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Estimating the number and inheritance of controlling genes for some important quantitative traits in crossing of Omid bread wheat and la/b tritipyrum primary line

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In order to heritability estimate and identify the number of controlling gene of some traits in crossing Omid bread wheat and La/b tritipyrum primary line, parent seeds and F1, F2 and F3 generations obtained from crossing Omid wheat variety and La/b tritipyrum primary line were planted in farm condition. The traits such as tiller number, high plant, stem length, leaf number, node number, inter node distance, flag leaf length, flag leaf width, ear number, number of spikelet per spike, ear length, own length, spike diameter, leaves length of non flag leaf were measured and noted. The obtained results from variance analysis showed that generations squares average were segregation for all traits, therefore generations mean analysis for all mentioned traits were performed. The results obtained show that dominant variance played most roles in controlling traits inheritance. Also, averages of broad sense heritability were estimated from 0.52 to 0.93. The numbers of controlling gene in reviewed traits were estimated from 1 to 4.

Key words: Wheat, tritipyrum, generation mean analysis, gene number, broad sense heritability.

INTRODUCTION

Estimation of the number of controlling gene of traits, identification of the inheritance method, and the amount of heritability for every one of the traits can be useful in selecting suitable breeding methods. One of the most suitable genetic analysis methods, that is, generation average analysis method which can estimate reciprocal effects beside additive and dominant effects (Ahmadi, 1992; Baghizadeh et al., 2008; Kang, 1994).

The transfer of genetic material of thinopyrum genus into the wheat genome through far crossing for increasing the genetic diversity in wheat. Increasing in order to improve the resistance against diseases, drought salinity and other traits in late fourth decade of 20th century (Taleei, 2000). One of them is production of artificial amphiploids of primary tritipyrum. This artificial cereal has been obtained from agronomy varieties of durum (AABB, 2n = 4X = 28) and bread wheat (AABBDD, 2n = 6X = 42)

with diploid wild varieties, *Thinopyrum bessarabicum* (E^bE^b, 2n = 2X = 14), and after production of the obtained F_1 that has been barren and chromosomes duplication, production of hexaploids and octaploids tritipyrum (AABBE^{b}E^b, 2n = 6x = 42 and AABBDDE^{b}E^b, 2n = 8X = 56) has been possible in the past decade, although in new cereal tritipyrum, especially hexaploids varieties, we can see potential reasons to be come a new high salt tolerant cereal crop too is born to problems similar to those exhibited by early triticale, such as chromosome instability and low fertility which in that crop were eventually overcome by breeding (Hassani et al., 2000; King et al., 1997). So the deletion of undesirable traits with breeding method is considerable in the tritipyrum plant. In order to identify suitable breeding methods for some important quantitative traits, genetic-breeding parameters for every one of the considerable traits were identified by generation average analysis method. Also, broad heritability for each trait was estimated in this study. Finally, the best breeding method for each trait has been certain and offered by estimating the number of

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controlling gene. This is the first research that is performed about tritipyrum lines, although research has been varied out on the wheat as one of the tritipyrum parent. Siyahpoosh et al. (2003) has studied the 25 wheat genotype in two farms in model randomized complete block design with three replications. They have measured different morphologic and physiologic traits in five stages and most heritability related to the number of spikelet per spike trait (h^2 = 80.14%) and the least heritability was related to spike to stem ratio at s_3 trait (h^2 = 1.05%). Seed yield heritability was estimated about 21.58%. Kashif and Khalig (2004), heritability, inter relationship and path coefficient studies were performed in a 5×5 diallel cross of wheat. Moderate to very high broad sense heritability was estimated for all the morphological characters except fertile tillers per plant. Plant height exhibited the highest heritability value of 92.08% while fertile tiller per plant showed a minimum value of 40.71%. Genotypically plant height, spike length, spikelet per spike, grains per spike and 1000-grain weight was positively and significantly correlated with grain yield while highly significantly associated phenotypically. Flag leaf area was positively but non significantly associated with grain yield; whereas, fertile tillers per plant was negatively and non significantly correlated with grain yield. Plant height, flag leaf area, spike length and grain per spike had positive direct effects on grain yield. While fertile tiller per plant, spikelet per spike and 1000 grain weight exhibited negative direct effects on grain yield are considered to be suitable selection criteria for evolving high yielding genotypes.

Waqar et al. (2008), ten wheat genotypes were evaluated for estimation of heritability and genetic advance of various yield related parameters viz. spike length, number of spike per plant, number of spikelet per spike, number of grains per spike, 1000 grain weight and grain yield per plant showed high values of heritability coupled high genetic advance that result in prevailing suitable condition for selection.

MATERIALS AND METHODS

In order to heritability estimate and identify the number of controlling gene of some traits in crossing Omid bread wheat and La/b tritipyrum primary line, parent seeds (Omid wheat as male parent and La/b tritipyrum as female parent), F_1, F_2 and F_3 generations obtained from crossing Omid wheat variety and La/b tritipyrum primary line were planted in model design simple observation in the farm of agriculture college of Kerman Shahid Bahonar university. The traits such as tiller number, high plant, stem length, leaf number, node number, inter node distance, flag leaf length, flag leaf width, ear number, number of spikelet per spike, ear length, own length, spike diameter, leaves length of non flag leaf were measured and noted. Data average for each trait as the main data were considered in statistic analysis for different traits in the form of variance analysis. The generation average analysis for all traits was performed through segregation of different observation among generations. The Mather and Jinks method (Mather and Jinks, 1982) were used for generations' average analysis. Equation 1 shows the general average for each trait

(Kang, 1994).

$$Y = m + \alpha d + \beta h + \alpha^2 i + 2\alpha\beta j + \beta^2 l \tag{1}$$

Where, Y= generations average, m = average of total generations d= sum of additive effects, h= sum of dominant effects, i = sum of reciprocal effect among additive effects, l = sum of reciprocal effect among dominant effects and j = sum of reciprocal effect among additive and dominant effects.

And α, β, α^2, $2\alpha\beta$ and β^2 are the coefficients for every one of the model parameters different genetic parameter were estimated by using P_1, P_2, F_1, F_2 and F_3 generations and least square method. 2, 3, 4 and 5 parameters models were used for describing observed average which was reviewed by using common scale test. The best model for every one of the traits was identified base on χ^2 test (Mather and Jinks, 1982). Then the sum of F_2 plants variance (V_{F2}) (Equation 2), F_3 progeny average variance ($V \overline{F}_3$) (Equation 3), F_2 plants covariance and F_3 progeny average of them ($W_{F2, \overline{F}_3}$) (Equation 4), f_3 progeny variances average ($\overline{V}_{F3}$) (Equation 5), separation generations variance average (E_1) and separation generations average variance (E_2), were calculated by the following formula and amounts:

$$V_{F2} = 1/2D + 1/4H + E_1 \tag{2}$$

$$V \overline{F}_3 = 1/2D + 1/16H + E_2 \tag{3}$$

$$W_{F2.} \overline{F}_3 = 1/2D + 1/8H \tag{4}$$

$$\overline{V}_{F3} = 1/4D + 1/8H + E_1 \tag{5}$$

Genetic variance details (D and H) and environment effects variance (E_1 and E_2) were calculated by creating 4 normal equation base on least square method for every trait (Ahmadi, 1992; Taleei, 2000). Then Mahmud and Keramer method (Mahmud and Keramer, 1951) were used for calculating broad heritability h^2_{bs} according to Equation 6:

$$h^2_{bs} = \frac{Vf2 - \sqrt{Vp1 \times Vp2}}{Vf2} \tag{6}$$

Finally, the Panes method (Panes, 1940) was used in order to calculate the number of controlling effective factor for every trait base on the following formula (Equation 7):

$$n = \frac{\text{Variances mean of F3 families} - E1}{\text{Variances variance of F3 families} - E2} \tag{7}$$

RESULTS AND DISCUSSION

The average and standard division for reviewed traits in different generations are given Table 1. Table 2 shows the estimate of averages genetic details for different traits that 3 parameters model included [m], [d], [h] was obtained for flag leaf length, ear number, own length Traits, 4 parameters model included [m], [d], [h], [l] for tiller number trait, 4 parameters model included [m], [d],

Table 1. The average and standard division for all traits in different generations.

Generation	Number tiller	Plant high	Stem length	Number node	Inter node distance	Flag leaf length	Flag leaf width
P_1	13.1±2.91	76.51±7.26	49.5±3.02	0.28±3.67	16.2±1.05	13.3±1.82	0.1±0.88
P_2	12.2±3.26	74.29±8.25	43.2±3.16	2.9±0.34	14.7±1.16	14.7±1.96	0.8±0.79
F_1	8.2±3.16	84±9.11	52.5±3.56	3.61±0.4	9±1.21	15.13±2.15	0.14±0.97
F_2	14.64±9.86	61.81±18.16	42.65±11.58	3.8±0.9	7.76±1.58	15.43±4.65	0.19±0.62
F_3	10.5±5.8	69.38±8.71	49.04±3.22	3.9±0.6	8.69±2.26	13.14±4.76	0.78±0.21

Generation	Leaf number	Ear number	Number of spikelet per spike	Ear length	Own length	Spike diameter	Other leave length
P_1	4.26±0.5	11.1±3.26	18±89.1	9.61±0.78	7.99±0.9	1.1±0.12	17.3±1.15
P_2	3.74±0.3	6.37±2.97	13±1.52	8.34±0.89	1.88±0.81	0.91±0.16	1.8±1.92
F_1	4.3±0.4	5.4±3.91	11±2.98	9.25±0.72	4.83±0.79	1.5±0.11	15.3±1.71
F_2	4.5±1.1	10.91±10.66	13.39±3.01	9.8±2.88	4.44±1.86	0.91±0.21	14.83±3.08
F_3	4.2±0.9	7.5±4.65	14.17±1.67	10.77±0.84	3.18±1.08	0.89±0.15	15.64±0.48

Table 2. The estimate of average genetic details for all traits.

Traits	m	[d]	[h]	[i]	[j]	[l]	χ^2
Number tiller	10.21±1.75**	-1.11±0.63 ns	21.87±7.8**	-	-	-18.23±6.15**	1.34262
Plant high	63.24±9.11**	6.15±1.16**	82.73±12.86**	18.76±3.91**	-	-61.03±7.26**	0.00000
Stem length	34.27±4.16**	4.11±1.42*	53.11±6.9**	12.29±2.17**	-	27.15±5.21**	0.00000
Leaf number	3.11±0.21*	0.26±0.08 ns	9.16±1.96**	4.35±0.82**	-	-	0.18215
Node number	2.91±0.18**	0.17±0.05 ns	5.11±0.42**	2.98±0.14**	-	-	0.081256
Inter node distance	10.76±2.1**	0.71±0.26 ns	21.11±3.6**	4.81±0.77**	-	-13.22±1.72**	0.00000
Flag leaf length	11.13±2.18**	-1.16±0.71 ns	9.25±1.93**	-	-	-	1.26723
Flag leaf width	0.52±0.17*	0.15±0.08*	1.26±0.52**	0.81±0.21**	-	-	0.29914
Ear number	6.21±2.16**	0.72±0.6 ns	4.15±1.33**	-	-	-	1.92267
Number of spikelet per spike	12.26±1.72**	-1.72±1.1 ns	51.15±4.9**	18.21±1.92**	-	-27.82±3.96**	0.00000
Ear length	6.92±1.29**	2.41±0.93**	15.63±2.19**	5.21±1.17**	-	-8.96±1.05**	0.00000
Own length	4.37±2.76**	0.61±0.83 ns	3.79±2.16**	-	-	-	1.82151
Spike diameter-	0.73±0.09**	0.09±0.03 ns	2.18±0.45**	1.15±0.19**	-	1.75±0.31**	0.00000
Other leave length	13.75±3.72**	-2.19±0.92 ns	20.19±4.1**	9.11±2.16**	-	-	1.71263

Ns, non significant; *= significant ($P \le 0.05$); **= high significant ($P \le 0.01$).

[h], [i] for leaf number, node number, flag leaf width and leaves length of non flag leaf traits and 5 parameters model included [m], [d], [h], [l], [i] for plant high, stem length, inter node distance, spikelet number per spike, ear length and spike diameter Traits. We can see only additive effects and dominant effects in the model for flag leaf length, ear number and own length Traits. Therefore, dominant-additive simple model is sufficient for describing the effects. For the number of tiller epitasis, reciprocal effects (dominant × dominant) have a role for controlling this trait beside dominant-additive effects. Additive effects, dominant effects and reciprocal effects (additive × additive) play a role in controlling the inheritance of traits such as leaf number, node number,

flag leaf width and leaves length of non flag leaf. Additive effects, dominant effective, reciprocal effects (additive × additive) and reciprocal effects (dominant × dominant) are very important in controlling the inheritance of traits like plant high, stem length, inter node distance, spikelet number per spike, ear length and spike diameter. We should consider that dominant effects and reciprocal effects (dominant × dominant) had opposite signs about the traits like tiller number, plant high, stem length, inter node distance, spikelet number per spike and ear length. That can result from duplication epitasis. The point is that the amount of additive effects in all review traits even if the model had reciprocal effects (dominant × dominant); the effect was more than the additive effect although the

Table 3. The estimate of diversity details for all traits.

Traits	D	H	E_1	E_2
Number tiller	-159.4	915.1	18.9	71.3
Plant high	-144.9	519.7	29.2	56.7
Stem length	-52.3	396.8	13.1	25.9
Leaf number	1.2	5.8	0.3	0.41
Node number	-5.4	61.9	2.8	3.9
Inter node distance	-58.15	291.7	21.2	35.1
Flag leaf length	-72.8	316.7	11.6	24.3
Flag leaf width	-0.44	5.16	0.52	0.61
Ear number	-53.9	344.6	7.15	31.2
Number of spikelet per spike	-37.2	298.2	8.3	25.9
Ear length	9.2	29.1	1.2	2.8
Own length	-5.2	28.7	2.81	1.7
Spike diameter	-11.18	72.8	5.1	6.9
Other leave length	-59.8	248.3	11.8	32.8

Table 4. The estimate of broad sense heritability and gene number for all traits.

Traits	Broad sense heritability	Gene number
Number tiller	0.9	2.3
Plant high	0.82	4.1
Stem length	0.93	3.4
Leaf number	0.88	2.1
Node number	0.88	1.8
Inter node distance	0.52	1.4
Flag leaf length	0.83	1.6
Flag leaf width	0.76	1.7
Ear number	0.91	3.1
Number of spikelet per spike	0.68	2.4
Ear length	0.92	3.9
Own length	0.79	1.7
Spike diameter	0.56	1.2
Other leave length	0.77	1.7

most of review traits had non segregation effect. It is clear that dominant effects in inheritance of all review traits had important role at the generations which were studied. Naturally, selection under self pollination condition for the above traits can not be performed and we offer that hybridization method and selection can be used for generations that are separating for breeding these traits. Table 3 shows the amount of D, H, E_1 and E_2 for all reviewed traits. The amount of dominant variance is more that the additive variance for all reviewed traits so breeding methods base on hybridization should be used for the above traits. Table 4 shows the broad heritability estimation, according to Mahmud and Kramer method that all traits have shown high broad heritability. The most amount of heritability is due to stem length and the least

amount is due to inter node distance trait. The number of controlling gene for every trait was estimated according to Panes method, needs to special presumption such as lack of linkage, epitasis effects and etc. therefore will cause to estimate less number of real limit separating genes (Baghizadeh et al., 2008).

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