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ORIGINAL ARTICLE

Genetic Analysis for Some of Morphological Traits in Bread Wheat under Drought Stress Condition Using Generations Mean Analysis

Jamileh Abedi[1], Amin Baghizadeh[2], Ghasem Mohammadi-Nejad[3]

[1] *Post graduate Student, Department of Plant Breeding, Graduate University of Advanced Technology, Kerman-Iran. Email: jabedi89@gmail.com*

[2] *Department of Biotechnology, Institute of Science and High Technology and Environmental Sciences, Graduate University of Advanced Technology, Kerman-Iran. Email: amin_4156@yahoo.com*

[3] *Department of Agronomy and Plant Breeding, College of Agriculture, Shahid Bahonar University, Kerman-Iran. E-mail: Mohammadinejad@uk.ac.ir*

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Perception of genes action controlling of quantitative traits is very important in genetic breeding methods the plant populations. to study and estimate the parameters of genetic and appointment the best genetically model for justification the genetic changing some of traits the bread wheat under drought stress condition, parents (P1 & P2) and F3, F4, F5 generations together the four control cultivars (Kharchia, Gaspard, Moghan and Mahuti) were evaluated by generation mean analysis using a agoment design including six blocks. Generation mean analysis was performed for all traits with Mather and Jinks model using joint scaling test. Three parameter model [m d h] provided the best fit for all traits expect harvest index, main spike grain weight, number of grain per plant, Total spike weight of plant with significant at 5% and 1% levels . Though additive and dominance effect both had interfered in controlling often the traits but with attention to difference effects and variety component was determined that dominance is more impressive than additive effect for traits of number of tiller, main spike weight, grain yield and grain number of main spike. Therefore will benefit using of these traits in the collection and to improve these traits hybridization would be much efficient than the selection strategies. In this study additive × additive epistasis effect only observed for traits of Total spike weight of plant, number of grain per plant, main spike grain weight and harvest index and other traits hadn't any epistasis effect that it was demonstration lack of existence the genes reciprocal effect in the inheritance studied traits. Therefore we can suggest that the selection strategies perform in terminal generations and additive × additive epistasis effect would be confirmed in selection under self-pollination condition.

Key words: bread wheat, drought stress, generation mean analysis, genes action

Bread wheat (*Triticum aestivum* L.) is an important crop worldwide and is cultivated on about 217 milion ha in a range of environments, with an annual production of about 651 milion tons (FAO., 2012). Global wheat production must continue to increase 2% annually until 2020 to meet future requirements of an increasing population and prosperity growth (Abdel-Ghany *et al.*, 2004). Iran is ranked as 14th in world wheat production. According to the recent reports, wheat was cultivated more than seven million ha and its total production was about 14.3 million tons in Iran, during 2010-2011 cropping season (FAO, 2011). This adaptability of wheat is an advantage, but drought as the most important abiotic stress is a major restriction to wheat and other agricultural production in arid and semi-arid regions (Delmer, 2005; Rajala *et al.*, 2009). Approximately 32% of the wheat growing regions in developing countries face some sort of drought stress during the cropping season (Rajaram, 2001). The occurrence and severity of soil water deficit is generally greater for rainfed wheat crops. However, changing weather patterns and worldwide water deficiencies will probably result in irrigated wheat being cultivated with lessapplied water, increasing the likelihood of soil water deficits (Rebetzke *et al.*, 2006). Insufficient water is the most critical threatto world food production (Farooq *et al.*, 2009). Breeders can use different mating designs to estimate the genetic components of controlling the traits in plant population under study. These mating designs differ in terms of genetic material used to estimate parameters (Sadrabadi Haghigi *et al.*, 1991; Vaezi *et al.*, 2000). Accurate evaluation of these traits is made difficult by the importance of the genotype × environment (G×E) interactions (Robert *et al.*, 2001). Generation means are used in analysis of generation means to estimate genetic effects (Vaezi *et al.*, 2000; Hauluer and Miranda, 1985).Generation means allow us to obtain additive, dominance and epistatic effects. Utilization of six generations in generation means analysis is simple but useful method for computation of genetic effects for the quantitative plant traits and its greatest merit reside in the capability to measure the epistatic effects like additive × additive [i], additive × dominance [j] and dominance × dominance [l] types (Novoselovic *et al.*, 2004). Accurate evaluation of these traits is made difficult by the importance of the genotype × environment (G×E) interactions (Robert *et al.*, 2001). The kind of genetic material used, will determine the ability to estimate the additive, dominance and epistasis components (Sadrabadi Haghigi *et al.*, 1991; Vaezi *et al.*, 2000). Based on the evaluated genetic parameters, selection in advanced generations might be effective for number of kernels per spike, kernel weight, fertile tillers number and grain yield, due to dominance and epistatic effects (Erkul *et al.*, 2010). Information of how gene action is important in a breeding program, because knowledge in this field can help the researcher to perform breeding programs. Thus the aim of this study was identification the effect of genes on the inheritance of traits such as spike length, peduncle length, stem length, height, number of spike, number of seed per plant, seed weight per main spike, weight grain thousand, biological yield, number of tillers, grain yield, grain number spike and main spike weight, the total weight of spike per plant and harvest index under drought stress through generation mean analysis and determine the best breeding method to use in breeding strategies effective in the bread wheat.

MATERIALS AND METHODS

Plant materials used in this study were including different generations of F3, F4, F5 derived from crosses of two parents of Gaspard (sensitive) and Kharchia (tolerante). After supply genotypes and necessary generations to obtain the best genetic model for different traits under drought stress, experiment is planned in agoment design with four controls Gaspard, Kharchia, Mahouti and Moghan in 6 blocks in the research farm of Graduate University of Advanced Technology -Kerman Iran in the agronomic year of 2011-2012. In each block created 35 plots with an area of ½ square meters with 30 cm distance between rows. In each of these blocks reserve 6 plots the family of F3, 15 plots the family of F4, 9 plots the family of F5 and 1 plot each of controls. Seeds were planted in 3 rows and 10 seeds in each row. Measured traits includes plant height, spike length, peduncle length, number of teller, spikelets number, stem length, biological yield, number of kernel per plant, number of kernels per main spike, grain weight per main spike, weight of main spike, grain yield, grain thousand weight, harvest index and weight total spike per plant. Then these were evaluated the single plant. In order to calculate of error and correction of data obtained was used from the generations P1, P2 and Mahouti and Moghan variates as control in a randomized complete block design for analysis of variance.

Genetic effect estimated using generations mean analysis with (Mather and Jinks, 1982) model. This model can show the relationship between the components of the mean. Total mean for each trait were calculated in the following way:

$$y=m+\alpha[d]+\beta[b]+\alpha^{2}[i]+2\alpha\beta[j]+\beta^{2}[l]$$

where y, m, d, h, i, l and j represent mean for one generation, mean of all generations, sum of additive effects, sum of dominance effects, sum of additive × additive, sum of additive × dominant and sum of dominant × dominant reciprocal, respectively. α, β, $2\alpha\beta$, α^2, β^2 are the coefficients for the additive, dominant effects and their interactions in the model, respectively. The joint scaling test was used to using of data the all generations. In this study, each five generations were tested with models the two, three, four, five parameters to the most appropriate model could describe observed means. All models were compared with the joint scale test (χ^2) with four, three, two and one degree of freedom (Mather and Jinks, 1982). SAS and Minitab software were used for calculations. Data analysis did base on augment design and necessary corrections were performed on each block and used from data corrected in statistical analysis.

RESULTS

Results of analysis of variance (Table 1) showed that there are significant difference among studied controls for all traits at 1% and 5% probability level Therefore, generations mean analysis is possible.

The mean and standard deviation of each of the measured traits in different generations under drought condition has been shown in Table 2. Average traits height, spike length, peduncle length, number of spikelets, stem length, plant weight, the weight of main spike, the weight of total spike, number of kernel per main spike, kernel number of total spike, harvest index in generations of F5, F3 and kernel weight main spike, grain thousand weight and grain yield in generation of F4 have significant difference with their parents.The mean of greater progenies to the parents in these traits is represented separate of transgressive (superior of progeny than parents). The amount of standard error in different generations was represented difference the individuals within the generations.

According to Mather & Jinks method (Mather and Jinks, 1982), all models, two, three, four and five parameters were fitted to identify how genes function in the inheritance of all traits and finally the model was selected that firstly all of its components be significant, secondly its standard error be less than other states and the chi-square be no significant. results of generation mean analysis based on the joint scale for all the traits under drought stress are presented in table 3 and for most traits, the three-parameter model including [m], [d], [h] had the best fit at significance levels of 1 and 5%. Golabadi with co-authors (Golabadi *et al.*, 2008) in both water environment reported three-parameter model including [m], [d], [h] with the best fit for most traits at the 1% and about the height plant and peduncle length detected four-parameter model [i], [h], [m], [d] with the best fit of significant in the environmental stress condition at the 5%. Erkul *et al.* (2010) in their investigation on wheat have expressed that for kernel weight per spike, number of kernel per spike and spikelet three-parameter model is responsible the inheritance of these traits under drought stress. Mostafavi with co-authors (Mostafavi *et al.*, 2005) in a study using different generations of bread wheat were identified that the model of additive – dominance is not adequate for most traits of studied due to non-allelic reciprocal effects. Estimated more values of h than d in tiller number, main spike weight, number of kernels per main spike and grain yield showed that the dominant genes in parents has accumulated in the hybrids of these two parents and although the additive effects is significant in the generation mean analysis of main spike weight, number of kernel per main spike but its amount is smaller than the effects of dominance. Therefore the hybridization methods are appropriate for breeding these traits.

Bigger amounts of [d] in comparison with the values of [h] in the grain 1000 weight indicates that selection methods are appropriate for breeding this trait which is according to modifying the findings obtained from (Golparvar *et al.*, 2004; Sung and Chiu, 1995). In traits of weight of main spike and number of main spike were significant both additive and dominance components that is the effects of additive and non-additive in the controlling genetic of these traits. Positive or negative sign of the additive genes effect [d] depends on which parent as P1 and which parent as P2 can be considered and in the dominance effect of its sign is as a function of mean F1 generation in relation to the parents mean and indicate which parent has a role in the dominance effect of genes (Miller and Pikett, 1956). About the spike length, peduncle length, stem length, plant height, number of spikelets and grain yield the due to the significant additive effect than dominance effect is represented the greater role this effect in controlling the inheritance of these traits. In case Khattab *et al*., (2010) in their study on three wheats crosses were reported additive, dominance and epistatic effects for plant weight and plant height. (Sharma and Sign, 2002) reported more additive effect in comparison with dominance effect for the peduncle level trait in durum wheat. (Lonc, 1988) showed that genes with over dominance effect control tiller number and dominant genes are involved in increasing plant height. However, increasing the grain yield per plant be inherited by recessive genes. He was determined allelic reciprocal effects for number of tiller, spike length and 1000-grain weight. He showed that plant height, spike length, number of spikelets per spike, number of kernel per spike, main spike yield, yield of plant and 1000-grain weight is controlled by genes partial dominance effects.

Dhanda and Sethi (1996) in the genetic analysis of different traits the bread wheat in both normal and drought conditions were determined that both additive and dominance gene effects are played an important role in controlling the inheritance of traits in each environment but for different traits were different the significance of these effects in different environments. For the total weight of spike per plant and harvest index additive × additive reciprocal effect plays an important role in controlling traits. Thus it can be suggested to accomplish the selection in the terminal generation and epistatic effect of additive × additive can be stabilized providing the selection under self-pollination condition. Exsiccation epistasis for yield and its components is seen in earnings (Akhtar and Chowdhry, 2006; Blank *et al*., 2006). Opposite sign [i] and [d] on the total weight of spike per plant, number of kernel per plant, kernel weight per main spike and harvest index is demonstrator exist epistatic effects of multiple for different loci. Overall different and significant epistatic effects of the total weight per spike and harvest index are indicating the nature of the polygene and insufficient three-parameter model for them. (Gamble and Burke, 1984) were reported for epistatic effects harvest index. Positive degree of dominance ($0 < h / d < +1$) means that partial dominance is happened for the trait under study towards parents who have a higher mean and the negative this ratio ($0 < h / d < -1$) can be concluded that partial dominance is to reduce the relative trait (Forouzanfar *et al*., 2009; Mather and Jinks, 1982) and partial dominance is happened towards parents to have a smaller mean for trait studied. In the most of the traits except number of spikelets, kernel weight per main spike, total spike weight per plant, 1000-grain weight the degree of dominance was greater than one that it is representing existence over dominance phenomenon in these traits that it may be result from the accumulation of large numbers of genes effects with partial dominant or complete and linkage desirable and undesirable dominance genes (Falconer, 1989). Stabilizing effects of over dominance are not allowed but can enjoy with crossing homozygous individuals and produce hybrid of them (Mola *et al.*, 1962). For the spike length is obtained over dominance that it is opposite the results of Golabadi *et al*, (2008) that for this trait have reported the partial dominance it is similar to results (Shirkavand *et al.*, 2011).

Table 1: Analysis of variance (Means squares) for traits interaction Gaspard × Kharchia under drought stress

	MEAN SQUARES	
CHARACTERS	**GENOTYPES**	**REPLICATION**
Plant height	524.82**	86.29^{ns}
Spike length	13.69**	3.98**
Peduncle length	272.25**	17.87^{ns}
Number of tillers	106.04**	39.27**
Number of spikelets	26.67**	12.48**
Stem length	6745.63**	8913.78*
The biological function	0.33*	0.35**
The main spike weight	3.88*	5.89*
Total weight Spikes	164.39**	336.32**
The number of grains per main spike	143.35*	171.53*
The total number of grains per spike	25.16*	19.45^{ns}
Grain weight per main spike	37.28*	27.65^{ns}
Grain yield	4.52*	0.058^{ns}
Thousand grain weight	1.36*	0.045^{ns}
Harvest index	8.861*	3.01^{ns}

*P ≤ 0.05, ** P ≤ 0.01, ns = Not-significant

Table 2: Mean and standard error for different traits in crosses Gaspard × Kharchia

Treats	P$_1$	P$_2$	F$_3$	F$_4$	F$_5$
plant height	45.27 ±1.31	52.58 ±1.75	87.90 ±0.77	71.49 ±0.48	72.44 ±0.58
spike length	1.69 ±0.25	1.11 ±0.25	1.77 ±0.11	1.88 ±0.07	2.27 ±0.10
peduncle length	14.92 ±1.15	22.73 ±0.5	37.24 ±0.5	30.11 ±0.31	56.31 ±0.51
number of tillers	22.08 ±0.92	23.00 ±1.16	21.11 ±0.38	22.24 ±0.27	21.24 ±0.31
Number of spikelets	6.48±0.49	3.75 ±0.42	6.44 ±0.20	6.47 ±0.40	4.37 ±0.14
Stem length	39.35 ±1.23	44.67 ±1.62	74.73 ±0.73	261.39 ±0.92	95.33 ±1.26
biomass	77.3±1.72	44.29 ±1.61	95.68 ±0.80	119.04 ±0.62	102.22 ±0.69
weight of main spike	0.60 ±0.08	0.40±0.06	3.20±0.14	1.01 ±0.05	1.53±0.08
spike weight	7.87 ±0.55	4.99 ±0.54	28.76 ±0.44	19.72 ±0.25	19.84 ±0.30
number of grains per main spike	133.14±2.26	48.98±1.69	91.2±0.79	109.54±0.6	87.94±0.64
number of grains per spike	6362.9±15.6	5670.01 ±18.26	10966.4±8.7	13984.6±6.8	9598.4 ±672
grain weight per main spike	0.50±0.05	0.34 ±0.04	0.12 ±0.01	0.21 ±0.02	0.35 ±0.01
grain yield	3.71 ±0.35	2.18±0.32	4.24±0.17	5.16 ±0.13	3.20±0.12
Thousand seed weight	14.67 ±1.39	11.49±1.59	9.16±0.48	22.5 ±0.78	21.56 ±0.42
harvest index	17.06±2.32	14.32±2.74	11.33±0.90	29.483±3.11	35.34±5.72

Table 3: Estimates of genetic components of the best fit model on generation means morphological traits of the wheat cross Gaspard × Kharchia evaluated under drought condition

Treats	Genetic components						
	m±SE	[d]±SE	[h]±SE	[i]±SE	[l]±SE	X^2	h/d
plant height	43.87±0.615**	-1.95±1.06*	4.671±4.48 ^{ns}	-	-	0.2106	-2.39
spike length	7.820±0.103**	0.377±0.180*	1.100±0.685 ^{ns}	-	-	0.0126	2.91
peduncle length	17.260±0.494**	-1.700±0.663**	5.506±3.030^{ns}	-	-	0.111	-3.23
number of tillers	11.630±0.347**	-0.649±0.726^{ns}	-3.026±1.710*	-	-	0.283	4.65
Number of spikelets	14.120±0.501**	1.097±0.353**	1.030±0.856**-	-	-	0.007	-0.947
Stem length	35.93±1.24**	-2.38±1.38*	4.307±6.430 ^{ns}	-	-	0.039	-1.806
biomass	16.360±0.696**	1.699±1.000**	-3.415±4.820^{ns}	-	-	0.225	-2.009
weight of main spike	0.806±0.050**	0.202±0.054 **	1.446±0.501**	-	-	0.021	7.132
spike weight	5.570±0.398**	0.669±0.386*	0.129±2.870^{ns}	-1.050±0.555*	-	0.002	0.192
number of grains per main spike	25.350±0.704**	2.53±1.37*	8.88±4.86*	-	-	0.152	3.506
number of grains per spike	110.21±8.67**	14.060±8.003**	18.012±8.430**	-21.611±4.820**	-	0.66	1.281
grain weight per main spike	0.510±0.024**	0.101±0.038**	0.040±0.142^{ns}	-0.069±0.045^{ns}	-	0.0003	0.442
grain yield	1.920±0.134**	0.235±0.240 ^{ns}	1.398±0.770*	-	-	0. 09	5.935
Thousand seed weight	19.025±0.490**	2.49±1.05 *	-0.82±3.21 ^{ns}	-	-	0.096	-0.329
harvest index	69.85±5.85**	0.49±1.80 ^{ns}	-7.23±6. 81 ^{ns}	-57.140±6.127**	-	0.001	-14.67

m = Mean, [d] = Additive effects, [h] = Dominance effects, [i] = Additive × additive effects, [l] = Dominance × dominance effects.

* $P < 0.05$, ** $P < 0.01$

DISCUSSION

Information about genes action will determine breeding strategy for a trait. The high estimation of dominance and epistasis effects and overhand the high estimated additive effects feature attention to hybrid seed production and usage of different methods of action selection as the original strategy breeding a trait respectively. with attention to the non-significance component of the additive and significant the dominance component about the tiller number and grain yield were more role of genes with dominance effects than the genes with additive effects thus it can be suggested that in genetic breeding this trait in the cultivars of studied wheat this research is used of hybrid seed production. Of course should be noticed that Hybrid seed production technology is currently more is focused on the cross pollination plants such as corn and is being developed in plants such as rice too. in wheat because achieve a good success with the classical methods the breeding plant such as hybridization terms of grain yield and also due to being self-pollination this plant and spend high charges to of hybrid seed production bodily using this genetic method has not practically succeed in wheat breeding.

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