GENETIC ANALYSIS OF TWO EGYPTIAN WHEAT CROSSES (*Triticum aestivum, L.*)

Salama, S.M.
Central Laboratory for Design and Statistical Analysis Research Crop Research Institute, A.R.C., Giza Egypt

ABSTRACT

Non-allelic interaction scaling test (A, B, and C) coupled with joint scaling test χ^2 and six parameters model were applied to test the adequacy of genetic model and estimates the genetic components for days to heading, flag leaf area, (cm)^2 number of spikes / plant, number of grains/spike, 1000-grain weight (g.) and grain yield plant (g.) using six generation (P_1, P_2, F_1, B_1, B_2 and F_2) of two wheat crosses; 1. sids1 X Gemmeiza 7 and 2. Gemmeiza 9 X Sakha 92, A randomized complete block design with three replications was used. The obtained results indicated the importance of additive genetic variance (D) in the genetic control of days to heading and flag leaf area for Gimmeiza 9 X Sakha 92 and number of spikes / plant in two crosses. Heritability in narrow sense was more than 0.50. While the dominance genetic variance (H) was found to be the prevalent type controlling for the remaining crosses in the studied characters and the value of $(H/D)^{0.5}$ was more than one for these characters and heritability in narrow sense was less than 0.50. The non allelic interaction (A, B and C) coupled with joint scaling test (χ^2) revealed that simple genetic model was adequate for explaining the inheritance of number of spikes/plant for Gemmeiza 9 X Sakha 92, epistasis played a great role of controlling remaining characters in two crosses. Additive (d) and additive X dominance (J) were significant for days to heading and number of grains / spike (1st and 2nd crosses), 1000 grain weight and grain yield / plant for 2nd cross. The digenic interaction type dominance X dominance (L) controlling days to heading (1st, and 2nd crosses), number of spikes/plant (1st cross), number of grains/spike, 1000-grain weight and grain yield / plant for 2nd cross. Understanding the type of gene action controlling mechanism of the yield and yield components couped with the reproduction system are considered the main limiting factors for choosing the appropriate breeding method. These information are of great interest for plant breeder to release high yielding wheat cultivars as well as early mature ones.

INTRODUCTION

Decision making about effective breeding method to be used is mainly dictated by the type of gene action controlling the genetic variation, such information is helpful for the breeders to predict in early generation of breeding. Programme, the potential of recombinant lines that could be derive following a series of selfing generations in this respect, additive and dominance gene effects, with great importance of dominance were found to be controlled heading date, number of grains/spike, and grain yield/plant (Pawar *et al.* (1988) and Alkadoussi and Eissa (1990)); flag leaf area, number of spikes / plant and 1000-grain weight Shehab El-Din (1997) and Salama (2002). The inheritance and genetic model for grain weight/spike were investigated by Alkaddoussi and Eissa (1989). They indicated that digenic model was appropriate to as certain the genetic model for grain yield/plant. Non allelic interaction parameters genetic model to test for epistasis were

studied by Salama (2002). Mitkess and Dawla (1983), Chatrath *et al.* (1986), Awaad (1996) and Salama (2007) indicated that additive gene action was the predominant type controlling heading data, number of grains/spike and grain yield/plant. Very limited studies were carried out to study the genetic control of yield and yield attributes characters in wheat, Sharma *et al.* (1996) Esmail (2002) and Sultan, *et al.* (2005).

MATERIALS AND METHODS

1- Description of the parental genotypes and experimental procedures:

The present study was carried out at Tag El-Ezz Research Station, Dakhlia Governorate during three winter successive growing seasons i.e. 2004/2005, 2005/2006 and 2006/2007. In 2004/2005 season the parental wheat genotypes of local origin were grown and two crosses were made by hand; Sids1 X Gimmeiza 7 and Gimmeiza9 X Sakha 92. The pedigree of the parental wheat genotypes are shown in Table (1). In second season 2005/2006 seeds of two F_1's were sown to produce F_1 plants and crossed between P_1, P_2 and F_1 to obtain backcross 1 (B_1) (F_1 X P_1), backcross 2 (B_2) (F_1 X P_2) and P_1 X P_2 (F_1 seeds) and the F_1 plants were selfed to produce F_2 seeds. In the third season 2006/2007 obtained seeds of the six populations (P_1, P_2, F_1, F_2, B_1 and B_2) of the two crosses were sown on 20th November 2006 and evaluated using a randomized complete block design with three replications. Rows was 2m length. Spacings between rows was 20 cm. While it was 10 cm between plants. Plot area was $6m^2$ (2 x 3m). The experimental plot consists of two rows for each parent, F_1 and backcrosses and five rows for F_2 generations. The recommended agricultural practices of wheat production were applied.

Table (1). Pedigree of the studied parental wheat genotypes.

Serial number	Genotypes	Pedigree
1	Sids 1	HD 2171 / Pavan "S"//1158. 57 / rlaya 74 "S"
2	Gimmeiza 7	CMM 74 A. 630 / SX // Seri 82/3/Agent
3	Gimmeiza 9	ALD "S" / Huac "S" // CM 74 A / 6301
4	Sakha 92	Napo 63 / Inia 66 // wern "S"

2- Recorded data:

The studied characters were; days to heading (day), flag. Leaf area $(cm)^2$, number of spikes /plant, number of grains/spike, 1000- grain weight (g.) and grain yield / plant (g.). Data were recorded on 10 individual plants for each of the parental genotypes as well as F_1's, 20 in B_1 and B_2 and 50 in F_2 were labeled in each replicate.

3- Biometrical analysis:

The "t" statistical test was applied to test the differences between parental genotypes for the studied characters before considering the biometrical analysis.

a- Testing for the genetic model:

The scaling test A.B. and C were applied according to Mather and Jinks (1982), formulae to test the presence of non-allelic interactions were as follows:

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}.$$

$$B = 2\overline{B_2} - \overline{P_1} - \overline{F_1} \quad \text{and}$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

Joint scaling test proposed by Cavalli (1952) as indicated X^2 was applied to test the adequacy of the genetic model controlling the studied characters. Due to the unknown biased effect of nonallelic interaction the simple genetic model (m), (d) and (h) was applied when epistasis was absent, whereas, in the presence of nonallelic interaction the analysis was proceeded to estimate the interaction types involved using the six-parameters genetic model of Jinks and Jones (1958) as follows:

m = Mean of $\overline{F_2}$.

d= Additive gene effects = $\overline{B_1} - \overline{B_2}$

h= Dominance gene effect = $\overline{F_1} - 4\overline{F_2} - (½) \overline{P_1} - (½) \overline{P_2} + 2\overline{B_1} + 2\overline{B_2}$,

i= Additive x Additive=$2\overline{B_1} + 2\overline{B_2} - 4\overline{F_2}$,

j= Additive x Dominance= $\overline{B_1} - ½ \overline{P_1} - \overline{B_2} + ½ \overline{P_2}$ and

l= Dominance x Dominance = $\overline{P_1} + \overline{P_1} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$.

The significancy of genetic components were tested using "t" test as follows:

$$\pm\, t = \frac{\text{effect}}{\sqrt{\text{variance of effect}}}$$

The genetic components of variance for each character in the studied crosses were partitioned into additive (D), dominance (II) genetic variance and environmental variance (E) using Mather (1949) and Mather and Jinks (1971) formula as follows:

Ew= ¼ ($V\overline{P_1} + V\overline{P_2} + 2V\overline{F_1}$).

D = 4 $V\overline{F_2} - 2$ ($V\overline{B_1} + V\overline{B_2}$).

H = ($V\overline{B_1} + V\overline{B_2} - V\overline{F_2} - Ew$) and

F = ($V\overline{B_2} - V\overline{B_1}$)

$(H/D)^{0.5}$ = Average degree of dominance

$F/(DxH)^{0.5}$ provides Little evidence that the dominance at different loci are particularly consistent in sign or magnitude.

Heritability in narrow sense (T_n) and Heritability in broad sense (T_b) were estimated.

RESULTS AND DISCUSSION

1- Mean performance:

Before considering the biometrical analysis for the studied characters, the "t" statistical test was applied for testing parental genotypes involved. The "t" value was significant, suggesting that employed displayed enough amount of genetic variability. Thus, genetic differences for the genes controlling the studied characters were detected Table (2).

Mean and Standared error of the six populations (P_1, P_2, F_1, F_2, B_1 and B_2) of two wheat crosses for studied characters are given in Table (2). According to the mean of F_1 as compared with its standard error (S.E.). Results indicated that the F_1 was earlier than the early heading for cross (2) (Gimmeiza 9 X Sakha 92) whereas, the F_1 exceeded its high performing parent (HP) for remaining studied characters in two crosses. The results provide evidence for present of overdominance gene effects and increasing alleles were more frequent in the genetic constitution of wheat parental genotypes, and that dominant gene were dispersed. The F_2 mean of the two studied crosses in each character indicated high value from high parent for all studied characters in two crosses except cross 2 for days to heading indicated appreciable amount of genetic variability for these characters in the corresponding crosses. The (h) value which indicated dominance deviations. (F_1-MP = F_1 − P_1 + $P_2/_2$) was positive and significant for all studied characters in two crosses except days to heading in two crosses. Significant and positive (h) value indicating that, presence heterotic effects and the increasing alleles were more frequent than the decreasing ones in the genetic constitution of the parental genotypes. However the negative and significant (h) value was obtained for days to heading at cross 2 providing evidence for the predominant of decreasing alleles over the increasing ones and the important role of dominance and / or dominance x dominance gene effects in the genetic control of these characters.

2- Component of genetic variance:

The assessment of the genetic variance Table (3), revealed that, the dominance genetic variance (h) were higher in magnitude than the corresponding additive (D) ones for days to heading and flag leaf area of 1st cross, number of grains/spike, 1000-grain weight and grain yield/plant for 1st and 2nd crosses. This resulted in average degree of dominance $(H_1/D)^{0.5}$ was more than unit. However, additive component (D) was found to be the prevailed type controlling for the remaining character in two crosses. Thus phenotypic selection would be effective in early segregating generations. The negative value "F" together with the ratio F $(H_1/D)^{0.5}$ for flag leaf area (1st and 2nd crosses), number of spikes / plant and grain yield/plant (2nd cross). Thus the decreasing alleles were more frequent. But, for the remaining characters in two crosses the increasing alleles exceeded the decreasing ones. Heritability in narrow sense was high for days to heading and flag leaf area (2nd cross) 0.65 and 0.58, respectively, number of spikes/plant (1st cross) (0.60) and (2nd cross) (0.63). suggesting the importance of straight forward

phenotypic selection method to improve characters in this respect Al Kaddoussi and Eissa (1989), Hassan (1993) and Salama (2002). But for the remaining characters heritability values ranged from (0.12) for flag leaf area (1st cross) to 0.48 for grain yield /plant (1st cross). These results are in accordance with those at Al Kaddoussi (1996), Sultan, *et al.* (2005) and Salama (2007).

3- Adequacy of genetic model:

The non allelic interaction tests (A, B and C) for studied characters, Table (4) provide evidence for the importance of epsitasis in the inheritance of studied characters in two crosses except number of spikes/plant (2nd cross). Significance χ^2 suggested that the additive –dominance model is not sufficient to explain the inheritance of these characters. Thus results confirm the findings of Al Kaddoussi and Eissa (1990) and Salama (2002) . Separation out the interaction types using six parameter genetic model revealed significant (d) gene effects for all studied characters in two crosses except number of spikes/plant in two crosses positive and significant dominance (h) was shown for days to heading (2nd cross) and grain yield/plant (1st cross). Similar results were obtained Hassan (1993) and Salama (2002). The most important digenic interaction as computed by the six parameter genetic model were; additive x dominance (J) for days to heading and number of grains/spike (two crosses), 1000-grain weight and grain yield / plant (2nd cross). Significant dominance x dominance (L) were the prevailed type that controlled days to heading (1st and 2nd crosses), number of spikes/plant (1st cross), number of grains/spike, 1000-grain weight and grain yield / plant (2nd cross).

These information are of great interest for wheat genotypes to raise grain yield and early mature ones to overcome the gap between production and consumption in Egypt.

2

3

REFERENCES

Al Kaddoussi, A.R. (1996). Using genetic components for predicting new recombinant lines in some crosses of Egyptian wheat *(Triticum aestivum L.)*. Zagazig J. Agric. Res. 23 : 463-475.

Al Kaddoussi, A.R. and M.M. Eissa (1989). Genetic analysis of main spike characteristics in durum wheat. Egypt J. Appl. Sci. 4 : 208 – 218.

Alkaddoussi, A.K. and M.M. Eissa (1990). Gene action and prediction of some yield attributes in four wheat crosses *(Triticum aestivum L.)* Annals of Agric. Sci. Moshtohor 28 : 2013-2023.

Awaad, H.A. (1996). Genetic system and prediction for yield and its attributes in four wheat crosses *(Triticum aestivum L.)*. Annals of Agric. Sci. Moshtohor, 34, 869-890.

Cavalli, L.L. (1952). An analysis of linkage in quantitative inheritance (ed. E.C.R. Rieve and Waddington, G.H.) PP 135-144 H MSO, London.

Chatrath, R.D.R.; Satija and V.P. Gupta (1986). Genetic analysis of grain yield in wheat. Indian J. Genet. 46:466-471.

Esmail, R.M. (2002). Estimates of genetic parameters in F_1 and F_2 generation of diallel crosses of bread wheat *(Triticum aestivum L.)*. Bul. of National Res. Center, Cairo 27 : 85 – 106.

Hassan, E.E. (1993). Genetic analysis of some main spike characteristics in four wheat crosses *(Triticum aestivum L.)*. Zagazig. J. Agric. Res. 20:611-621.

Jinks J.L. and Jones R.M. (1958). Estimation of the components of heterosis. Genetics, 43:223-234.

Mather, K. (1949). Biometrical genetics, Dover publication, Inc. New York.

Mather, K. and Jinks J.L. (1971). Biometrical genetics. Chapman and Hall Ltd, London.

Mather, K. and Jinks J.L. (1982). Biometrical genetics. 3rd ed. Chapman and Hall Ltd, London.

Mitkees, R.A. and N.F. Dawla (1983). Genetic analysis of a bread wheat cross. Annals of Agric. Sci, Moshtohor 20 : 225-236.

Pawar, I.S., R.S. Paroda and S. Singh (1988). Gene effects for six metric traits in four spring wheat crosses Indian J. Genet. 48 : 195-199.

Salama, S.M. (2002). Genetic analysis of yield and some yield attributes in some Egyptian wheat cultivars. Zagazig J. Agric. Res. 29 : 1395 – 1410.

Salama, S.M. (2007). Detecting epistasis, genetic correlations and new recombinant lines for grain yield and its components in bread wheat *(Triticum aestivum L.)* using triple test cross analysis. Zagazig J. Agric. Res. 34 : 1021 1038.

Sharma P.K.; D.K. Garg and P.C. Sharma (1996). Genetic characterization of some quantitative characters in wheat *(Triticum aestivum L.)*. EM. Thell). Indian J. Genet., 56: 281-284.

Shehab El-Din, T.M. (1997). Three methods for studying the genetic behaviour of heading date and plant height in several wheat crosses. J. Agric. Sci. Mansoura Univ., 22 : 1297-1306.

Sultan, M.S.; M.H. El-Hindi; S.M. Salama and E.M. EL-Morshedy (2005). Genetic variance for some main spike characters in bread wheat *(Triticum aestivum L.)*. J. Agric. Sci. Mansoura Univ. 30 : 2347-2354.

التحليل الوراثى لهجينين من قمح الخبز المصرى
سليمان محمد جمعة سلامة
المعمل المركزى لبحوث التصميم والتحليل الإحصائى – معهد بحوث المحاصيل – مركز البحوث الزراعية – جيزة – مصر

أجريت هذه الدراسة بالمزرعة البحثية لمحطة البحوث الزراعية بتاج العز — دقهلية فى الموسم الشتوى لأعوام ٢٠٠٤ / ٢٠٠٥، ٢٠٠٥ / ٢٠٠٦ وموسم ٢٠٠٧/٢٠٠٦. وأستخدم إختبار التفاعلات الغير آليلية (C, B, A) (χ²) والنموذج الثلاثى والسداسى الوراثى لدراسة النظام الوراثى المتحكم وكذلك دراسة الإختلافات الوراثية وطبيعة الفعل الجينى فى دراسة صفات عدد الأيام حتى طرد السنابل ومساحة ورقة العلم بالسم٢ وعدد السنابل وعدد حبوب السنبلة ووزن الألف حبة بالجرام ومحصول الحبوب للنبات الفردى بالجرام. وذلك بإستخدام العشائر الستة (الآباء والجيل الأول والهجن الرجعية لكلا الأبوين والجيل الثانى) فى هجينين من قمح الخبز المصرى وهما: سدس ١ × جميزة ٧ وجميزة ٩ × سخا ٩٢.

ويمكن تلخيص أهم النتائج فى الآتى:

1) أوضحت النتائج أهمية التباين الراجع للفعل الجينى المضيف فى وراثة عدد الأيام حتى طرد السنابل ومساحة ورقة العلم للهجين الثانى (جميزة ٩ × سخا ٩٢) وعدد السنابل فى الهجين الأول والثانى وكان معامل التوريث بالمعنى الضيق أعلى من ٠,٥٠ لهذه الصفات.

2) كان التباين الراجع للفعل السيادى للجين معنوياً لباقى الهجن فى الصفات المدروسة وكانت قيمة درجة السيادة أعلى من الوحدة لهذه الصفات ومعامل التوريث بالمعنى الضيق أقل من ٠,٥٠.

3) وجد أن النموذج الوراثى البسيط كان ملائماً لدراسة السلوك الوراثى لصفة عدد السنابل للنبات فى الهجين الثانى بينما كان النموذج غير ملائماً لدراسة السلوك الوراثى لباقى الصفات المدروسة.

4) كان الفعل الجينى المضيف والتفاعل المضيف × السيادى معنوياً لصفة عدد الأيام حتى طرد السنابل وعدد الحبوب للسنبلة فى كلا الهجينين ووزن الألف حبة ومحصول الحبوب للنبات الهجينى الثانى. وكان التفاعل السيادى × السيادى معنوياً لصفة عدد الأيام حتى طرد السنابل لكلا الهجينين وعدد السنابل الهجين الأول وعدد حبوب السنبلة ووزن الألف حبة ومحصول الحبوب للنبات الهجين الثانى.

5) وعلى وجه العموم معرفة النظام الوراثى المتحكم فى المحصول ومكوناته من الأسس الهامة لتحديد طريقة التربية المستخدمة. وهذه المعلومات مهمة لتربية أصناف عالية المحصول ومبكرة النضج.

Table (2): Mean performance $\pm$ standard error of the six populations (P_1, P_2, F_1, F_2, B_1 and B_2) of the two Egyptian wheat crosses for studied characters.

Characters	Days to heading (day)		Flag leaf area (cm)^2		Number of spikes/plan		Number of grains / spike		1000-grain weight (g.)		Grain yield / plant (g.)	
Populations	1	2	1	2	1	2	1	2	1	2	1	2
P_1	99.5	100.10	42.97	43.80	7.66	6.45	65.82	69.11	59.33	62.17	19.70	21.12
	±0.23	±0.19	±0.29	±0.34	±0.11	±0.09	±0.36	±0.31	±0.29	±0.38	±0.10	±0.08
P_2	93.0	92.5	45.0	40.23	6.33	5.83	62.14	58.32	65.46	57.35	18.51	26.49
	±0.20	±0.13	±0.18	±0.20	±0.13	±0.15	±0.29	±0.28	±0.24	±0.31	±0.14	±0.07
F_1	96.32	91.85	47.24	45.81	8.13	6.92	69.18	73.81	67.28	66.53	25.93	24.54
	±0.31	±0.26	±0.33	±0.37	±0.17	±0.19	±0.39	±0.41	±0.35	±0.34	±0.16	±0.11
F_2	102.01	99.53	46.16	44.82	7.73	6.52	68.88	72.53	66.21	65.42	24.17	23.34
	±0.71	±0.93	±0.84	±0.92	±0.28	±0.37	±0.91	±0.82	±0.84	±0.79	±0.28	±0.23
B_1	103.36	100.52	46.02	44.51	6.82	6.14	69.88	71.93	61.72	64.81	23.09	22.08
	±0.54	±0.48	±0.94	±0.91	±0.19	±0.38	±0.67	±0.65	±0.51	±0.58	±0.23	±0.26
B_2	92.01	90.10	47.93	42.13	6.98	6.73	65.16	59.99	68.16	58.35	24.73	20.49
	±0.75	±0.92	±0.65	±0.61	±0.27	±0.20	±0.93	±0.88	±0.95	±0.87	±0.26	±0.16
"t" test	**	**	**	**	**	**	**	**	**	**	**	**
h=F_1-½	0.07	-4.45**	3.26**	3.79**	1.13**	0.78**	5.20**	10.09**	4.88**	6.77**	6.82**	3.73**
(P_1+P_2) $\pm$ S.E	±0.33	±0.28	±0.37	±0.41	±0.18	±0.20	±0.44	±0.45	±0.39	±0.42	±0.18	±0.12

Table (3): Components of genetic variance, derived parameters and narrow sense heritability (T_n) for studied characters in two wheat crosses.

Characters	Days to heading (day)		Flag leaf area (cm²)		Number of spikes/plant		Number of grains / spike		1000-grain weight (g.)		Grain yield / plant (g.)	
	1	2	1	2	1	2	1	2	1	2	1	2
Genetic parameters												
D	0.28	1.28	0.18	0.99	0.096	0.172	0.72	0.66	0.46	0.29	0.074	0.022
H	1.16	0.68	2.12	0.96	0.048	0.084	1.44	1.28	1.52	1.44	0.08	0.108
E	0.07	0.05	0.08	0.11	0.02	0.03	0.13	0.12	0.09	0.12	0.02	0.015
F	0.28	0.62	-0.47	-0.45	0.04	-0.11	0.44	0.37	0.65	0.43	0.02	-0.04
Derived parameters												
$\sqrt{H/D}$	2.03	0.72	3.43	0.98	0.71	0.70	1.41	1.39	1.81	2.23	1.04	2.22
$F/\sqrt{DH}$	0.49	0.67	-1.15	-0.46	0.19	-0.91	0.43	0.40	0.77	0.66	0.26	-0.83
T_n	0.28	0.65	0.12	0.58	0.60	0.63	0.42	0.41	0.33	0.23	0.48	0.21

Table (4): Testing for non allelic interaction (A, B and C), χ² and six parameters genetic model for studied characters of two wheat crosses.

Parameters		Non-allelie interaction test			Joint scaling test	Six – parameter genetic model					
Characters	Cross No.	*A*	B	C	X²	M	(d)	(h)	(i)	(j)	(L)
Days to	1	10.92** +0.47	-1.3 +1.55	22.9 +2.91	**	102.01** +0.71	11.35** +0.93	-17.23** +3.96	-17.66** +4.14	8.1** +1.69	11.70** +3.97
Heading (day)	2	9.09** +1.013	-4.15* +1.86	21.82** +3.75	**	99.53** +0.93	10.42** +0.13	21.33** +4.92	-16.88 +4.91	6.62** +2.65	11.94** +4.49
Flag leaf area	1	1.83 +1.97	3.62** +1.35	2.19 +3.42	**	46.16** +0.84	-1.91 +0.14	6.51 +3.93	3.26 +4.95	-0.89 +1.83	-8.71 +6.71
(cm²)	2	4.94** + 1.83	0.23 + 1.29	3.63 + 3.77	**	44.82** + 0.92	2.38* + 1.09	-2.20 + 4.06	-6.0 + 4.13	0.59 2+.85	8.37 + 6.01
Number of spikes/plant	1	-2.15** + 0.43	-0.50 + 0.59	0.67 + 1.19	**	7.73** + 0.28	-0.16 + 0.33	-2.18 + 2.25	-3.28 + 2.23	-0.82** + 0.26	5.97** + 1.95
	2	-1.09 +0.78	0.71 + 0.47	-0.04 + 1.54	N.S	6.52** + 0.37	-0.59 + 0.43	0.44 + 1.61	-	-	-
Number of grains / spike	1	4.76** +1.43	2.36 +1.93	9.2** 3.75	**	68.88** +0.91	4.72** +1.15	-0.24 +5.99	-5.44 +4.96	2.88** +0.81	1.68 +4.89
	2	0.94 +1.39	2.15 + 1.84	15.07** +3.63	**	72.53** + 0.88	11.94** + 1.10	-16.18** +4.92	-26.28** +3.89	6.54** + 1.86	37.49** +6.95
1000-grain weight (g)	1	-3.17** +1.11	3.58 + 1.96	5.49 +3.43	**	66.21** + 0.84	-6.44** +1.08	-15.19** + 3.62	-5.08 + 3.60	-3.37** + 0.69	4.67 + 4.35
	2	3.01* +1.27	-7.18** +1.80	9.1** + 3.27	**	65.42** + 0.79	6.46** + 1.05	-8.59** + 3.48	-15.36** + 3.46	4.05* + 1.75	21.62** +4.32
Grain yield / plant (g.)	1	0.55 +0.49	5.02** +0.56	6.61** + 1.17	**	24.17** + 0.28	-1.64** + 0.34	5.78** + 1.92	-1.04 + 1.61	-2.23** + 0.83	-4.53* + 2.01
	2	-1.5** +0.55	-4.05** +0.34	2.67** +0.95	**	23.34** +0.23	1.59** +0.31	-0.4.48 +1.42	-8.22** +1.43	1.27** + 0.31	13.77** +2.27