

GRAIN SIZE AND PLANT HEIGHT CORRELATION IN DOUBLED-HAPLOID (DH) PROGENIES OF A CROSS BETWEEN CONTRASTING WINTER WHEAT (*Triticum aestivum* L.) PARENTS

Aurel Giura

National Agricultural Research and Development Institute Fundulea, 915200 Fundulea, Călărași County, Romania

*Corresponding author. E-mail: agiura@ricic.ro

ABSTRACT

Grain size is an important yield component in wheat. Knowing its relationship with plant height can facilitate breeding for increased thousand kernels weight in optimum plant height cultivars. A set of 85 doubled-haploid obtained from the F₁'s of G.603-86 (large grains and tall plants) and F.132 (normal size grains and semidwarf with plants) was tested along with the parents during three seasons. DH lines showed near normal distributions for plant height and thousand kernels weight, suggesting that many genes were involved in the control of both traits. Strong correlations were found between plant height and thousand kernels weight on average for the three years of testing, but also for each year. This suggests that transferring the favorable alleles from the high thousand kernels weight parent to semidwarf wheat is not an easy breeding task.

Keywords: thousand kernels weight (TKW), plant height, correlation.

INTRODUCTION

Grain size, as described by the weight of thousand kernels (TKW), is important in wheat, being, along with the spike number per unit area and the number of grains per spike, a decisive yield component. Because of the frequent compensation among the yield components, most trials performed in typical conditions prevalent in Romania, showed practically no correlation of grain yield with TKW (Mandea et al., 2019), but high and stable wheat yields cannot be conceived without a relatively high TKW.

Correlation analysis for interdependence among agronomical important traits may represent a valuable information source for prediction in plant breeding. With the possibility of creating homozygous genotypes at all loci in genome without any residual heterozygosity by using biotechnological methods, the analysis of genotype-phenotype interrelationships for important characters of agronomic interest has become more precise, eliminating also the transient expression of some genes with a dominant effect or non-additive epistasis, as in the case of classical methods. Using this new way,

the necessary information can be obtained faster, in two-three years, compared to classical methods, by which a relative homozygous status can be achieved after several generations of selection and not concomitantly for entire plant architecture genes expression of parental genomes.

This paper presents and discusses data obtained from a study of 85 doubled haploid (DH) lines created by using biotech *Zea* system on F₁'s between two parental genotypes differing in plant height and weight of 1000 kernels (TKW) traits. The study was conducted in three different years.

MATERIAL AND METHODS

A set of 85 doubled-haploid were obtained from the F₁'s of G.603-86 (large grains and tall plants) and F.132 (normal size grains and semidwarf plants).

The wheat line G.603-86 was selected from the cross *Cologna* x F6-75, where *Cologna* is an Italian local population known for its very long grains. G.603-86 has a grain weight over 60 mg in most years at Fundulea, while most cultivars have grain weights

between 35 and 45 mg. The high grain weight of G.603-86 is associated with increased grain length (8.5 to 9 mm as compared with 6 to 7 mm in most cultivars) (Giura and Săulescu, 1996). The Italian local population *Cologna* can be found in the pedigree of several wheat cultivars (*Fiorelo*, *Lovrin 231*, *Transilvania 1*, *Arieșan* etc.),

which have long grains associated with high TKW.

The lines and their parents were studied in trials at NARDI Fundulea in 2004, 2005 and in 2016 seasons, using a randomized block design with three replications.

Weather conditions during the three testing years were quite different.

Table 1. Monthly sums of precipitation (mm) recorded at NARDI Fundulea during experiment

Year / Month	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Sum
2003 / 2004	69.4	55.9	39.9	40.5	10.6	22.8	7.1	73.9	79.3	65.1	464.5
2004 / 2005	20.2	96.8	42.9	31.4	35.8	23.9	18.1	99.0	154.6	175.4	698.1
2015 / 2016	47.0	94.3	2.8	53.3	10.3	54.9	73.7	81.2	43.7	31.3	492.5
LTA	43.0	42.0	43.7	35.1	32.0	37.4	45.1	62.5	74.9	71.1	486.8

Table 2. Monthly averages of mean air temperatures (°C) recorded at NARDI Fundulea during experiment

Year / Month	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Average
2003 / 2004	9.7	6.9	-0.1	-4.2	0.8	6.5	11.8	15.8	19.8	22.4	8.9
2004 / 2005	12.4	6.1	1.2	1.1	-2.4	3.5	10.9	17.3	19.4	22.5	9.2
2015 / 2016	10.7	7.8	3.0	-4.3	6.2	7.3	13.9	15.9	22.9	24.1	10.8
LTA	11.3	5.4	0.0	-2.4	-0.1	4.9	11.3	17.0	20.8	22.7	9.1

Agricultural year 2003/2004 was wetter than normal in the first months of winter wheat development but overall, it was drier than long term average (LTA), especially due to a droughty period in February-April 2004 (Table 1). The next year was wetter than usual, the months May to July being very rainy.

The precipitation in agricultural year 2015/2016 was close to normal but the most part of the grain filling period of winter wheat was drier than usual. In the first two years the thermal conditions were close to LTA, but, in 2015/2016 the weather was warmer than LTA with 1.7°C and the grain filling period was warmer than usual (Table 2).

The lines and parents were sown in pair of rows of 1 m long, spaced apart at 25 cm

between rows and 50 cm between pairs. At maturity, thirty spikes per plot were randomly harvested for each genotype. The thousand kernels weight (TKW) was estimated by weighing the seeds per each spike and dividing by seed number. The plant height was estimated by measuring ten plants per replicate from the soil level to the top of the spike, excepting the awns.

RESULTS AND DISCUSSION

The two histograms that present three years average data of plant height and TKW (Figure 1 and 2) show near normal distributions of DH lines, suggesting that many genes were involved in the control of both traits.

AUREL GIURA: GRAIN SIZE AND PLANT HEIGHT CORRELATION IN DOUBLED-HAPLOID (DH) PROGENIES OF A CROSS BETWEEN CONTRASTING WINTER WHEAT (*Triticum aestivum* L.) PARENTS

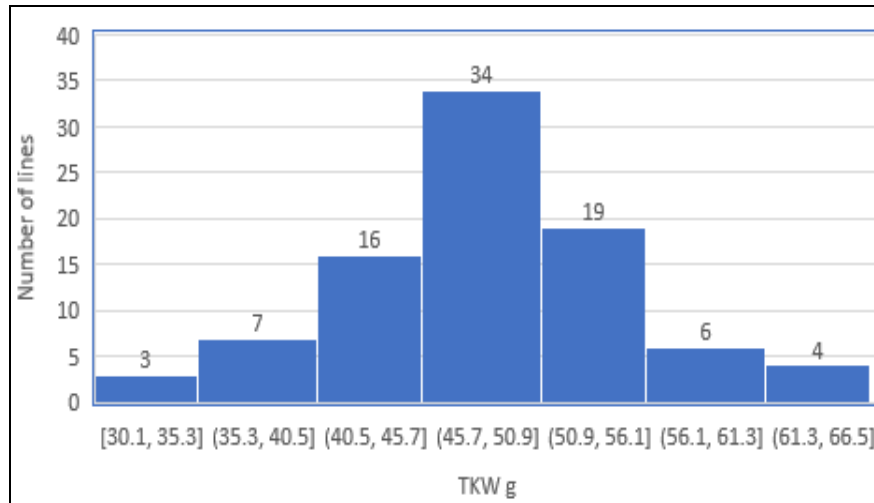


Figure 1. Histogram for DH-lines distribution for thousand kernels weight (average of 3 years)

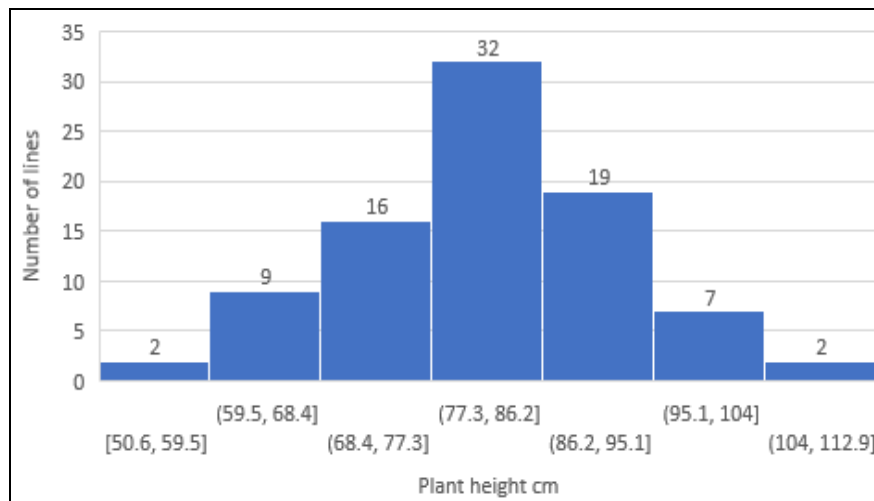


Figure 2. Histogram for DH-lines distribution for plant height (average of 3 years)

Strong correlations were found between plant height and TKW on average for the three years of testing (Figure 3, $r^2 = 0.469$),

but also for each year, i.e. 2004 (Figure 4, $r^2 = 0.372$), 2005 (Figure 5, $r^2 = 0.375$) and 2016 (Figure 6, $r^2 = 0.376$).

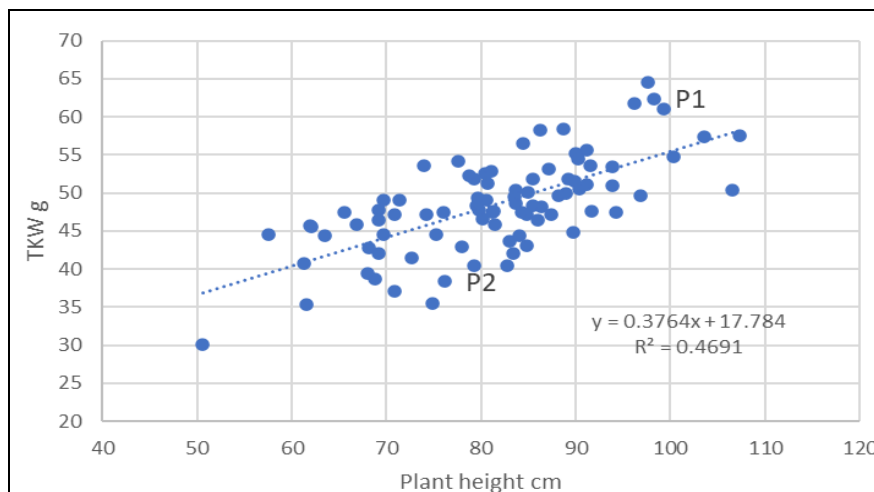


Figure 3. Correlation between plant height and thousand kernels weight (average 2004, 2005 and 2016)

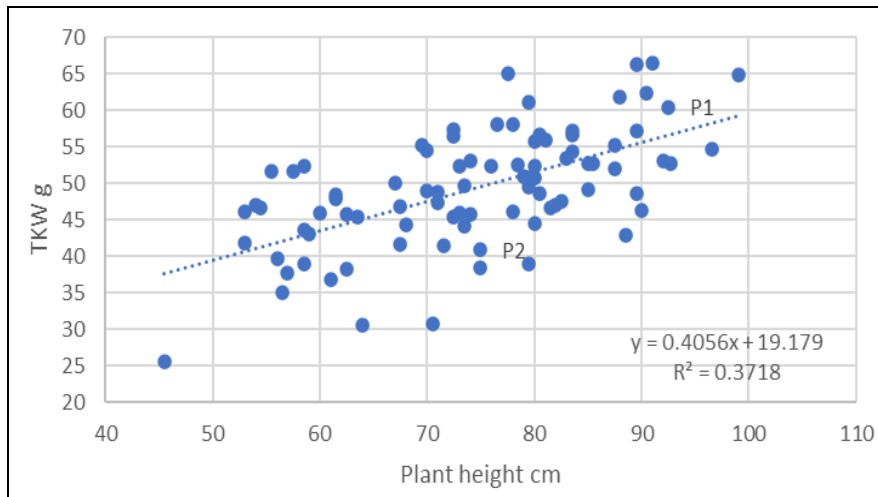


Figure 4. Relationship between plant height and thousand kernels weight in 2004

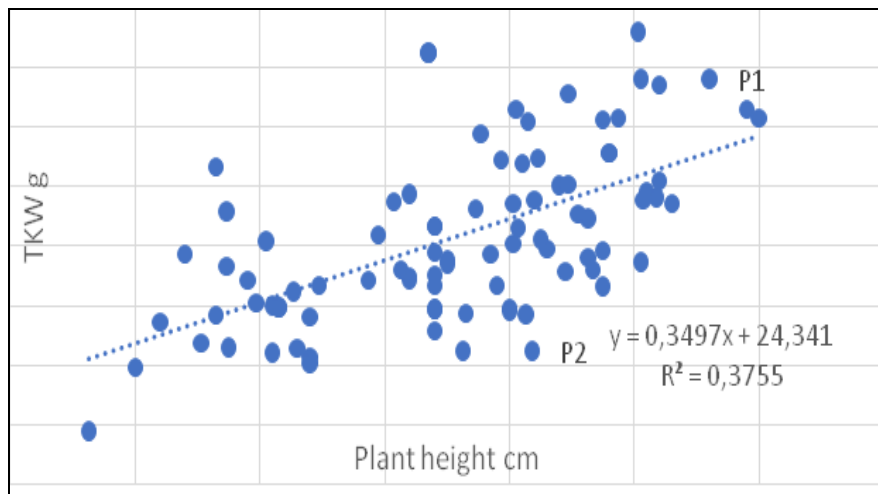


Figure 5. Relationship between plant height and thousand kernels weight in 2005

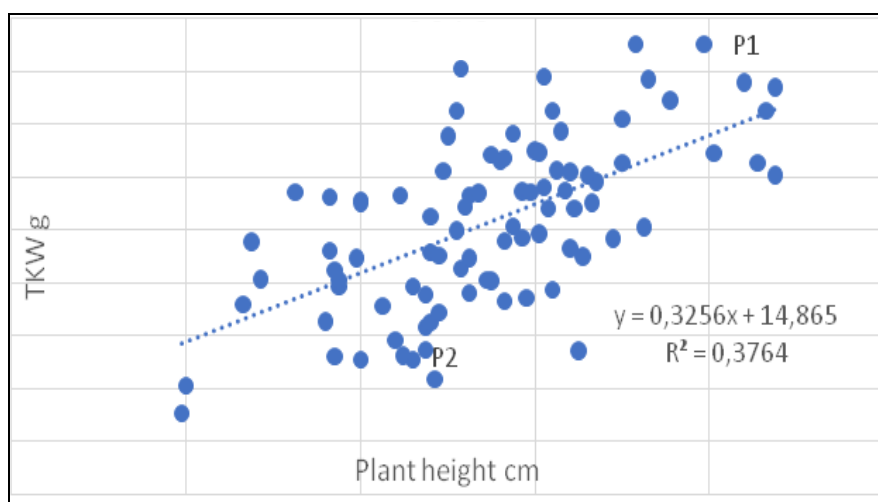


Figure 6. Relationship between plant height and thousand kernels weight in 2016

Histograms confirm the results of a previous study with F3 disomics selected cytologically from F2 monosomics (mono Favorit / G.603-86), which showed that the

weight and the size of the kernels are controlled by several genes located on different chromosomes, some with positive effects, other with negative effects (Giura and

Săulescu, 1996). In homozygous condition the alleles of these genes, both for TKW and plant height, should be equally grouped around the average.

The normal distribution of the analyzed traits suggests that in modern wheat cultivated germplasm, many genes have been accumulated, which can interact for adequate plant architecture to a better expression for plant height, seed size and thousand kernels weight, respectively. Several studies suggested that the progress in cultivar performances has been related to the increase of the grain size and TKW (Sharma et al., 2014).

The correlated distribution of TKW and plant height show that in all conditions none of the DH lines did not have significantly higher TKW or plant height than the P1 parent G.603-86. Instead, several DH lines had lower TKW and plant height than parent P2. This suggests that G.603-86 cumulates most or all of the positive alleles present in the cross for the analyzed traits.

The strong correlation between plant height and TKW might be explained by the fact that a longer stem can provide larger assimilation area and allows storing more assimilates that could be available for grain filling. Zhang et al. (2013) found that the major QTL for TKW were strongly linked to Rht-B1 and Rht-D1 loci and the positive effects were associated with the wild-type alleles, Rht-B1a and RhtD1a that control longer stem.

This suggests that combining short stem with very high TKW inherited from G.603-86 and related germplasm could face difficulties. A possible approach in overcoming these difficulties could be to recombine the lines that show deviations

from the general regression line in further recombination cycles.

CONCLUSIONS

Indifferently of environmental conditions for a specific cultivation area, the strong relationship between important plant traits makes evident a common co-evolution of responsible genes during both empirical and modern wheat breeding. The strong correlation between plant height and thousand kernels weight found in progenies of the cross between G.603-86 and a short stem line suggests that transferring the favorable alleles from this parent to semidwarf wheat is not an easy breeding task.

REFERENCES

- Giura, A., and Săulescu, N.N., 1996. *Chromosomal location of genes controlling grain size in a large grained selection of wheat (Triticum aestivum L.)*. Euphytica, 89: 77-80.
- Mandea, V., Mustăţea, P., Marinciu, C.M., Şerban, G., Meluca, C., Păunescu, G., Isticioaia, S.F., Dragomir, C., Bunta, G., Filiche, E., Voinea, L., Lobonţiu, I., Domokos, Z., Voica, M., Ittu, G., Săulescu, N.N., 2019. *Yield components compensation in winter wheat (Triticum aestivum L.) is cultivar dependent*. Romanian Agricultural Research, 36: 27-33.
- Sharma, R.C., Morgounov, A., Akin, B., Bespalova, I., Lang, I., Litvinenko, M., Mustăţea, P., Ozturk, I., Postolatiy, A., Rajarem, S., Braun, H.J., 2014. *Winter wheat Eastern European regional yield trial: identification of superior genotypes and characterization of environments*. Crop Sci., 54: 1-12.
- Zhang, J., Dell, B., Biddulph, B., Drake-Brockman, F., Walker, E., Khan, N., Wong, D., Hayden, M., Appels, R., 2013. *Wild-type alleles of RHT-B1 and RHT-D1 as independent determinants of thousand-grain weight and kernel number per spike in wheat*. Mol Breeding, 32: 771-783.
DOI: 10.1007/s11032-013-9905-1