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Frequency of heterosis in different cultivars of durum wheat

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Abstract

Five cultivars and ten their F1 and F2 hybrids were tested for inheritance of quantitative traits To achieve this aim, the difference between mean values of each F1 and F2 trait were used. These values represent the loss of allelic gene interaction during reproductive process. Using a method different from standard methods, we have determined the parental general combining ability (GCA) and influence of allelic and non allelic gene interaction, that arise during hybridization. The results revealed that these values are negative or positive, influencing negatively or positively on traits value of progeny. When the values of allelic and non-allelic interaction are equal, but inverse sign, have not heterotic effect. Analyzing the results can see also, that between allelic and non-allelic gene interaction, for cultivars in this study, exist an opposite dependency , as you can see in their rankings. According to GCA, 5/11-1 cultivar had higher values of GCA, so it is better than others, to insure a better inheritance of traits.

Key words: cultivar, inheritance, gene, allelic and non allelic gene interaction, heterosis, hybrid

Introduction.

Heterosis effect has been used in breeding of open pollinated plants such as maize. At present, hybrid breeding also being focused on self-pollinated plants, including wheat [6,8]. Development of hybrid durum wheat rests on the premise that there is heterosis in this crop [3,9].

Optimum combination of yield contributing characters and components influence the yield substantially in genetically different genotypes and their F1 hybrids [10]. Heterosis is related with genetic differences in parental components In accordance with the theory of domination and super domination, heterosis is result of allelic and non-allelic genes interaction that arise during hybridization [3,4,7] But really, there is not an exact way of measuring the effectiveness of the genes interaction that conditioned heterosis and new traits occurrence [1,5]. Moreover, in any case is not possible separation, even approximately, the effect of allelic and non-allelic genes interaction and determination of positive or negative effect of each of them in the development of trait under study. Recent studies, based on the variability of the mean values of quantitative traits of F1 and F2 hybrids and their parental forms, have developed a method to predict the effectiveness of breeding in hybrid populations and assessing the general combining ability of participants in crossing schemes [1,2,6]. This method is based on elements of analysis and measurement of effect, arise during hybridization

The present study was designed to measurement genes interaction effect that determine occurrence of heterosis in Durum wheat.

Materials and methods

The scheme of allelic and non allelic genes interactions in a hybrid, can be presented as follows: AABBCC x aabbcc → F1AaBbCc, where the A ↔ B, A ↔ C, B ↔ C interactions, are non allelic genes interactions in initial genotype AABBCC. a ↔ b, a ↔ c, b ↔ c interactions, are non allelic genes interactions of other genotype aabbcc; A ↔ b, A ↔ c, a ↔ B, B ↔ c, a ↔ C, b ↔ C are non allelic interactions, and A ↔ a, **B** ↔ b, C ↔ c are allelic genes interactions that arise as result of hybridization. This indicates that the trait value of F1 hybrids, derived from the geometric average size of trait of parental forms and allelic and non allelic interactions effects that arise during hybridization. So the model of development of quantitative traits has this form: F1=PM + AGI + NAGI, where, PM – mean parental value, AGI – allelic gene interaction, NAGI – non allelic gene interaction

It is assumed that the effect of non-allelic gene interaction of parental forms on development of F1 hybrids traits, responds to the geometric average trait size of the parental forms: $Pm=\sqrt{P_1 \times P_2}$, which are always positives. Gene allelic interaction disappears during reproduction of self-pollinated plants, and non allelic increases during transition of plants in homozygote form, in the absence of selection process The way we used to analyze the inheritance of quantitative traits in self-pollinated plants (wheat), relies on usage of changes of average size trait in F1 and F2 hybrids. This value determines the loss effect of allelic gene interaction during the process of reproduction of the population, Their effect on development of quantitative traits is calculated by formula: Allelic interaction = 2(F_1 – F_2). This is because of the population of older generations (Fk), remain in constant state, as far as in changing the trait value F1-Fk , while the relative difference F1-F2 should be doubled. This relates to the fact that heterozygous in F2, compared to F1, decreased twice as many as homozygous increased. F1-F2 difference is inbreeding depression indicator of studying population. Effects of non allelic gene action was determined by formula: NAGI=2F2-F1-PM where 2F2-F1 is the trait value of Fk population. The formula that gives the effect of non-allelic gene interaction arises from the initial formula, replacing NAGI with its actual value 2 (F1-F2) In our study we have take into consideration the weight grains variability of spike of 10 F1 and F2 hybrids, derived from crossing of 5 Durum wheat cultivars: Creso, 5/11-1, Dyarbakir, QFN, and Latino. The seeds were planted using furrows on lines with 1.0 m in length and 20 cm in width on the basis of a randomized complete block design with three replications. Every line contains 20 plant, sowing in distance 5 cm from each other. Five plants per plot were collected and the mean data points were used for analysis.

Results and discussion

The results show that among variants in the study exist significant differences, for grain weight/spike Since there are differences, the procedure continues with determining the average size of trait in parental forms, and their F1 and F2 hybrids, while their absolute values are expressed in percentage. (Table 1) According to methodology, quantitative values of allelic and non-allelic genes interaction effect, that appears during hybridization were calculated. The data in Table 1, showed that signs of this values in different hybrids, were positive or negative. So the values of allelic gene interaction effect of Dyarbakir x Latino hybrid was - 60.4, i.e. negative, which indicates that allelic genes interaction in this hybrid tends to reduce the weight grain value of the spike. But, at the same time, significative increase of the value of this interaction, causes the emergence of non-allelic gene interaction. In above mentioned hybrid, positive value of non allelic interaction (+ 45.7) opposes the negative effect of allelic interaction on the trait. The sum of allelic and non-allelic gene interaction effect in a given combination, determined by the difference between the trait size of F1 hybrid and geometric average of its parental forms PM

Table1 Effect of allelic and non allelic gene interaction on grain spike weight in some hybrids of durum wheat

Nr	*Cultivar and hybrids*	*F_1*		*F_2*		*Fk %*	*MP %*	*NAGI %*	*AGI %*
		gr	%	gr	%				
1	Dyarbakir	1.95	100.0	2.31	111.6	-	105.8	-	-
2	QFN	1.80	92.3	2.01	97.1	-	94.7	-	-
3	L-5/11-1	2.25	115.4	2.19	105.8	-	110.6	-	-
4	Latino	2.00	102.6	2.02	97.6	-	100.1	-	-
5	Creso	1.75	89.7	1.82	87.9	-	88.8	-	-
	PM	**1.95**	**100.0**	**2.07**	**100.0**	**-**	**100.0**	**-**	**-**
6	Dyarbakir x QFN	1.83	93.8	2.01	97.1	100.4	100.1	+0.3	-6.6
7	Dyarbakir x L-5/11-1	1.90	97.4	2.42	116.9	136.4	108.2	+28.2	-39
8	Dyarb x Latino	1.72	88.2	2.45	118.4	148.6	102.9	+45.7	-60.4
9	Creso X Dyarbakir	2.27	116.4	2.15	103.9	91.4	96.9	-5.5	+25.0
10	L-5/11-1 x QFN	2.12	108.7	2.17	104.8	100.9	102.3	-1.4	+7.8
11	QFN x Latino	1.54	79.1	2.09	101.0	122.9	97.4	+25.3	-49.8
12	Creso x QFN	2.33	119.5	2.15	103.9	88.3	91.7	-3.4	+31.2
13	L-5/11-1 x Latino	2.60	133.3	2.36	114.0	94.9	105.2	-10.3	+38.4
14	Creso x L-5/11-1	1.98	101.5	2.08	100.5	99.5	99.1	+0.4	+2.0
15	Creso x Latino	2.01	103.1	2.12	102.4	101.7	94.3	+7.4	+1.4
	Hybrids mean	**2.03**	**104.1**	**2.20**	**106.3**	**108.5**	**-**	**+8.7**	**-5.0**
18	LSD 0.05	0.22	18.6	0.27	14.3	-	-	-	-

If, allelic and non allelic genes interaction effects are manifested to the same degree, but with opposite sign, then we have not heterosis effect. So, during the hybrids creation process, need to study its dual nature, because there is a possibility that heterosis caused by allelic action, offset by the conditioned effect of non-allelic gene interaction Selection value of hybrids in accordance with this method, determined by the trait of population Fk. The results showed that higher selection value for this trait (weight grain/spike) had Dyarbakir x Latino and Dyarbakir x L-5/11-1 hybrids (Fk= 148.6 and 136.4% respectively), while Creso x QFN hybrid had lower value (88.3%). During further reproduction process of populations of the two above mentioned hybrids, variability of this trait is such, even, in the absence of selection, they can be stabilized at a higher level, than the best parent, for this trait. In this case, the weight spike increasing, realized on account of non-allelic gene interaction effect, that occurs during hybridization Such tendency, noted for the mean value of all hybrid populations are studied, in which the value of non-allelic interaction was 8.7%

The data of Table 1 show also that mean values of weight grains/spike of F1 hybrids (2.03 g) have not significant differences, compared with mean value of parental forms (1.95 g). But, only in hybrids comes by crossing of Creso and L-5/11-1, used as parental components, was observed the increasing of this value. Otherwise occurs with the second generation (F2) where the increasing of this value was evident for most of hybrids. Following the received data (Table 2), the impact of allelic gene interaction that showed during hybridization, is higher for Creso (+11.92), while for Dyarbakir cultivar, this effect is lower and has the negative sign (-16.2)

Non-allelic gene interaction effects (Table 3), on the contrary, had maximum mean value for Dyarbakir cultivar (+ 13.74), and minimum mean values for Creso (- 0.22). Its mean, there is an opposite dependency, between allelic and non-allelic gene interaction, which verified by their ordering

Table 2 Impact on the grain weight depending by allelic gene interaction of parental forms

Nr	*Parents*	*Dyarbakir*	*QFN*	*L-5/11-1*	*Latino*	*Creso*
1	Dyarbakir	-	-6.6	-39.0	-60.4	+25.0
2	QFN	-6.6	-	+7.8	-49.8	+31.2
3	L-5/11-1	-39.0	+7.8	-	+38.4	+2.0
4	Latino	-60.4	-49.8	+38.4	-	+1.4
5	Creso	+25.0	+31.2	+2.0	+1.4	-
6	∑	-81.0	-17.4	+9.2	-70.4	+59.6
7	PM	-16.2	-3.5	+1.84	-14.08	+11.92
8	Ranking	5	3	2	4	1

Table 3 Impact on the grain weight depending by non allelic gene interaction of parental forms

Nr	*Parents*	*Dyarbakir*	*QFN*	*L-5/11-1*	*Latino*	*Creso*
1	Dyarbakir	-	+0.3	+28.2	+45.7	-5.5
2	QFN	+0.3	-	-1.4	+25.3	-3.42
3	L-5/11-1	+28.2	-1.4	-	-10.3	+0.4
4	Latino	+45.7	+25.3	-10.3	-	+7.4
5	Creso	-5.5	-3.4	+0.4	+7.4	-
6	∑	+68.7	+20.8	+16.9	+68.1	-1.1
7	PM	+13.74	+4.16	+3.38	+13.62	-0.22
8	Ranking	1	3	4	2	5

Table 4 GCA values of parental forms

Nr	*Parental forms*	*Trait value of parents*	*Allelic gene interaction of parents*	*Non allelic gene interaction of parents*	*GCA* ***(P + AGI + NAGI)***
1	Dyarbakir	105.8	-16.2	+13.74	103.04
2	QFN	94.7	-3.5	+4.16	95.36
3	L-5/11-1	110.6	+1.84	+3.38	115.78
4	Latino	100.1	-14.08	+13.62	99.64
5	Creso	88.8	+11.92	-0.22	100.5

In accordance with the methodology, to analyze and evaluate quantitative inheritance of traits that provide the highest trait value to next generations, was determined general combining ability (GCA) (Table 4), as sum of parents trait mean value, with allelic and non allelic gene interaction effect, that occur during hybridization. The data showed (Table 4), that excluding L-5/11-1, all others cultivars, have no significant differences for GCA. Since it has a high GCA (115.78%) and presence of allelic and non allelic gene interaction effects (+ 1.84 and + 3:38 respectively) that occur during hybridization, it can be used as a good parent, to ensure high inheritance (heterosis effect) for grain weight/spike.

Conclusions

Study the legality of trait variability using standard methods, not always gives positive results, because during their use, often does not appear allelic and non-allelic gene interaction effects. The method of analysis used in this study, has no limitations because of examines what quantitative traits (including yield) formed as a result of interaction of genetic system at the level of genetic product

In the using crossing scheme, even in every other schemes, through this method, not only is determined allelic and non allelic gene interactions, their signs, but is determined GCA of each parent, making it easier to further selection process

The genotype L-5/11-1 had higher GCA than the other genotypes, which makes it more suitable as parent, to guarantee high values of studied trait.

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