0.4 m<sup>2</sup>), situated at least 50 cm  
207 from the end of the plot. Plants were cut off at ground level in all cases. The fresh weight of  
208 the harvested plant material was recorded. Fifty fertile shoots (those with a spike) were  
209 randomly selected from the sample and the fresh weight and dry weight (after drying in oven  
210 for 48 hours at 75 °C) were recorded. Twenty fertile shoots were then taken randomly from  
211 the remaining sampled material and spikes were removed from the shoots at the spike collar.  
212 Both the spikes and straw were weighed after drying for 48 hours at 75 °C. In 2006, growth of  
213 the above-ground plant material was analyzed in 12 randomly sampled fertile shoots cut at  
214 ground level from each plot at GS61+5d. The spikes were separated from the straw, and the  
215 dry weight of each component recorded after drying for 48 hours at 75 °C.

216 In each year, rachis length and spikelets per spike were recorded on 12 randomly  
217 sampled fertile shoots per plot. In 2005, the 12 fertile shoots were randomly selected from the  
218 20 used for DM partitioning. In 2006, the 12 fertile shoots were those used for DM  
219 partitioning. The assessments were carried out before the spikes were placed into the oven.

220

### 221 *2.4.2 Measurements at GS31, GS41 and GS61+5d in LSP2 x R (8DH lines) experiment*

222 For the sub-set of eight DH lines in 2006, plant material was sampled in one 0.4 m<sup>2</sup>  
223 area per plot as described above at GS31 (onset of stem extension), GS41 (early booting) and  
224 at GS61+5d. The number of fertile and infertile shoots in a 25% subsample (by fresh weight)  
225 was counted. At GS31 and GS41, infertile shoots were classified as those that either had no  
226 green area or for which the newest fully expanded leaf was completely senesced; the  
227 remaining shoots were classified as fertile. At GS61+5d, fertile shoots were classified as  
228 those with a spike; the remaining shoots were classified as infertile. The weight of the  
229 infertile shoots was recorded after drying for 48 h at 75°C. The fertile shoots were separated  
230 into (i) spikes, (ii) dead leaf lamina, (iii) green leaf lamina, and (iv) stem with attached leaf  
231 sheath. Green leaf lamina area was measured using a leaf area meter (LI3050A/4; LICOR,  
232 Lincoln, NE). The green area of the stem plus attached leaf sheath and of the spikes was  
233 calculated by assuming the shape of the organs to be a cylinder and applying the formulas: (i)  
234  $\pi(\text{diameter}) \times (\text{length})$ , for the stem plus attached leaf sheath and (ii)  $[\pi(\text{diameter}) \times (\text{length})]$   
235  $+ [\pi(\text{diameter}/2)^2]$  for the spike. A calliper was used to measure the diameter of the stem or  
236 spike at its midpoint and a ruler to measure the length. Aboveground dry weight was  
237 measured on an additional 50% subsample (by fresh weight) from the original sample after  
238 drying for 48 h at 75°C. Dry matter of crop components (leaf lamina, stem and leaf sheath,  
239 etc.) was obtained by weighing components of the 25% subsample after drying for 48 h at  
240 75°C. Rachis length and spikelet number per spike were recorded on 12 randomly sampled  
241 spikes per plot at GS61. The percentage of water-soluble carbohydrate (WSC) content in  
242 stems and attached leaf sheaths was estimated at GS61+5d in 10 randomly sampled fertile  
243 shoots per plot, using the anthrone method of Yemm and Willis (1954) as described by Gay  
244 *et al.* (1998).

245 Interception of photosynthetically active radiation (400-700 nm; PAR) was measured  
246 using a Sunfleck Ceptometer (Delta-T Devices, Burwell, Cambridge, UK) in all plots at 2- to  
247 3-wk intervals from GS31 to GS61+5d. Readings were taken on cloudless, sunny days  
248 between 11.00 and 14.00 h above the crop and at ground level diagonally across the rows.  
249 Readings of the reflected PAR were taken by inverting the ceptometer approximately 5 cm  
250 above the crop. Radiation-use efficiency (RUE) was calculated over the period from GS31 to  
251 GS61+5d as the ratio of the aboveground dry matter increment between samplings to PAR  
252 interception over the same period. Values of daily fractional PAR interception were obtained  
253 by interpolation between readings of fractional interception; and these were applied to the  
254 daily incident solar radiation to calculate daily radiation interception, assuming PAR was

255 equal to 0.5 solar radiation (Monteith, 1972). Values for RUE were calculated individually  
256 for each plot, and the plot values subjected to analysis of variance (ANOVA).

257 In addition to the above measurements, degrading of spikes was performed 14 days  
258 after anthesis (GS61) on the subset of eight DH lines. Twelve spikes per plot were tagged to  
259 carry out the degrading treatment in which all spikelets were removed from one side of the  
260 spike and 12 control shoots were also tagged. At harvest, the 12 degrading shoots and the 12  
261 control shoots were sampled in each plot. The spikes were threshed separately and their  
262 grains counted and weighed after drying for 48 h at 75°C.

263

#### 264 2.4.3 Combine yield and growth analysis at harvest

265 In each experiment, after physiological maturity (PM) was reached, yield was  
266 measured by machine harvesting a plot area of 4.8 m<sup>2</sup> in each plot. Averaging across 57 LSP2  
267 x R DH lines, PM occurred on 15 and 19 April in 2005 and 2006, respectively. Prior to  
268 machine harvesting, a random sub-sample of 100 spike-bearing shoots was removed from  
269 each plot by cutting at ground level. The plant material was dried for 48 h at 75°C and  
270 weighed, and the spikes were then threshed. Dry weight of grains from 100 spikes was  
271 recorded. From this lot, 200 grains were randomly counted and weighed. Using these data,  
272 estimates of individual grain weight, all yield components, harvest index and final above-  
273 ground biomass were calculated.

274

#### 275 2.4.4. Statistical analyses

276 Data collected in field experiments were subjected to ANOVA, where replications and  
277 incomplete blocks within replications were regarded as random effects and genotype was a  
278 fixed effect. For spike traits (spikelet number, rachis length etc), the mean value for the 12  
279 spikes per plot was calculated and these plot means were then subjected to ANOVA. For  
280 ANOVAs across years, Bartlett's test (P = 0.05) was used to test for the homogeneity of  
281 variances, and years were regarded as random effects. The *Tin1* effect was tested as a contrast  
282 in the ANOVA model with one degree of freedom. Treatment means were compared using  
283 the least significant difference of the means of Fisher.

284 Since there were large differences in anthesis date (AD) amongst the DH lines, for all  
285 traits ANOVA was performed with AD as co-variable and probabilities presented for the  
286 statistical significance of the presence/absence of *Tin1* are those from ANOVA including AD  
287 as a covariable..The adjusted means from the ANOVA with AD as a covariable are used for

288 correlation and regression analysis. Regression analysis with a standard linear model was  
289 applied to two-year genotype means to calculate linear relationships between traits.  
290 Regression coefficients are presented for all variables for the linear regressions together with  
291 degrees of freedom for the error residual term in the regression model. Phenotypic  
292 correlations (Pearson's correlation coefficient) between traits were calculated using two-year  
293 genotype means. All analysis was carried out using Genstat version 15.1 (VSN International,  
294 Hemel Hempstead UK).

295

296

### 297 **3. Results**

298

#### 299 *3.1 Growing conditions in experiments*

300

301 Temperatures were similar in the two seasons, except during January (i.e. early-to-  
302 mid stem extension; GS31/33) when daily mean temperatures were on average 1.9 °C cooler  
303 in 2006 than 2005. Daily mean temperature increased during both seasons, from about 16°C  
304 at onset of stem extension to 18°C at anthesis to 21°C at harvest (Table 1). The 2004-5 season  
305 was brighter than 2005-6 during grain filling in March and April with a cumulative total  
306 solar radiation for these two months of 1619 and 1472 MJ m<sup>-2</sup>, respectively.

307

308

**Table 1 here**

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#### 311 *3.2 Grain yield, yield components, spike traits, plant height and anthesis date of 57 DH lines*

312

313 Averaging across years, grain yield, above-ground DM at harvest (AGDM<sub>H</sub>) and HI  
314 amongst the 57 lines ranged from 221-706 g m<sup>-2</sup>, 565-1904 g m<sup>-2</sup> and 0.22-0.52, respectively  
315 ( $P < 0.001$ ; Table 2). The lines differed for spike traits in the following ranges: spikelets  
316 spike<sup>-1</sup> (18.1-28.7), spikes m<sup>-2</sup> (211-542), grains spike<sup>-1</sup> (23.1-58.3), grains m<sup>-2</sup> (7,655-  
317 18,697) and grain weight (19.5-51.7 mg) ( $P < 0.05$ ; Table 2). Within these ranges, the  
318 distribution of lines was skewed towards the upper end of the range for GY, but  
319 approximated to a normal distribution for most other traits (data not shown). Variation above  
320 the LSP2 parent was observed in 2006 for GY (+19%), grains m<sup>-2</sup> (+46.6%), spikelets spike<sup>-1</sup>

321 (+28.9%), grains spike<sup>-1</sup> (+44.8%) and grain weight (+14.5%) (Table 2). Averaged across  
322 years, anthesis date ( GS61) ranged amongst lines from 21 February to 6 April and plant  
323 height from 51.1 to 103.6 cm ( $P < 0.001$ ; Table 2 and Fig. 1 ), reflecting segregation for  
324 developmental and plant height (*Rht-B1*) genes. In the present study, effects of  
325 presence/absence of the *Tin1* gene on spike fertility and yield potential traits are mainly  
326 analyzed averaged across the groups of DH lines (+*Tin1* and -*Tin1*) which overall were  
327 balanced for anthesis date and plant height, minimising any potential confounding effects of  
328 variation in anthesis date and plant height. In addition, the effect of *Tin1* was tested using  
329 anthesis date as covariable in the ANOVA as described above. .

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331

332

### Table 2 here

333

### 334 3.3 Effects of the presence/absence of *Tin1* gene in set of 57 LSP2 x R DH lines

335

336 In total 13 out of the 57 lines possessed the tiller inhibition +*Tin1* gene. The ANOVA with  
337 the *Tin1* gene showed that averaging across years +*Tin1* decreased spikes m<sup>-2</sup> (-5.7%,  $P <$   
338 0.01) and increased grains m<sup>-2</sup> (+6.6%,  $P < 0.05$ ), grains spike<sup>-1</sup> (+13.9%,  $P < 0.001$ ) and  
339 grains spikelet<sup>-1</sup> (+11.3%,  $P < 0.01$ ) (Table 3). In 2005, +*Tin1* conferred a non-significant  
340 increase in grains m<sup>-2</sup> (+6.6%), associated with an increase in grains spike<sup>-1</sup> (+6.0%,  $P <$   
341 0.01). In 2006, +*Tin1* decreased spikes m<sup>-2</sup> (-11.7%,  $P < 0.05$ ) and increased grains m<sup>-2</sup>  
342 (+6.7%,  $P < 0.001$ ), grains spike<sup>-1</sup> (+22.0%,  $P < 0.001$ ) and grains spikelet<sup>-1</sup> (+20.4%,  $P <$   
343 0.001). Overall *Tin1* increased grains m<sup>-2</sup> from 13,071 (-*Tin1*) to 13,936 (+*Tin1*) (+6.6%;  $P <$   
344 0.05), the effect of +*Tin1* on grain yield was not statistically significant. The +*Tin1* allele also  
345 increase spikelets spike<sup>-1</sup> overall from 23.3 to 23.9 ( $P < 0.05$ ). There was a year x *Tin1*  
346 interaction for grains spike<sup>-1</sup> ( $P < 0.01$ ); the increase with +*Tin1* was relatively greater in  
347 2006 than in 2005. There was also a year x +*Tin1* interaction for spike partitioning index  
348 (spike DM/above-ground DM at GS61+5d; SPI); the presence of +*Tin1* increased SPI overall  
349 from 0.32 to 0.34 ( $P < 0.001$ ), but the effect was only significant in individual years in 2005.  
350 In addition, the year x  $\pm$ *Tin1* interaction was significant for the spike fertility index (grains  
351 per g spike DM at GS61+5d); in this case +*Tin1* allele increased SFI from 38.8 (-*Tin1*) to  
352 45.5 grains g<sup>-1</sup> DM (+*Tin1*) in 2006 ( $P < 0.001$ ), but there was not significant effect in 2005.

353 , Overall there was no effect of +*Tin1* on anthesis date. There was a small overall effect for  
354 plant height to decrease with *Tin1* from 74.4 (-*Tin1*) to 73.3 (+*Tin1*) cm ( $P < 0.05$ ) .

355

356

**Table 3 here**

357

### 358 3.4 Relationship between grain $m^{-2}$ and its determinants and plant height for *Tin1* groups

359 For each of the +*Tin1* and -*Tin1* groups there was positive linear regression between grains  
360 spike $^{-1}$  and grains pikelet $^{-1}$  ( $R^2 = 0.76$  and  $0.81$ , respectively,  $P < 0.001$ ; Fig. 1a), whereas the  
361 relationships between grains spike $^{-1}$  and spikelets spike $^{-1}$  was not statistically significant (Fig.  
362 1b). Therefore spikelet fertility was the main determinant influencing variation in grains per  
363 spike amongst the DH lines rather than spikelets spike $^{-1}$ , albeit there was overall increase in  
364 spikelets spike $^{-1}$  in the +*Tin1* (23,9) compared to -*Tin1* (23.3) groups of lines ( $P < 0.05$ ),  
365 Table 3) . The linear positive relationship of grains  $m^{-2}$  on grains spike $^{-1}$  was stronger in the  
366 +*Tin1* lines ( $R^2 = 0.27$ ,  $P < 0.05$ ) than the -*Tin1* lines ( $R^2 = 0.19$ ,  $P < 0.07$ ) (Fig. 1c). The  
367 range in plant height within the +*Tin1* (51 - 93 cm) and -*Tin1* (51 - 104 cm) groups of lines  
368 was broadly similar (Fig. 1d); there was no relationship between plant height and grains  $m^{-2}$   
369 in either of the +*Tin1* and -*Tin1* groups or across all 57 DH lines.

370

**Figure 1 here**

371

372

373

374

### 375 3.5 Interactions between *Tin1* gene and *Rht-B1b* gene and presence/absence of awns

376 The dwarf (*Rht-D1b/Rht-B1b*) genotypes (64 cm) showed decreased plant height compared to  
377 the semi-dwarf (*Rht-B1a/Rht-D1b*) genotypes (84 cm; -23%,  $P < 0.01$ ), and decreased grain  
378 yield (-20.4%,  $P < 0.01$ ), associated with increases in both HI (from 0.37 to 0.39,  $P = 0.053$ ;  
379 Table 4) and AGDM<sub>H</sub> (from 1090 to 1178 g  $m^{-2}$   $P < 0.05$ ). There was a decrease in grains  
380 spike $^{-1}$  (from 39.5 to 36.4,  $P < 0.01$ ) and a decrease in grain weight (36.3 to 30.7 mg  $P <$   
381 0.001) in the dwarf compared to the semi-dwarf group of lines. However, the effects of *Tin1*  
382 were generally observed consistently in both the semi-dwarf and dwarf backgrounds, e.g. for  
383 grains  $m^{-2}$ , grains spike $^{-1}$  and spike partitioning index. For two of the 15 traits the *Tin1* x  
384 *RhtB1b* interaction was significant: above-ground DM and rachis length ( $P < 0.05$ ). The +*Tin1*  
385 allele increased biomass in the semi-dwarf background; and had a neutral effect in the dwarf

386 background. The increase in rachis length with *Tin1* was relatively greater in the semi-dwarf  
387 background than the dwarf background (Table 4).

388

389

390 Of the 57 DH lines, 30 were awned and 27 were unawned. Averaging across years,  
391 the presence of awns did not have a statistically significant effect on grain yield, but  
392 decreased grains  $m^{-2}$  (-9.1%;  $P < 0.001$ ) and increased grain weight (+16.2%;  $P < 0.001$ )  
393 (Table 5). The effect of awns was also not statistically significant on either anthesis date or  
394 plant height. There was *Tin1* x awned/unawned interaction for grain yield ( $P < 0.001$ ). In the  
395 unawned DH lines, +*Tin1* increased grain yield (+14.0%); but in the awned lines it decreased  
396 grain yield (-7.4%). A similar interaction was observed for grains  $m^{-2}$  ( $P < 0.05$ )

397

398

#### 399 **Tables 4 and 5 here**

400

401

#### 402 *3.7 Effects of +Tin1 gene in sub-set of 8 LSP2 x R DH lines in 2006*

403

404 The subset of eight DH lines was selected for detailed study of physiological traits in  
405 the additional field experiment in 2006. The DH lines were chosen to represent a narrow  
406 range for anthesis date and plant height and overall to be balanced across +*Tin1* and -  
407 *Tin1* groups of lines, (Table 6). There were only small differences in either anthesis date (19  
408 March -*Tin1* versus 18 March +*Tin1*) or plant height (70 cm -*Tin1* versus 69 cm +*Tin1*)  
409 between the groups of lines. The plant density at GS31 did not differ amongst the eight DH  
410 lines in the range 141 - 169 plants  $m^{-2}$ , or between the +*Tin1* (151 plant  $m^{-2}$ ) and -*Tin1* (160  
411 plants  $m^{-2}$ ) group of DH lines (Table 7). At GS61+5d, +*Tin1* decreased spikes  $m^{-2}$  (-13%;  $P =$   
412 0.06) and increased grains spike<sup>-1</sup> (+19.0%;  $P < 0.001$ ). There was a trend for +*Tin1* to  
413 increase grains  $m^{-2}$  (+11.0%;  $P = 0.09$ ), although the effect of +*Tin1* on grain yield was not  
414 statistically significant.

415

416 Overall green canopy area, light extinction coefficient ( $k$ ), aboveground DM at  
417 GS61+5d and radiation interception from GS31 to GS61+5d and were not affected by the  
418 presence/absence of the *Tin1* allele (Table 7). Spike DM partitioning at GS61+5d was  
419 increased with +*Tin1* from 0.28 to 0.33 (+14%;  $P < 0.001$ ), so that spike DM per  $m^2$  at

419 GS61+5d was boosted from 308 g m<sup>-2</sup> in the *-Tin1* group of DH lines to 363 g m<sup>-2</sup> (+17.9 %;  
420 *P* < 0.05) in the *+Tin1* lines. The effects of *+Tin1* on the spike partitioning index and stem  
421 soluble carbohydrate accumulation at GS61+5d were not statistically significant in the subset  
422 of eight DH lines.

423

424

**Tables 6 and 7 here**

425

426 The responses of grain weight to the degrading treatment imposed at GS61+ 14d are  
427 shown in Figure 2. A response of grain weight of ca. +0-10% to degrading would indicate  
428 sink limitation of grain growth and of ca. +10-20% co-limitation by source and sink (Acreche  
429 *et al.*, 2008). The response of grain weight to degrading did not differ significantly between  
430 the *+Tin1* (+10.6%) and the *-Tin1* (+14.7%) groups of lines. In the degraded shoots, where  
431 source per grain is theoretically increased by 100% in the degraded spikes (assuming no  
432 negative feedback on photosynthesis), the final grain dry weight is an indicator of potential  
433 grain weight; the grain weight in degraded shoots did not differ significantly between the  
434 *+Tin-1* lines and *-Tin1* lines.

435

436

**Fig. 2 here**

437

#### 438 **4. Discussion**

439

440 Firstly, we discuss the physiological basis of effects of the presence/absence of the  
441 *Tin1* gene on grains m<sup>-2</sup> and grain yield, then we consider further effects of large-spike  
442 phenotype on grains m<sup>-2</sup> and grain yield determined independently of the *Tin1* gene and lastly  
443 we consider the prospects for exploiting *+Tin1* and large-spike phenotype in breeding for  
444 enhanced grains m<sup>-2</sup> and yield potential.

445

##### 446 *4.1 Physiological basis of effects of presence/absence of Tin1 on grains m<sup>-2</sup> and grain yield*

447

448 The reduction in spikes m<sup>-2</sup> with *+Tin1* (-6% in the 57 DH lines and -13% in the  
449 subset of 8 DH lines) was smaller than reported in previous field investigations, e.g. -30% in  
450 Australia in wheat grown at 170 seeds m<sup>-2</sup> under high nitrogen fertilizer input (Duggan *et al.*  
451 *et al.*, 2005). Plant density was likely similar in our study to that of Duggan *et al.* (2005).

452 Although plant density was not recorded in the experiments examining 57 DH lines in 2005  
453 and 2006, in the experiment examining the subset of 8 DH lines in 2006 plant density was  
454 on average 156 plants m<sup>-2</sup>. Moreover, this experiment was located in the same field as the  
455 experiment examining 57 DH lines in 2006 with the same sowing date, seed rate, irrigation  
456 and other management inputs, so plant densities were likely similar in these two  
457 experiments. The experimental field and seed rate used for the 2005 and 2006 experiments  
458 examining the 57 DH lines was the same and sowing dates and other plot management were  
459 similar, so plant density was also probably close to 156 plants m<sup>-2</sup> in the 2005 experiment.  
460 *Tin1* decreased spikes m<sup>-2</sup> by 6% in the present study (57 DH line experiments), but there  
461 was a wide range of quantitative variation within the *Tin1* group of lines (240 - 520 spikes  
462 m<sup>-2</sup>). This suggested that in the +*Tin1* lines, axillary buds were at least partially released  
463 from tiller inhibition during tiller development by modifying tiller promoting genes.

464 Overall grains m<sup>-2</sup> was increased by 7% in the +*Tin1* group; this was associated with  
465 more grains per spike (+14%). The increase in grains per spike was associated mainly with  
466 more grains per spikelet (+11%), with only a small increase in spikelets spike<sup>-1</sup> (+3%). Our  
467 previous work indicated in a growth-room experiment that the LSP2 parental line produced 5  
468 more spikelets spike<sup>-1</sup> than a check CIMMYT cultivar (Bacanora) and that the thermal  
469 duration of spikelet primordia production was primarily responsible for the increased spikelet  
470 number (Gaju *et al.*, 2009). However, in the field the increase in spikelets per spike for LSP2  
471 compared to the Bacanora check was only 4% compared to 31% in the spaced plants in the  
472 growth-room experiment. In the present study, the increase in spikelets spike<sup>-1</sup> with +*Tin1* of  
473 3%, was broadly consistent with the findings of Gaju *et al.* (2009).

474

475 Increased grains per m<sup>2</sup> with +*Tin1* was overall associated with higher SPI (both in 57  
476 DH line experiments and 8 DH line subset experiment). Spike DM per m<sup>2</sup> at anthesis was  
477 similarly increased with *Tin1* in the 57 line and 8 DH line experiments. Enhanced spike  
478 DM per m<sup>2</sup> therefore appeared to be one mechanism driving the increase in grains m<sup>-2</sup> with  
479 +*Tin1*. However, there was also a contribution from the spikelet fertility index according to the  
480 results of the 57 DH lines experiments. The SFI averaging across years was increased with  
481 +*Tin1*, although the effect was only significant individual years in 2006. Overall our results  
482 showed that the physiological basis of increased grain m<sup>-2</sup> with *Tin1* depended partly on the  
483 season, with SPI the predominant mechanism in 2005 and SFI in 2006.

484 Encouragingly present results suggested increased SPI with *+Tin1* was not  
485 associated with a trade-off with SFI; nor was there a trade-off between SPI and potential  
486 grain weight. In previous work on large spike phenotype, increased SPI was associated with  
487 decreases in both FE and potential grain weight (as indicated by the grain DW in the  
488 degrained treatment) (Gaju *et al.*, 2009).

489 The mechanism underlying the differences in SFI in the present study cannot be  
490 certain. Slafer and Andrade (1993) observed higher grains  $m^{-2}$  amongst bread wheat  
491 genotypes was associated with allocating a higher proportion of spike DM to reproductive  
492 (developing florets) rather than structural (rachis, glumes and paleas) organs within the  
493 spikes. A higher concentration of soluble carbohydrate in the spikes in slower-growing spikes  
494 was shown to increase fertile florets per ear (Ghiglione *et al.*, 2008).

495 The positive effect of *+Tin1* on grains  $m^{-2}$  did not overall translate in the present study  
496 to a positive effect on grain yield. There was an apparent interaction with *+Tin1* increasing  
497 grain yield (+14.0%) in the unawned lines; but decreasing grain yield (-7.4%) in the awned  
498 lines. However, this interaction must be interpreted cautiously since the anthesis dates were  
499 not completely balanced in the four  $\pm Tin1/\pm awns$  groups; and the relatively earlier anthesis  
500 date for *+Tin1* lines compared to *-Tin1* lines in the unawned background (*+Tin1* 3 days  
501 earlier than *-Tin1*) than in the awned background (*+Tin1* 2 days later than *-Tin1*) could partly  
502 account for this apparent interaction. The overall neutral effect of *+Tin1* on grain yield  
503 reflected a trade-off between grains  $m^{-2}$  and grain weight. This trade-off could be due to a  
504 trade-off between grains  $m^{-2}$  and potential grain weight or alternatively a dilution of post-  
505 anthesis assimilate supply amongst the increased grain number affecting final grain weight.  
506 Present results were not conclusive with regard to these two alternatives. There was no  
507 significant effect of presence/absence of *+Tin1* on the final grain weight in degrained spikes,  
508 an indicator of potential grain weight. Furthermore, there was no significant effect of  
509 presence/absence of *+Tin1* on source-type traits: e.g. green canopy area at anthesis, RUE  
510 during the stem-elongation period or stem WSC at GS61+5d. However, the similar grain  
511 growth responses to degrading between the *+Tin1* and *-Tin1* groups indicated source: sink  
512 balance did not differ between the lines. Further investigations with the degrading  
513 treatment applied across all 57 lines as well as additional source-sink manipulation  
514 treatments, e.g. defoliation at GS61+14 d, across all 57 DH lines are required to ascertain  
515 the physiological basis of the trade-off between grains  $m^{-2}$  and grain weight in the DH lines.  
516 Encouragingly, similar grain weight responses to degrading for *+Tin1* and *-Tin1* suggested

517 that *+Tin1* is not associated with impeded vascular connections to grain sites as has been  
518 postulated in relation to shrivelled grain of many large-spike lines.

519 The present analysis provides a quantitative assessment of the physiological basis of  
520 effects of *Tin1* on grains per m<sup>2</sup> and grain yield in a relatively uniform genetic background.  
521 For example, similar comparisons across groups of DH lines were used to examine effects of  
522 an awn suppressor gene and *Rht* genes on grain yield and yield components in a winter wheat  
523 Beaver x Soissons DH population (Aravinda Kumar et al., 2011). It is recognised that the  
524 present results on the effects of the presence/absence of *Tin1* should be confirmed by a more  
525 precise analysis of near isogenic lines for *Tin1* gene derived from individual LSSP2 x R DH  
526 lines. .

527

528

#### 529 *4.2 Implications for plant breeding*

530

531 Large-spike phenotype associated with restricted tillering has been of interest to breeders in  
532 recent decades with a view to boosting grains m<sup>-2</sup>, but there are several factors which have so  
533 far limited its utility. Firstly, there is the consideration of the extent to which large-spike  
534 phenotype is expressed at higher plant densities in a crop environment. Our results indicated  
535 that an increase in grains spike<sup>-1</sup> and grains m<sup>-2</sup> was obtained with *+Tin1* at standard  
536 agronomic plant densities in spite of the decrease in spikes m<sup>-2</sup>. These results therefore  
537 indicated potential scope for commercial exploitation of *Tin1* in optimal high radiation,  
538 irrigated environments, if *Tin1* could be combined with traits conferring ability to maintain  
539 or ideally, increase individual grain weight. Such a conclusion would also be supported by  
540 results in a recent field experiment in the UK where *+Tin1* decreased spikes m<sup>-2</sup> (-6.4%) and  
541 increased grains m<sup>-2</sup> (+14.5%) and grain yield (+7.8%) (Aiswai, 2011). To combine high  
542 grain number and grain weight in the same genotype has however been to date a difficult task  
543 for wheat breeding. One strategy to avoid the trade-off between grain number and grain  
544 weight was proposed by Gaju *et al.* (2009) by selecting genotypes with high spikelets spike<sup>-1</sup>  
545 and high rachis length per spikelet number of spikelets which were shown to have higher  
546 grain number spike<sup>-1</sup> and grain weight. An alternative strategy may be to cross parental lines  
547 contrasting in grain number and grain weight as a way to combine both desired traits (Bustos  
548 *et al.*, 2013). Those authors reported the two highest yielding lines in a spring wheat DH  
549 population derived from a cross between Bacanora (high grain number) and Weebil (high

550 grain weight) attained between 22 and 31% increment in grain yield compared to the parents  
551 in a field experiment in southern Chile.

552 In future work the +*Tin1* germplasm should be grown at still higher plant densities of  
553 approximately 200 to 400 m<sup>-2</sup> to examine if the gain in grains per spike can be maintained at  
554 these higher levels of interplant competition. Exploitation of large-spike-phenotype traits by  
555 breeders in the longer term will also depend on maintaining lodging resistance. Useful traits  
556 in this respect to select for may be crown roots that spread widely and wide stems with  
557 increased material strength of the stem wall (Berry *et al.*, 2004). In this regard, large-spike-  
558 phenotype may have an advantage since stem material strength is readily expressed at low  
559 plant population density while spike size can compensate for low density.

560

561

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567

568

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705

**Table 1.** Mean daily temperature, mean daily relative humidity (RH), monthly rainfall and daily solar radiation at CIMMYT experimental station at Ciudad Obregon in NW Mexico in 2004-5 and 2005-6

	<u>2004-5</u>					<u>2005-6</u>				
	Dec	Jan	Feb	Mar	Apr	Dec	Jan	Feb	Mar	Apr
Mean daily temp (°C)	15.5	16.4	16.0	17.7	20.8	16.1	14.5	16.5	17.2	21.1
Mean daily RH (%)	62.2	72.3	75.0	61.1	47.3	58.2	57.4	66.1	62.3	47.2
Monthly rainfall (mm)	0.1	1.7	1.7	0.0	0.0	0.0	0.7	0.0	0.0	0.0
Daily solar rad. (MJ m <sup>-2</sup> )	13.9	14.8	17.4	25.5	27.6	15.8	16.1	19.3	22.7	25.6

**Table 2.** Maximum, minimum and mean values for anthesis date (GS61), spike traits at GS61+5d, grain yield (at 1000 g DM kg<sup>-1</sup>), yield components and above-ground dry matter at harvest (AGDM<sub>H</sub>) for 57 DH lines of LSP2 x R population in 2004-5 and 2005-6 and SEDs from cross-year ANOVA for year, DH line and interaction. Probability † < 0.10, \* < 0.05, \*\* < 0.001, and \*\*\* < 0.001.

	Anthesis date	Plant height (cm)	Grains m <sup>-2</sup>	Grains spike <sup>-1</sup>	Rachis length (cm)	Spikelets spike <sup>-1</sup>	Spikes m <sup>-2</sup>	Grain weight (mg)	Grain yield (g m <sup>-2</sup> )	AGDM <sub>H</sub> (g m <sup>-2</sup> )
2005										
Min	18 Feb	46.8	6,813	26.2	10.2	18.9	224.6	20.8	204.4	672
Max	11 Apr	106.0	19,391	51.7	16.1	29.7	543.0	52.9	727.3	2176
Mean	10 Mar	72.2	13,322	38.2	12.9	24.1	354.6	35.2	460.8	1247
S.E.D. DH line (D.F.=56)	-	1.95	2,059	5.62	0.51	1.37	66.25	2.33	66.50	269.1
DH line Prob.	-	<0.001	<0.001	<0.001	<0.001	<0.001	<0.01	<0.001	<0.001	<0.001
2006										
Min	24 Feb	52.0	8,496	20.1	9.6	17.3	197.9	18.2	202.5	457
Max	1 Apr	101.9	17,966	64.8	15.1	27.6	541.4	50.5	646.5	1632
Mean	13 Mar	74.5	13,199	38.2	12.6	22.7	363.2	32.8	427.5	1072
LSP2	24 Feb	93.4	12,258	44.8	13.2	21.4	275.1	44.1	543.4	1064
S.E.D. DH line (D.F.=56)	-	3.39	1,442.7	6.42	0.58	1.41	56.47	2.15	37.85	116.4
DH line Prob.	-	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
SED DH line vs LSP2 (D.F.=57)	-	2.344	1,440.1	6.41	0.59	1.40	56.61	2.14	38.71	152.71
Cross-Year ANOVA										
S.E.D. (D.F.=112) DH line	2.30***	1.97***	1259.2***	4.27***	0.39***	0.99***	43.68***	1.59***	38.28***	146.8***
S.E.D. (D.F.=2) Year	0.50*	0.30*	612.8	0.41	0.21	0.51	16.9	0.39*	15.8	94.2
S.E.D. (D.F. = 112) Yr*line	3.26***	2.78***	1869.1	6.01***	0.59***	1.47***	63.52*	2.27**	55.93*	226.3†

**Table 3.** Rachis length (R. Len.), spikelets per spike, spike DM partitioning index at anthesis (GS61) (Spike Part. Index), spike fertility index (SPI), spike DM per unit area at GS61 (Spike DM<sub>anth</sub>), plant height, harvest index, above-ground dry matter (AGDM) at harvest, grain yield (at 1000 g DM kg<sup>-1</sup>), yield components, and anthesis date (GS61) for groups of *-Tin1* (44 lines) and *+Tin1* (13 lines) lines of the LSP2 x Rialto DH population in 2005 and 2006. ns = not significant.

Trait	2005			2006			2005-6			
	<i>-Tin1</i>	<i>+Tin1</i>	Prob.	<i>-Tin1</i>	<i>+Tin1</i>	Prob.	<i>-Tin1</i>	<i>+Tin1</i>	Prob. $\pm Tin1$	Prob. $\pm Tin1$ x Year
<u>Anthesis</u>										
Anthesis date	71.1	70.3	n/a	74.20	74.35	n/a	72.7	72.3	n/a	n/a
R. Len. (cm)	12.78	13.11	0.08	12.48	12.77	0.04	12.6	12.9	0.005	ns
Spikelets spike <sup>-1</sup>	23.9	24.8	0.02	22.62	22.90	Ns	23.3	23.9	0.020	ns
Spike Part. Index	0.32	0.34	0.00	0.33	0.33	Ns	0.32	0.34	0.001	0.019
SFI. (grns g <sup>-1</sup> DM)	55.6	56.2	ns	38.89	45.49	0.002	47.3	50.8	ns	0.010
Spike DM <sub>anth</sub> (g m <sup>-2</sup> )	299.4	352.2	0.01	365.1	343.5	ns	332.3	347.8	ns	0.013
<u>Harvest</u>										
Plant height (cm)	72.4	71.6	ns	74.45	73.0	0.010	73.4	72.3	0.003	ns
Grain yield (g m <sup>-2</sup> )	456.6	474.9	ns	425.4	426.1	ns	441.0	450.5	Ns	ns
AGDM (g m <sup>-2</sup> )	1222.6	1329.3	ns	1084.9	1030.1	0.03	1153.8	1179.7	Ns	ns
Harvest Index	0.38	0.37	ns	0.39	0.43	<0.001	0.388	0.399	0.001	<0.001
Grains m <sup>-2</sup>	13125	13990	ns	13017	13883	0.013	13071.2	13936.4	0.013	ns
Spikes m <sup>-2</sup>	354.0	356.5	ns	374.70	330.91	0.001	364.4	343.7	0.003	ns
Grains spike <sup>-1</sup>	37.7	40.0	0.02	36.2	44.2	<0.001	37.0	42.1	<.0001	0.003
Grains spikelet <sup>-1</sup>	1.59	1.62	ns	1.61	1.95	<0.001	1.60	1.79	<.0001	0.007
Grain weight mg	35.4	34.4	0.06	33.02	31.05	0.001	34.2	32.7	<.0001	ns

**Table 4.** Anthesis date, rachis length, spikelets per spike, , spike partitioning index, spike fertility index, plant height, harvest index, above-ground dry matter (AGDM) and grain yield (t ha<sup>-1</sup>; 1000 g DM/kg) and yield components for semi-dwarf (*Rht-B1a* + *Rht-D1b* ; 31 lines) and dwarf (*Rht-B1b* + *Rht-D1b* ; 26 lines) groups of lines of the LSP2 x Rialto DH population. Probability † < 0.10, \* < 0.05, \*\* < 0.001, and \*\*\* < 0.001.

Traits	<u>RhtB1b</u>		<u>RhtB1a</u>		SED RhtB1 (DF = 195)	SED RhtB1 x <i>Tin1</i> (DF=195)
	<i>+Tin1</i>	<i>-Tin1</i>	<i>+Tin1</i>	<i>-Tin1</i>		
<u>Anthesis</u>						
Anthesis date	16 Mar	17 Mar	14 Mar	10 Mar	1.558 ***	5.90 ns
Rachis length (cm)	13.06	12.81	13.72	12.58	0.162 ns	0.367 *
Spikelets spike <sup>-1</sup>	24.3	23.7	24.5	23.1	0.33 ns	0.754 ns
Spike partitioning index	0.367	0.358	0.314	0.289	0.0062 ***	0.0142 ns
SFI (grains g <sup>-1</sup> DM)	43.8	41.4	54.3	51.8	2.483 ***	5.62 ns
<u>Harvest</u>						
Plant height (cm)	62.5	64.2	84.4	82.9	1.63 ***	3.67 ns
Grain yield (t ha <sup>-1</sup> 100% DM)	415.1	401.6	467.9	458.1	15.05 **	34.07 ns
AGDM (g m <sup>-2</sup> )	1073	1094	1325	1141	39.55 *	89.52 *
Harvest index	0.401	0.373	0.379	0.406	0.011 0.053†	0.0263 †
Grains m <sup>-2</sup>	14040	13144	14179	12557	377.8 ns	855.2 ns
Spikes m <sup>-2</sup>	353.1	386.5	331.5	346.3	12.00 ***	27.16 ns
Grains spike <sup>-1</sup>	41.4	35.2	43.2	38.6	1.25 *	2.83 ns
Grains spikelet <sup>-1</sup>	1.71	1.50	1.79	1.68	0.0589 **	0.129 ns
Grain weight (mg)	29.6	30.9	33.2	37.1	1.075 ***	2.43 ns

**Table 5 .** Antheiss date, rachis length, spikelets per spike, , spike partitioning index, spike fertility index, plant height, harvest index, above-ground dry matter (AGDM) and grain yield (t ha<sup>-1</sup>; 1000 g DM/kg) and yield components for +*Tin1A*/awned (7 lines), -*Tin1A*/awned (23 lines), +*Tin1A*/unawned (6 lines) and -*Tin1A*/unawned (21 lines) groups of lines of the LSP2 x Rialto DH population. Values represent means across 2004-5 and 2005-6. Probability < 0.10 denoted by †

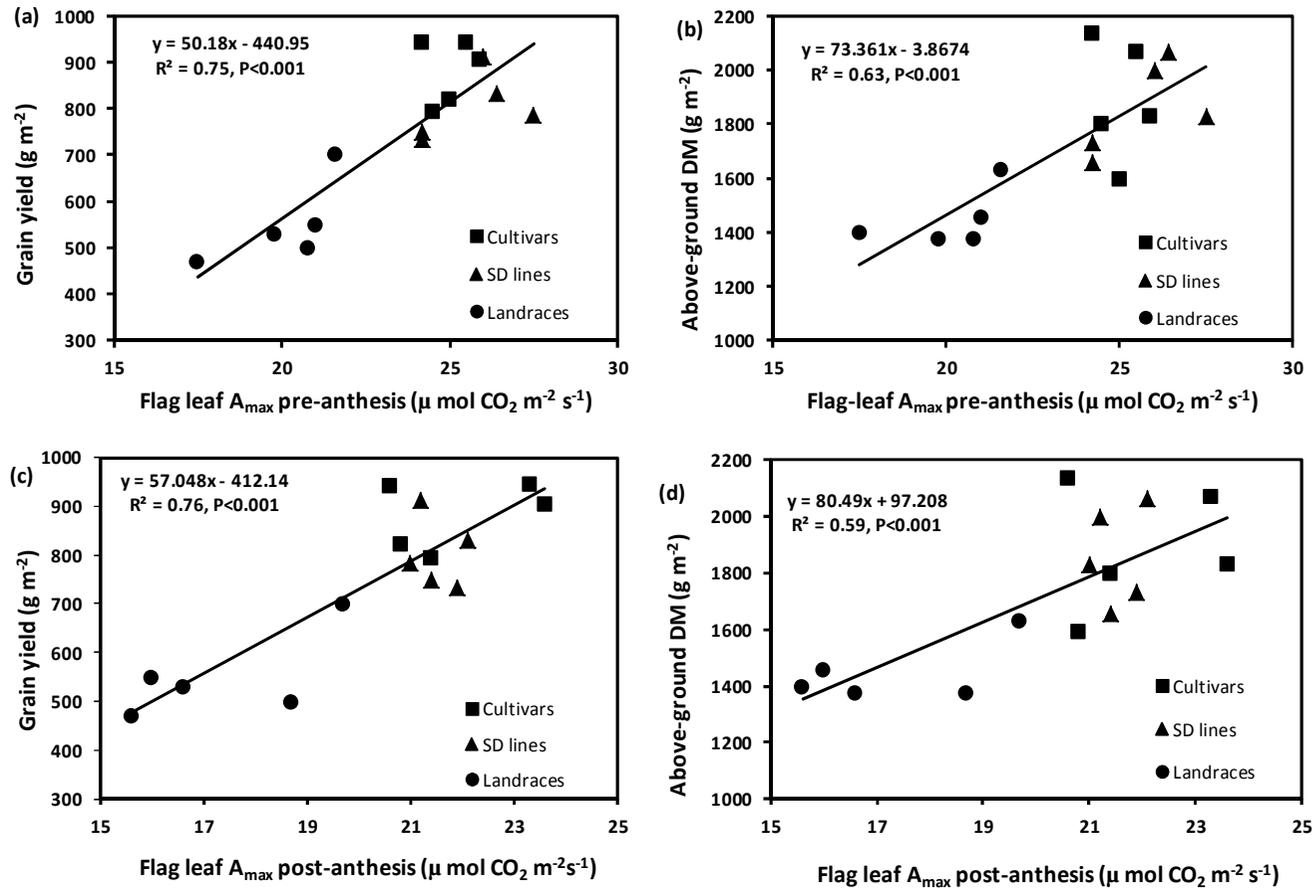
Traits	<u>Awned</u>		<u>Unawned</u>		SED Awned/Unawned (DF = 109)	SED <i>Tin1A</i> x Awns (DF=109)
	+ <i>Tin1A</i>	- <i>Tin1A</i>	+ <i>Tin1A</i>	- <i>Tin1A</i>		
Anthesis						
Anthesis date	12 Mar	10 Mar	11 Mar	14 Mar	0.351 ns	4.39 ns
Rachis length (cm)	12.7	12.4	13.3	12.9	0.3456 ***	0.32 ns
Rachis length spikelet <sup>-1</sup> (cm)	0.55	0.55	0.54	0.54	0.01436 ns	0.012 ns
Spikelets spike <sup>-1</sup>	23.1	22.7	24.7	23.9	0.714 ***	0.65 ns
Spike partitioning index	0.341	0.325	0.333	0.322	0.01747 ns	0.0159 ns
SFI (grains g <sup>-1</sup> DM)	45.7	45.9	56.8	48.7	5.705 ns	5.31 ns
Harvest						
Plant height (cm)	69.7	74.5	75.3	72.2	4.67 ns	4.14 ns
AGDM (g m <sup>-2</sup> )	1180	1213	1180	1088	87.05 ***	86.1 ns
Harvest index	0.383	0.381	0.417	0.394	0.0247 *	0.024 ns
Grain yield (t ha <sup>-1</sup> 100% DM)	4.26	4.60	4.89	4.14	0.337 ns	0.315***
Grains m <sup>-2</sup>	12574	12699	15525	13479	813.2 **	711.6*
Spikes m <sup>-2</sup>	346.2	364.0	340.8	364.8	27.60 ns	24.01 ns
Grains spikelet <sup>-1</sup>	1.69	1.58	1.90	1.63	0.12618 *	0.113*
Grains spike <sup>-1</sup>	38.1	35.6	46.8	38.5	2.661 ***	2.33*
Grain weight (mg)	34.1	36.9	31.1	31.2	0.24 ***	2.15 ns

**Table 6** Grain yield (t ha<sup>-1</sup>; 1000 g DM kg<sup>-1</sup>), harvest index (HI), above-ground dry matter (AGDM), grain yield (t ha<sup>-1</sup>; 1000 g DM kg<sup>-1</sup>) and yield components for +*Tin1A* and -*Tin1A* groups of lines of the LSP2 x Rialto DH population in 2005-6. Probability < 0.10 denoted by †

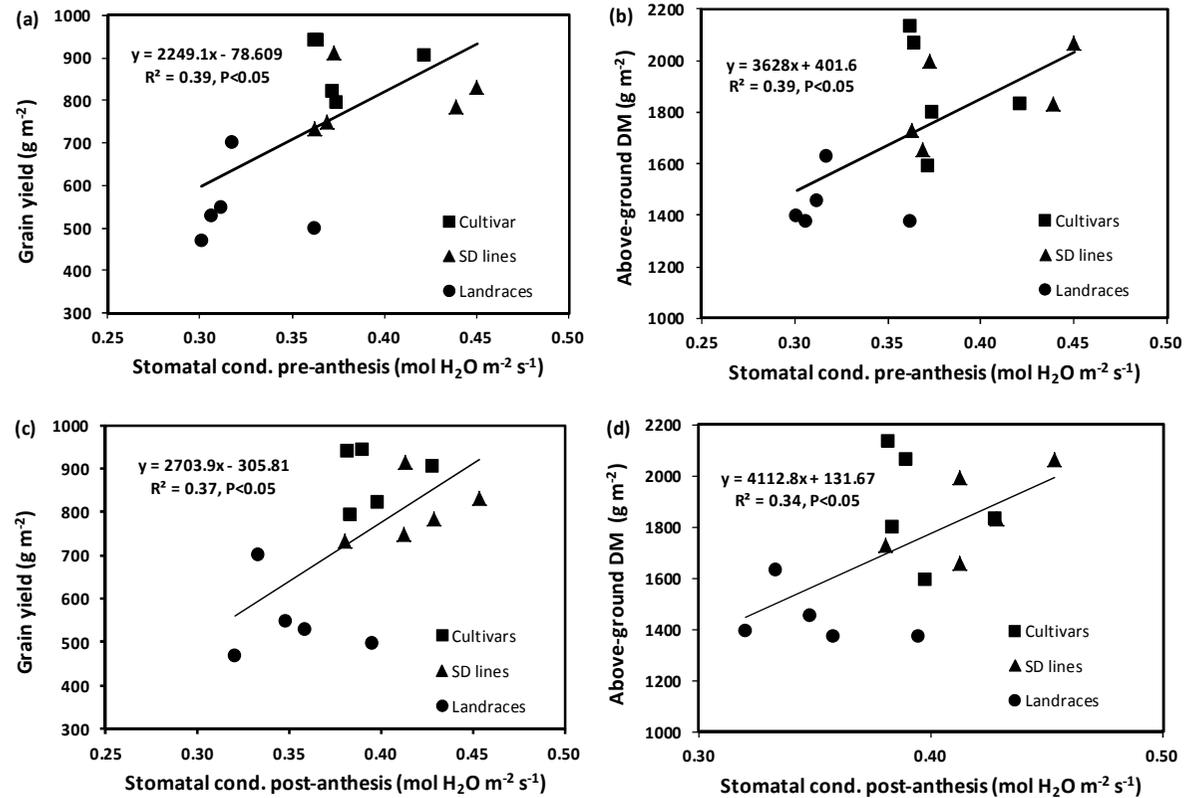
Lines	<i>Tin1A</i>	Grain yield (t ha <sup>-1</sup> )	Grains spike <sup>-1</sup>	Spikes m <sup>-2</sup>	Grains m <sup>-2</sup>	AGDM (g m <sup>-2</sup> )	HI	Grain weight (mg)	Rachis length (cm)	Spikelets Spike <sup>-1</sup>	Plant height (cm)	Anthesis date
1	+ <i>Tin1A</i>	666.1	52.3	497.2	25981	1811	0.37	25.8	13.4	26.3	72.1	20 Mar
21	+ <i>Tin1A</i>	710.4	45.5	453.8	20596	1712	0.42	34.6	13.2	23.7	70.6	15 Mar
31	+ <i>Tin1A</i>	667.3	42.4	457.7	19327	1718	0.39	34.6	13.2	24.8	66.9	21 Mar
124	+ <i>Tin1A</i>	558.2	47.0	444.3	20911	1443	0.39	26.7	14.5	26.3	65.9	17 Mar
Mean		650.5	46.8	463.3	21704	1671	0.40	30.4	13.575	25.3	68.9	68.9
7	- <i>Tin1A</i>	473.1	30.5	542.2	16390	1403	0.34	29.0	11.7	22.7	61.0	27 Mar
17	- <i>Tin1A</i>	704.3	37.3	565.0	20864	1946	0.36	33.8	11.6	22.1	93.9	16 Mar
116	- <i>Tin1A</i>	658.6	47.9	410.0	19604	1468	0.45	33.6	14.5	25.8	61.2	20 Mar
106	- <i>Tin1A</i>	682.4	41.6	529.2	22082	1713	0.40	31.1	13.2	26.2	61.9	16 Mar
Mean		629.6	39.3	511.6	19735	1632.5	0.38	31.9	12.75	24.2	69.5	69.5
SED (df=20)		32.61	2.282	23.56	1134.1	87.0	0.015	1.457	0.433	0.584	4.56	4.56
Prob.		ns	**	*	0.09	ns	ns	ns	0.065	ns	Ns	ns

**Table 7** Fertile shoots per m<sup>2</sup>, spike DM per m<sup>2</sup>, above-ground DM per m<sup>2</sup> (AGDM) and spike partitioning index (SPI) at GS61+5d; fruiting efficiency (grains per gram spike DM at GS61+5d; FE), accumulated photosynthetically active radiation ( PAR) from GS 31-61+5d, radiation use efficiency (RUE<sub>PAR</sub>) from GS 31-61+5d, green area index (GAI) at GS61+5d, plant height at harvest and anthesis date for +*Tin1* and - *Tin1* groups of lines of the LSP2 x Rialto DH population in 2005-6. Probability < 0.10 denoted by †

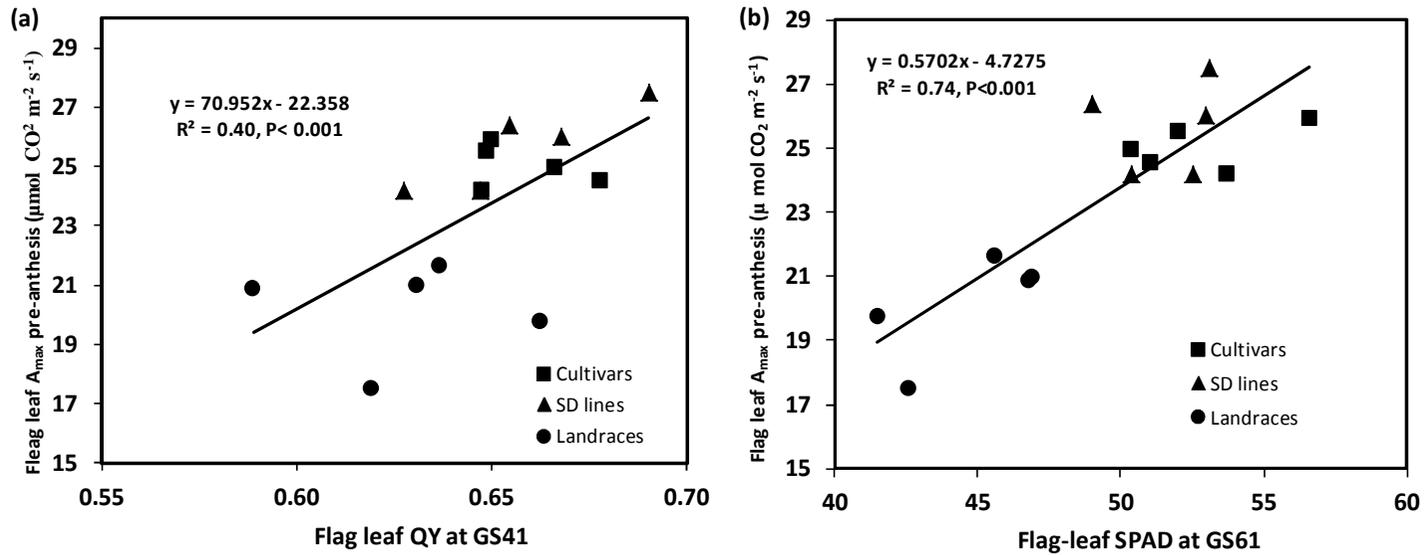
Lines	<i>Tin1A</i>	Plants m <sup>-2</sup>	Fertile shoots m <sup>-2</sup>	Spike DM (g m <sup>-2</sup> )	AGDM (g m <sup>-2</sup> )	SPI	FE (grains g <sup>-1</sup> )	Stem WSC t ha <sup>-1</sup>	Accumulated PAR (MJ m <sup>-2</sup> ) GS 31-61+5d	RUE <sub>PAR</sub> (g MJ <sup>-1</sup> )	GAI	Plant height (cm)	Anthesis date
1	+ <i>Tin1</i>	158.3	494	350.8	1138	0.31	74.1	0.58	1969	1.17	9.43	72.1	20 Mar
21	+ <i>Tin1</i>	140.8	417	310.9	1001	0.31	66.3	0.76	1756	1.15	7.73	70.6	15 Mar
31	+ <i>Tin1</i>	147.5	505	438.9	1344	0.33	44.0	0.89	1968	1.36	8.73	66.9	21 Mar
124	+ <i>Tin1</i>	157.5	451	352.7	999	0.35	59.3	0.70	1792	1.10	8.15	65.9	17 Mar
<b>Mean</b> + <i>Tin1A</i>		151.0	467	363.3	1121	0.33	60.9	0.73	1871	1.20	8.51	68.9	18 Mar
7	- <i>Tin1</i>	168.3	622	287.2	1159	0.25	57.1	0.80	2121	1.12	9.12	61.0	27 Mar
17	- <i>Tin1</i>	157.5	584	279.7	1154	0.24	74.6	1.09	1787	1.31	7.88	93.9	16 Mar
106	- <i>Tin1</i>	169.2	552	334.1	1154	0.29	66.1	0.90	1910	1.26	7.86	61.2	20 Mar
116	- <i>Tin1</i>	144.8	394	331.6	1054	0.32	59.1	0.79	1774	1.20	6.64	61.9	16 Mar
<b>Mean</b> <i>Tin1</i>	-	160.0	538	308.2	1130	0.28	64.2	0.90	1898	1.22	7.88	69.5	19 Mar
SED (df = 20)		5.90	35.8	19.85	62.8	0.0153	0.584	0.584	54.2	0.509	0.452	4.56	
Prob.		Ns	†	*	ns	**	ns	ns	ns	ns	ns	ns	



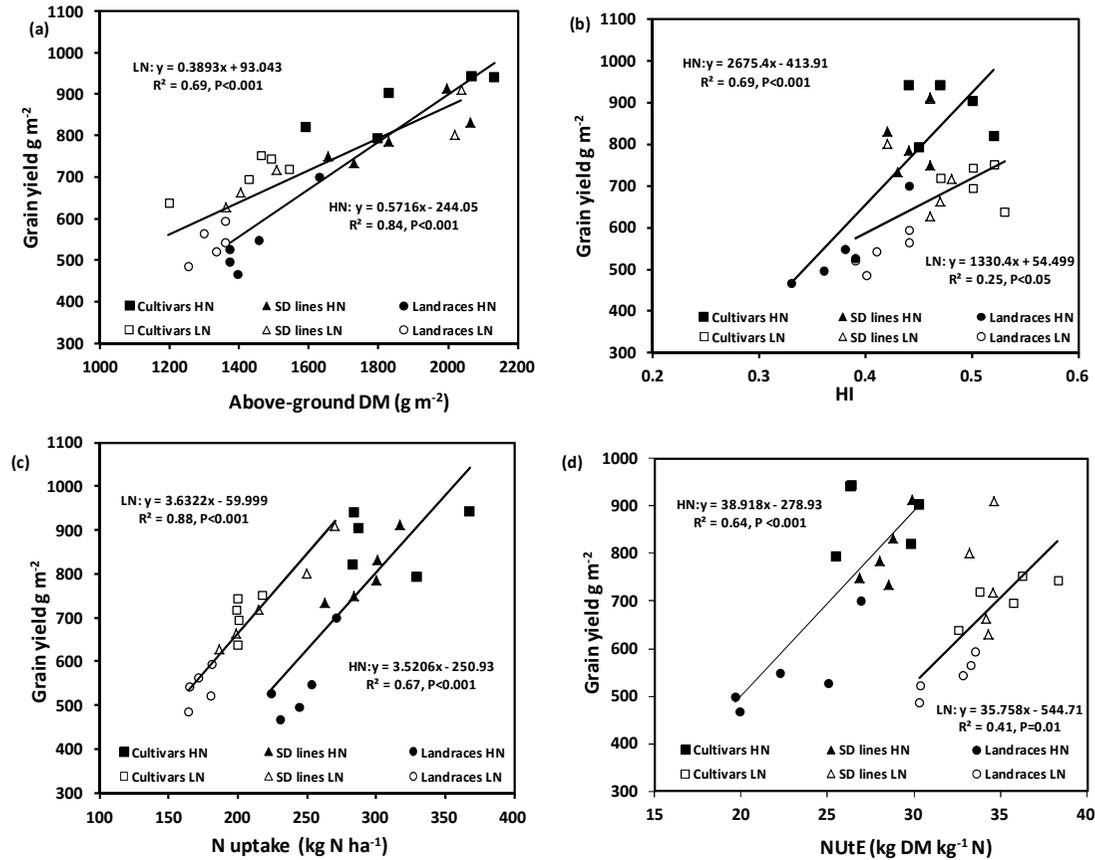
**Fig. 1.** Linear regression of a) grain yield (100% DM) on pre-anthesis flag-leaf photosynthetic rate ( $A_{max}$ ), b) above-ground dry matter on pre-anthesis flag-leaf photosynthetic rate, c) grain yield on post-anthesis flag-leaf photosynthetic rate and d) above-ground dry matter on post-anthesis flag-leaf photosynthetic rate for 15 wheat genotypes (5 modern cultivars, 5 synthetic-derived (SD) lines and 5 landraces) in the high N treatment (values represent means of 2011 and 2012).



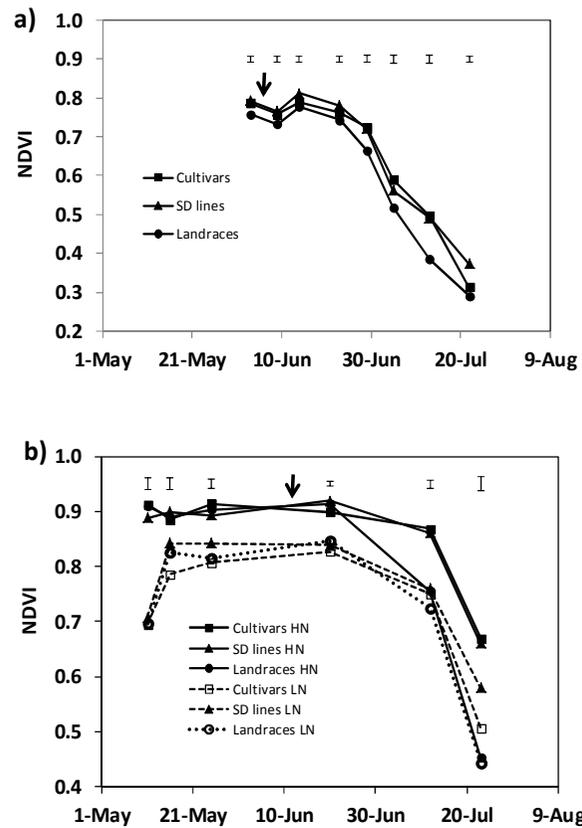
**Fig. 2.** Linear regression of a) grain yield (100% DM) on pre-anthesis flag-leaf stomatal conductance, b) above-ground dry matter on pre-anthesis flag-leaf stomatal conductance, c) grain yield on post-anthesis flag-leaf stomatal conductance and d) above-ground dry matter on post-anthesis flag-leaf stomatal conductance on 15 wheat genotypes (5 modern cultivars, 5 synthetic-derived (SD) lines and 5 landraces) in the high N treatment (values represent means of 2011 and 2012).



**Fig. 3.** Linear regression of: (a) pre-anthesis flag-leaf photosynthetic rate ( $A_{max}$ ) on flag-leaf chlorophyll fluorescence quantum yield at onset of booting (GS41) and (b) flag-leaf  $A_{max}$  pre-anthesis on flag-leaf relative chlorophyll content (SPAD) at anthesis (GS61) for 15 wheat genotypes (modern cultivars landraces and synthetic-derived lines) in the high N treatment (values represent means of 2011 and 2012).

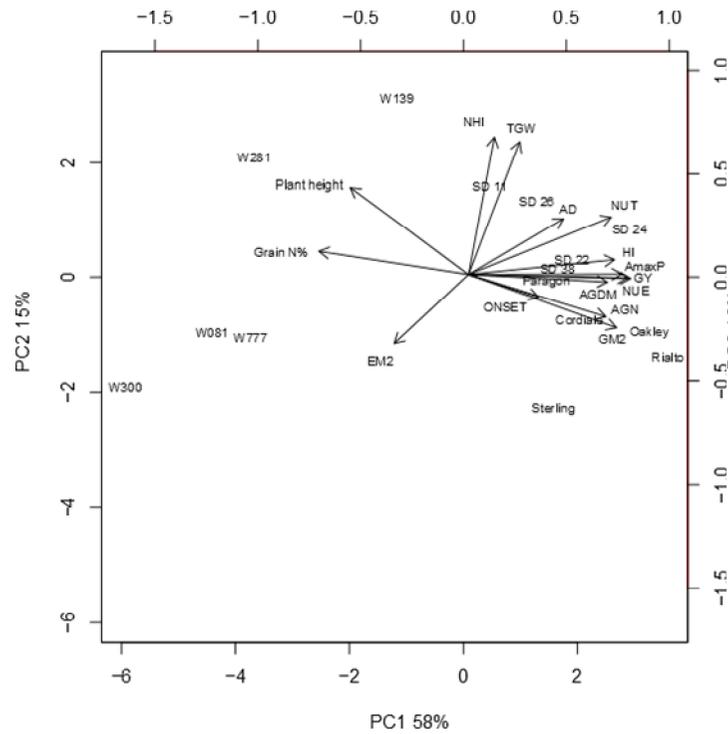


**Fig. 4.** Linear regression of (a) grain yield (100% DM) on above-ground dry matter, (b) grain yield on harvest index, (c) grain yield on above-ground N uptake at harvest and (d) grain yield on N-utilisation efficiency (NUtE) under HN (solid symbols) and LN (open symbols) conditions for 15 wheat genotypes (landraces, synthetic-derived (SD) lines and modern cultivars) (values represent means of 2011 and 2012).



**Fig. 5.** NDVI for genotype groups (landraces, synthetic-derived (SD) lines and modern cultivars under a) high N (HN) in 2011 and b) high N (HN) and low N (LN) conditions in 2012. Error bars show LSD (5%) for genotype in 2011 and N x Genotype in 2012. Arrows indicate date of anthesis (GS61) averaged across genotypes under HN in 2011 and across genotypes under HN and LN conditions in 2012.

**a) High N**



**b) Low N**

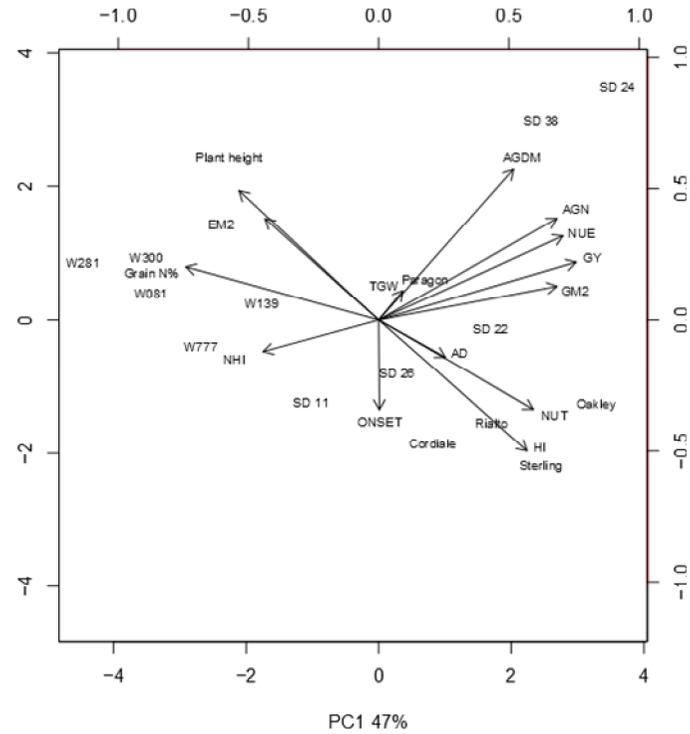


Fig. 6. Biplot for grain yield (GY), grains  $m^{-2}$  (GM2), N-use efficiency (NUE), N-utilization efficiency (NUT), N harvest index (NHI), above-ground N uptake at harvest (AGN), above-ground dry matter at harvest (AGDM), harvest index (HI), 1,000 grain weight (TGW), anthesis date (AD), onset of flag-leaf post-anthesis senescence (ONSET), grain N%, plant height and ears per  $m^2$  (EM2) for 15 wheat genotypes under a) HN conditions and b) LN conditions (values represent means of 2011 and 2012).

