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Genetic Analysis of Physiological Traits and Grain Yield in Bread Wheat under Drought Stress Conditions

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ABSTRACT: Physiological traits are very important in wheat breeding programs for drought prone environments. In order to study genetic parameters, a half diallel crosses with nine cultivars of wheat was performed.ParentsandF2 hybrids were planted in a randomized complete block design (RCBD) with three replicates in research field during 2013. Physiological traits including chla, chlb, chlT, carotenoids, protein, proline, carbohydrates, antioxidant enzymes (CAT, APX and GPX) and grain yield were evaluated. Diallel results based on method 2 of Griffing B model showed that GCA and SCA were highly significant for all traits. Results showed that the most of genetic variation was due to non-additive genetic variance. In the following, Hayman and Jinks analysis was done. The broad sense heritability for traits was between 0.49 to 0.74 and narrow sense heritability was varied between 0.12 to 0.35. Hayman, Jinks graphical analysis was showed that the control of genes action for traits was to over dominance. For breeding of these traits, Bulk, Bulk seed discent and Double haploeid method suggested.

Key words: Bread wheat, Drought stress, Gene action, Half diallel cross, Heritability, Physiological parameters

Abbreviations: Chla-chlorophyll a, Chlb -chlorophyll b, ChlT- Total chlorophyll, Car-Carotenoids, CAT -Catalase enzyme, APX -Ascorbate peroxidase enzyme, GPX- Guaiacol peroxidase enzyme

INTRODUCTION

Limitation water is the most critical threat to world food production (Farooq *et al,* 2009). About one-third of the world's cultivated land is in semiarid and arid regions (Atlin & Frey, 1990; Blum, 2011), and this includes Iran, which has90 million hectare of natural rangelands, 20 million hectare of cultivated land, with an average rainfall of 240 mm. Of the 20 million hectare of cultivated land in Iran, only 5 million hectare is under irrigation because of limited water supplies. As wheat (*Triticum aestivum* L.) is an important food crop for human nutrition (Altenbach, 2012), developing high-yielding plant cultivars for drought conditions in arid regions is an important aim of breeding programs (Painawadee *et al,* 2009; Kirigwi *et al,* 2004). However plants respond to drought stress by the induction of different morphological and physiological responses (Wang & Huang, 2004).

Many physiological parameters could be involved in drought stress which may promise for characterizing drought resistance in screening studies (Jiangand & Huang 2001). For example drought stress damages photosynthetic apparatus and reduces chlorophyll content (Fu & Huang, 2001). Drought stress leads to enhanced generation of reactive oxygen species (ROS) (Foyer *et al*, 2005). Accumulation of ROS leads to protein degradation, lipid oxidation, and pigment bleaching. Detoxification of ROS is accomplished by the antioxidant defense system comprising nonenzymatic components such as carotenoids (Della Pena & Pogson, 2006). Antioxidant enzymes including ascorbateperox-idase (APX), glutathionereductase (GR), guaiacolperoxidase (GPX) and dehydroascorbate reductase are known to detoxify H_2O_2 (Foyer *et al*, 2005; Wu *et al*, 2013).

Catalase (CAT) is a tetrameric heme and mostly located in peroxisomes also involved in deactivation of hydrogen peroxide, though its affinity to H_2O_2 is low and has the highest conversion efficiency of all antioxidant enzymes (Luna *et al*, 2004; Scandalios *et al*, 2007; Mhamdi *et al*, 2010; Gill & Tuteja, 2010). The balance between ROS production and activities of antioxidative enzyme determines whether oxidative signaling or damage will occur (Møller *et al*, 2007). Another important mechanism of protection against water stress is accumulation of osmolytes such as carbohydrates, amino acids, amides and proline (Taylor *et al*, 1996; Kuznetsov *et al*, 1999; Hare & Cress, 1997; Maggio *et al*, 2002). Proline is one of the most common osmolytes and there is a strong positive correlation with plant ability to survive upon high salinity and drought stress (Chaves *et al*, 2004; Taylor, 1996; Quartacci *et al*, 1995; Lizana *et al*, 2006). The increasing in stability of global climate necessitates investigations into the mechanisms of plant resistance to drought and other stresses. The knowledge of genetic association between selection indices, yield and morpho-physiological traits can be useful to improve the efficiency of breeding programs. Diallel analysis has been widely used by plant breeders to quantify the genetic variation among and relative merit of specific parents from a defined reference population (Griffing, 1956). In many circumstances plant breeders are interested in quantifying the breeding value of a specific selected set of parents. Estimates of the breeding values of parents can be obtained from the combining ability model in a diallel analysis. As there is not any genetic information on physiological parameters, the objective of the current study was to quantify the genetic variation of physiological parameters in a diallel analysis and to identify whether different cultivars with high drought tolerance differ in their patterns of combining ability for the physiological parameters.

MATERIALS AND METHODS

The experiment was conducted at Shahid Bahonar University research field, located at Iran (South-East of Kerman, 30°15" N and 56°58 E, 1753.8masl). The mean annual precipitation and temperature were 154.1mm and 25.5 °C, respectively. Summers are dry, and there is usually no rain from the end of May to mid-October. In this experiment, nine Wheat cultivars-namely 'Mahdavi', 'Ghods', 'Azar2', 'Shiraz', 'Roushan', 'Kavir', 'Kalheydari', 'Shahpasand', 'Excaliber' and their F_2 progenies were cultivated in randomized complete block design with three replicates in research field in 2013. Each of the blocks including the F_2 generation crosses and their parents and each genotype were planted on each plot was containing four rows with 2 meters length and distance of 20 cm from each other. The distance of planting on row was considered 5 cm. Agricultural operations such as fertilization, weeding and spraying was carried out uniformly and equally to all replicates. In order to create water stress due to climate conditions of the region, irrigation was cut from the shooting stage. Sampling from flag leaf con-ducted after signs of stress. Some physiological traits including, Chl a, Chl b, Chl T, Car, protein, proline, solution carbohydrates and antioxidant enzymes activity like CAT, APX and GPX were measured. Chla, Chlb and ChlT were determined spectrophotometrically using 80% acetone as a solvent (Lichtenthaler & Buschmann, 2001). Plant pigments concentrations were calculated using the following equations:

$Chla = (12.25A_{663.2} - 2.79A_{646.8})$

$Chlb = (21.21A_{646.8} - 5.1\ A_{663.2})$

$ChlT = Chl\ a + Chl\ b$

$Car = [(1000A_{470} - 1.8\ Chla - 85.02\ Chlb)/198]$

Proline was determined by the ninhydrin method described by Bates *et al*. (1973). Solution carbohydrate content was measured by the reagents anthrone method described by Roe *et al.* (1955). Protein was determined by the Bradford (1976) method. CAT activity (EC 1.11.1.6) was determined according to Dhindsa *et al.* (1981) from the rate of destruction and reduce the absorption of hydrogen peroxide in 240nm. The extinction coefficient was ε = 0/40 mM/cm. The enzyme activity was expressed in detoxification 1mmol of H_2O_2 per minute by catalase enzyme.APX activity (EC1.11.1.11) was determined according to Gerbling *et al*. (1984) from the rate of ascorbic acid oxidation by hydrogen peroxide in 290nm. The extinction coefficient of ascorbic acid was ε = 0/80mM/cm. One unit of APX was defined as the amount of enzyme required to consume 1 µmol ascorbate min^{-1}. GPX activity (EC1.11.1.7) was determined according to Zhang *et al*. (2005) from the rate of tetraguaiacol formation in 470nm. The extinction coefficient of tetraguaiacol was ε = 0/25 mM/cm. The enzyme activity was defined as the absorbance change of one unit per minute. After ripening, grain yield for all genotype was measured. Data statistical analysis were tested for normality by Kolmogorov Smirnov test and was subjected to two-way analysis of variance (ANOVA) using SAS (SAS Institute, 2008) to determine differences among genotypes for each trait. Diallel analysis based on method 2 of Griffing B Model (1956) and Hyman-Jinks (1956,57) was done. A combining ability analysis was conducted on the F_2 hybrids following Griffing method (1956), assuming a random effects model. Both general (GCA) and specific (SCA) combining ability effects were estimated.

The relative sizes of the two sources of variation, GCA and SCA were compared following Baker (1978) as $2V_g/(2V_g + V_s)$, where V_g is the variance of general combining ability effects and Vs is the variance of specific combining ability effects. In Hayman, Jinks method (1956,57) for the description of results, we used dispersion components as D, H_1, H_2, F, UV, E, sqr (H1/D), h^2/H_2, h^2b and h^2n each with a different genetic sense. D is a measure of the additive effect of genes, H_1 and H_2 are measures of the dominance effects, F is the ratio of dominant and recessive alleles, UV parameter is the balance of positive and negative alleles, E is environmental component of variation. Ratiossqr (H_1/D) determine the average degree of dominance in each locus. The h^2/H_2 estimates the number of groups of genes controlling and exhibiting dominance. h^2b and h^2n are broad sense and narrow sense heritability respectively. The significance of differences between the parameters D and H_1 were established by the Student-criterion based on the estimation of the value. In addition to calculating different genetic parameters, graphical method was used to analyze the best (Mather and Jinks, 1982). For verification of the compliance of the experimental material with additive-dominant model, we used the dispersion analysis of Wr + Vr as well as the regression analysis of the dependence of Wr from Vr, for testing the correspondence between repeats and equality of the regression coefficient to one, respectively(Hayman, 1957). For data analysis Diallel 98 software were used.

RESULTS

According to normality of data by Kolmogorov Smirnov test, the variance analysis was performed. The results of variance analysis of traits for all genotypes are presented in Table 1. The mean squares of all traits are significant at level 1% except for Car and proline traits, that these traits are significant at level 5%. Comparison of treatments mean was done with Multiple Rang Duncan's test for nine cultivars (Table 2) revealed that cultivars 'Roushan', 'Excaliber', 'Kalheydari', 'Ghods', 'Azar2', 'Shahpasand' and 'Kavir' had the highest amounts of the traits Chla & protein, Chlb & ChlT & CAT, GPX & APX, grainyield, Car, proline and carbohydrates respectively.

Table 1: Mean of squares of evaluated traits under drought stress.

S.O.V	Block	Genotype	Error	CV
Chla	27.15	32.97**	12.3	10.23
Chlb	1.23	13.25**	6.19	9.14
ChlT	36.56	84.16**	31.79	18.66
Car	0.13	0.42*	0.26	15.56
Protein	46257	48082**	26811	13.76
Proline	7460	23335*	15712	14.57
Carbohydrates	45071	93440**	35333	19.76
CAT	0.002	0.12**	0.03	16.34
APX	0.02	0.23**	0.04	17.45
GPX	0.04	0.32**	0.05	18.98
Grain yield	24035	316300**	21348	23.22
df	2	44	88	

*,**Significant differences at P≤0.05 or P≤0.01, respectively, as based on F test. CV: coefficient of variation.

Table 2: Multiple Rang Duncan's test among evaluated traits in 5% significant level.

Genotype	Chl a	Chl b	Chl T	Car	Protein	Proline
Mahdavi	12.46ab	8.58a	21.04ab	1.78abc	401.86ab	384.9ab
Azar2	13. 5ab	6.79b	20.29ab	2.33a	254.9b	253.7ab
Roushan	15. 01a	8.74a	23.8a	2.05ab	561.8a	255.2ab
Ghods	10. 97b	8.73a	19.7ab	1.45abc	261.2b	174.7b
Kavir	11. 79ab	8.35ab	20.15ab	1.8abc	160.31b	234.6ab
Excaliber	14. 73a	10.3a	25.04a	1.65abc	218b	234.2ab
Kalheydari	10. 81b	6.24b	17.06ab	1.16bc	251.64b	321.8ab
shiraz	10. 64b	5.89c	16.53ab	1.01c	537.2a	237.4ab
Shahpasand	5. 5c	8.5a	14b	1.5abc	393.6ab	442.2a

Any two values of mean having a common letter are not significantly different

Table 2 continued: Multiple Rang Duncan's test among evaluated traits in 5% significant level.

Genotype	Carbohydrates	CAT	APX	GPX	Grain Yield
Mahdavi	290.5b	0.21ab	0.65bc	0.58c	519.3ab
Azar2	331.3b	0.35ab	0.97bc	1.02bc	562.8a
Roushan	620.5ab	0.04b	0.31c	0.64c	510.9ab
Ghods	344.4b	0.19ab	0.91bc	1.36abc	607.3a
Kavir	808.9a	0.28ab	1.91ab	2.09ab	550.9ab
Excaliber	325.4b	0.44a	1.2abc	1.52abc	451.6b
Kalheydari	609.3ab	0.15ab	2.48a	2.32a	479.7b
shiraz	520.9ab	0.12ab	0.52c	0.61c	509.3ab
shahpasand	497.4ab	0.08ab	1.59abc	1.29abc	254.2c

Any two values of mean having a common letter are not significantly different

Table 3: Mean squares of GCA and SCA for evaluated traits under drought stress.

S.O.V	GCA	SCA	Error	GCA/SCA	Baker ratio[1]
Chla	40.5**	35.4**	11.42	1.14	0.69
Chlb	15.39*	14.71**	6.23	1.04	0.67
ChlT	104.85**	92.27**	31.03	1.13	0.69
Car	0.39**	0.42**	0.08	0.92	0.65
Protein	47104*	67740**	28924	0.69	0.58
Proline	25869*	37137**	14192	0.69	0.58
Carbohydrates	55048**	47403**	20585	1.16	0.69
CAT	0.28**	0.29**	0.08	0.96	0.56
APX	1.25**	2.26**	0.06	0.55	0.52
GPX	1.45**	1.88**	0.28	0.77	0.6
Grain yield	6645.9*	8413.7**	2337.1	0.78	0.61
df	8	27	70		

General combining ability (GCA) effects, and specific combining ability (SCA) mean squares for traits of nine parents in a half diallel mating design, 1 2Vg/(2Vg + Vs),* Significant at P≤0.05, **P ≤ 0.01

According to Griffing method (1956), differences of nine evaluated cultivars for GCA (Table 3) in terms of traits, Chla, ChlT, Car, carbohydrates and antioxidant enzymes CAT, APX and GPX were significant at level 1% and for other traits at 5%. The SCA was significant at 1% for all evaluated traits (Table 3). Also the ratio of general combining ability to specific combining ability for all traits is not significant and Baker ratio was varied between 0.52 to 0.69 for evaluated traits (table 3) that revealed non additive effect has a greater role in controlling the traits. Given, the GCA and SCA calculated values (Table 4), the cultivars' Ghods' for Chla, Chlb, ChlT, Carand' kavir' for protein and 'Shiraz', 'Shahpasand', 'Kalheydari', 'Azar2' and 'Roushan' for proline, carbohydrates, CAT, APX & GPX and grain yield respectively, have the highest general combining ability in a positive direction. 'Mahdavi × Kalheydari', 'Azar2 × Roushan', 'Ghods × Kavir', 'Kavir × Shiraz', 'Excaliber × Azar2', 'Excaliber × Ghods' and 'Roushan × Kavir' have the highest specific combining ability in a positive direction for the content of Chla & Chlb & ChlT, Car, protein, proline, carbohydrates, CAT & GPX & grain yield and APX. In order to increase traits content can be used the above cultivars and hybrids. Then, for further genetic analysis, Hayman and Jinks method (1956,57) was used. Hayman and Jinks (1956-57) analysis of variance was showed that additive effects and non additive effects are significant, but the role of dominant effects is more important (Table 5).

Table 4: General and Specific combinig ability for evaluated traits under drought stress.

Chl a									
	1	2	3	4	5	6	7	8	9
1	1.05	-5.12	-1.51	3.86	0.87	-0.62	4.36	0.23	1.29
2		-2.7	2.31	-0.92	0.84	3.32	0.77	0.1	-0.48
3			-1.85	2.73	2.88	-0.76	-1.14	-5.06	-1.07
4				1.43	-6.84	2.78	-3.56	0.18	-0.14
5					0.11	3.66	-2.59	-1.51	-0.6
6						0.67	-4.17	2.32	0.96
7							0.93	2.59	0.21
8								1.15	-0.16
9									0.29
Chl b									
1	0.56	-2.88	-0.74	2.49	-1.01	-0.2	3.75	-1.96	0.56
2		-1.57	0.75	-0.65	-0.63	3.65	0.52	-0.85	0.1
3			-1.35	2.19	0.94	-0.1	-0.09	-0.27	-2.68
4				0.64	-3.74	0.29	-2.42	2.95	0.04
5					-0.03	2.19	-0.75	2.95	0.04
6						0.56	-2.76	-4.32	1.25
7							0.58	1.54	0.21
8								0.21	0.78
9									0.39
Chl T									
1	1.59	-8	-2.24	6.33	-0.13	-0.83	8.1	-4.02	0.8
2		-4.27	3.07	-1.57	0.21	6.98	1.29	-2.16	0.19
3			-3.2	4.91	3.83	-0.87	-1.2	0.25	-7.75
4				2.07	-10.58	3.1	-5.98	3.88	0.09
5					0.08	5.85	-3.37	5.63	-1.44
6						1.24	-6.92	-10.86	-1.44
7							1.51	5.3	2.77
8								0.09	1.97
9									0.89
Car									
1	-0.25	-0.52	-0.24	0.15	-0.09	0.01	0.25	0.06	0.38
2		-0.1	0.73	-0.2	0.37	0.23	-0.28	-0.59	0.25
3			-0.07	0.27	0.18	-0.21	-0.52	0.07	-0.29
4				0.17	-0.54	0.26	-0.2	0.31	-0.05
5					-0.09	0.22	0.02	-0.06	-0.05
6						0.1	0.05	0.58	-0.23
7							0.02	0.71	-0.02
8								0.11	0.04
9									0.11

Protein									
	1	2	3	4	5	6	7	8	9
1	36.32	-50.34	-90.5	12.47	-42.67	91.12	30.97	-19.91	68.944
2		-54.5	171.6	-75.09	14.83	19.2	-49.05	48.06	-60.23
3			21.5	-30.69	-147.41	-59.61	-165.76	217.59	104.84
4				-43.37	258.11	109.63	120.89	-122.43	-53.64
5					96.91	38	166.81	-128.27	-159.46
6						-11.98	-19.86	120.76	-61.03
7							-0.07	-180.19	96.19
8								-12.08	64.4
9									-13.33
Proline									
1	20	14	42	-56	111	83	-88	-17	-90
2		28	-72	48	-3	100	57	105	76
3			-64	50	-19	-69	28	-69	109
4				25	-125	-53	79	-17	73
5					9	-5	-30	175	-102
6						-17	74	-117	-12
7							10	99	-104
8								34	51
9									-46
Carbohydrates									
1	-36.87	-80.3	183.21	-118.53	-181.38	-96	62.25	149	81.8
2		-29.3	112.75	62.53	48/92	188.71	-129.4	-158.9	-44.2
3			45.99	-121.9	-65/6	9.88	88.59	22/89	-229.6
4				-78.53	119/31	42.83	15.67	-100.3	100.49
5					7/25	-120.17	90.1	119.36	-10.55
6						-45.51	-115	-65.12	154.9
7							34.2	36.93	-49.08
8								51.79	-37.2
9									59.96
CAT									
1	-0.19	-0.01	0.03	-0.11	-0.01	-0.2	-0.13	-0.03	0.45
2		-0.09	-0.07	-0.19	-0.14	-0.27	0.25	0.06	0.27
3			-0.06	0.26	0.25	-0.22	-0.34	0/08	-0.1
4				0.06	-0.36	1.01	-0.25	-0.16	-0.2
5					0.05	-0.28	0.42	0.19	-0.18
6						0.12	0.19	-0.18	-0.16
7							0.15	0.13	-0.13
8								-0.1	0.05
9									0.08

APX									
	1	2	3	4	5	6	7	8	9
1	-0.24	0.24	0.05	-0.04	-0.59	-0.48	0.8	-0.3	0.31
2		0.36	0.61	1.01	0.52	0.52	0.97	0.03	0.58
3			-0.38	0.03	1.48	-0.08	-0.37	-0.18	-0.28
4				0.13	-0.73	-0.34	-0.95	-0.45	1.46
5					0.05	0.5	0.21	0.8	0.73
6						0.15	0.17	0.5	0.25
7							0.12	-0.18	0.22
8								0.04	0.22
9									0.06
GPX									
1	-0.23	0.25	1.15	-0.74	-0.16	-0.93	-0.28	-0.25	0.97
2		0.31	-0.23	0.92	-0.46	-0.3	0.64	-0.63	-0.19
3			-0.19	0.22	0.18	-0.77	-0.35	-0.11	-0.1
4				0.05	-0.78	1.32	-0.51	-0.03	-0.4
5					-0.2	0.13	0.95	0.42	-0.29
6						0.26	-0.36	0.53	0.37
7							0.22	0.16	-0.26
8								-0.14	-0.1
9									-0.09

Grain Yield									
1	-21.53	109.7	-4.8	30.59	-43.62	-44.8	67.64	-75.4	-39.28
2		12.71	2.68	-134.85	82.08	31.97	-6.47	-94.6	9.51
3			74.56	-63.2	15.64	-13.6	52	31.93	20.67
4				-14	-12.69	173.24	-27.36	73.21	-38.95
5					-8.19	-18.54	17.89	-72.77	32
6						-24.78	-202	89.88	-16.14
7							23.39	36.35	61.96
8								-12.28	11.56
9									-49.86

Estimates of general combining ability effects (gi) of each parent: 1. Mahdavi 2. Azar2 3. Roushan 4. Ghods 5. Kavir 6. Excaliber 7. Kalheydari 8. shiraz 9. shahpasand and estimates of specific combining ability effects (Sij) of each cross for traits.

Table 5: Mean squares of Hayman and Jinks method for evaluated traits in drought stress.

S.O.V	Block	a	b	b_1	b_2	b_3	Error
Chla	27.21	29.72*	37.67**	74.14*	29.46*	38.75**	12.27
Chlb	1.19	12.92*	14.81**	12.84	7.95	16.92**	6.2
ChlT	36.46	60.29*	96.71**	151.57*	63.13	104.63**	31.75
Car	0.12	1.5**	1.4**	0.03	0.73*	0.32	0.27
Protein	41007	45192*	61168**	224.5	62142*	41803	26928
Proline	7382	31517*	33795*	2334	30285	22666	15690
carbohydrates	56303**	43791*	72963**	86396**	20905	57519**	30438
CAT	0.35*	0.44**	0.28**	0.18	0.16	0.33**	0.09
APX	1.98	1.41*	2.18**	0.7	0.72	1.34*	0.72
GPX	2.27**	1.49**	1.32**	1.11*	0.82*	1.52**	0.22
Grain yield	266007**	40551*	63515**	158510**	15713	20827	21596
df	2	8	36	1	8	27	88

(a) :additive variation, (b): average square of domination, (b_1) average dominance, (b_2) symmetrical distribution of the alleles determining the dominance, (b3) residual dominance

* Significant at $P \leq 0.05$, **$P \leq 0.01$

Table 6: Genetic parameters of Hayman and Jinks for evaluated traits in drought stress.

Parameter	Wr+Vr	D	H_1	H_2	F	E	UV	h^2_b	h^2_n	Sqr(H_1/D)	h^2/H_1
Chla	14.43**	0.41	19.41	16.3	2.24	2.08	0.21	0.69	0.25	6.84	0.69
Chlb	11.06**	-19.45	-40.58	-25.9	-30.83	21.42	0.16	0.61	0.12	1.44	0.22
ChlT	39.9**	-1.26	98.03	86.34	1.13	10.36	0.22	0.65	0.23	3.45	0.41
Car	0.35**	0.07	0.53	0.37	0.22	0.09	0.17	0.51	0.22	2.62	0.78
Protein	29091	11233	53233	40896	20689	9163.7	0.19	0.56	0.24	2.17	0.71
Proline	9252	2002	24959	19511	6150	5169	0.19	0.51	0.35	3.5	0.72
Carbohydrates	51062	1197.5	35686.5	33139.9	6536.1	77506	0.26	0.54	0.14	5.3	0.24
CAT	0.13	0.012	0.031	0.016	0.026	0.02	0.13	0.62	0.31	1.59	0.83
APX	0.59	0.1	0.82	0.77	-0.04	0.39	0.26	0.49	0.27	2.6	0.46
GPX	0.52	0.15	0.93	0.91	0.17	0.24	0.24	0.53	0.23	2.47	0.54
Grain yield	4050	10584	11915	11585	276.6	7225	0.23	0.74	0.32	1.88	0.58

Wr+Vr dominant effect, D additive variance, H1 - H2 dominance variance, F relative frequency of dominant and recessive alleles in the parent, E environmental variance , UV the balance of positive and negative allels,h2b-h2n broad sense and narrow sense heritability respectively, Sqr(H1/D) mean degree of dominance, h2/H1 ratio dominant to recessive allels, * Significant at P ≤ 0.05, **P≤0.01

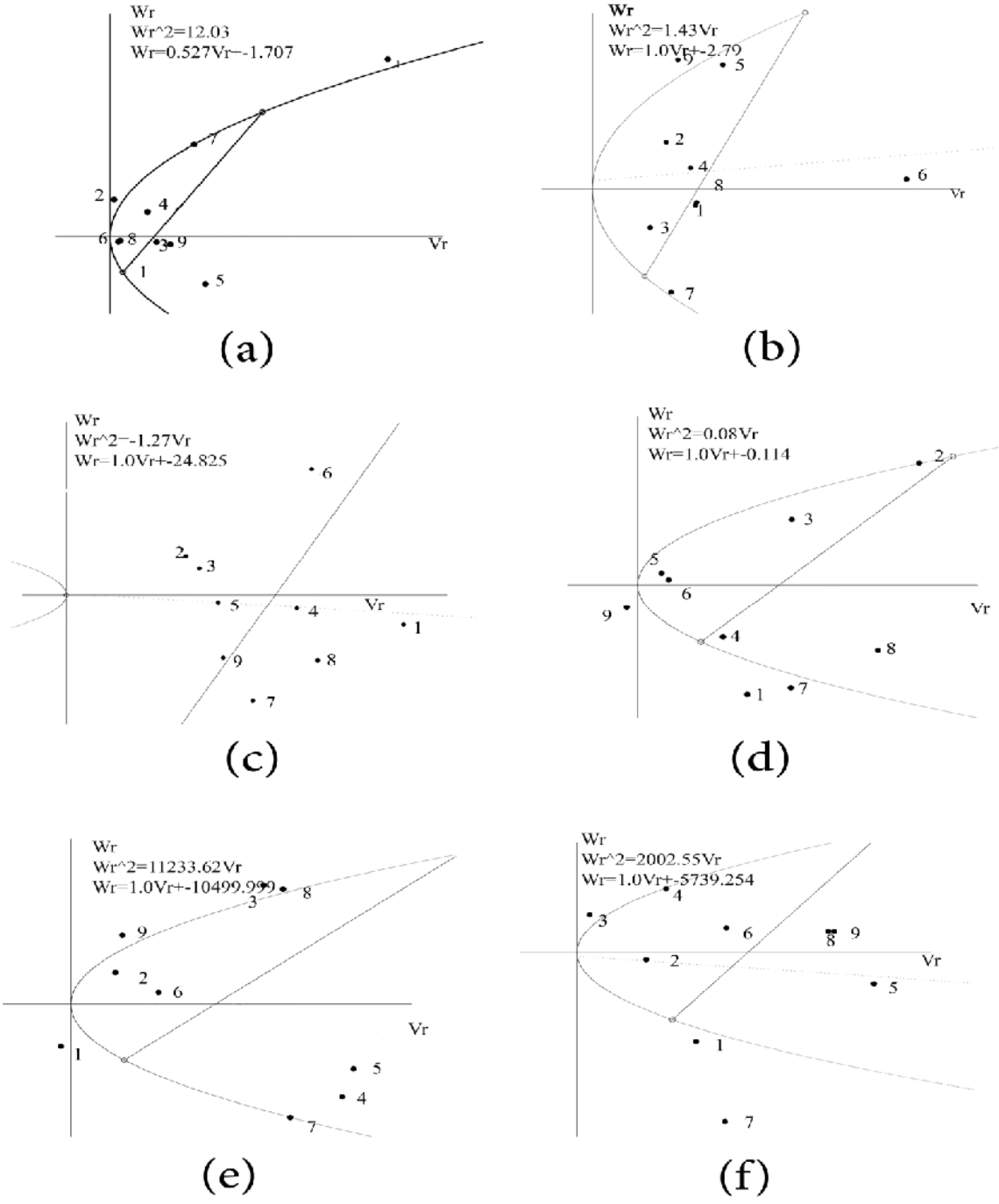
The components of b (b_1, b_2 and b_3) was shown in Table 5. In significance of b1 with the significance of the b3 components indicated the presence of the dominant effects in the genetic control of the most evaluated traits. The results of Hayman and Jinks analysis (1956,57) confirmed the results of Griffing method (1956) for all evaluated traits. According to Table 6, Wr+Vr statistic for Chla, Chlb, Chl T and Car traits were significant. Moreover, the amount of dominance components(H_1, H_2) for all traits were greater than additive effect (D), that are in harmony with the results of Griffing method (1956). UV parameter for the most traits is less than 0.25and b2 component is significant for some, therefore it can be concluded that the frequency of dominant and recessive alleles are not equal. The difference between dominance components (H_1, H_2) for all traits is positive, indicating non equality of dominant and recessive alleles in all loci controlling traits. F parameter for all traits except chlb and APX is positive, that revealed a higher frequency for dominant alleles. In addition, average degree of dominance (Sqr(H1/D)) (Table 6) for all traits is greater than one, that indicates over dominance of gene action for controlling the traits. The results of ratio dominant to recessive alleles (h2/H1) (Table 6) indicates the importance of dominant effect for all the traits except Chlb, ChlT, Car and APX. In addition, h2band h2n for evaluated traits was varied between 0.49 to 0.74 and 0.12 to 0.35respectively, that indicates the importance of nonadditive gene action in controlling the traits. In addition, Hayman's graphical analysis was conducted to assess the genetic relationship among homozygous parents for all traits (Fig. 1). The Wr/Vr regression coefficient was not significantly different from one, indicating the adequacy of the additive-dominance genetic model for Chla, Chlb, ChlT and Car but for the other traits, the Wr/Vr regression coefficient was significantly different from one, indicating non-allelic effects on controlling traits (Table 7 & Fig. 1).

Table 7: Validity of Hayman and Jinks model for evaluated traits in drought stress.

	Regration coefficient	b=0	b=1
Chla	0.55	3.95**	0.04
Chlb	0.49	2.65**	0.02
ChlT	0.57	4.28**	0.05
Car	0.4	1.5*	0.02
Protein	0.15	0.5	5.86**
Proline	0.35	0.34	3.34**
Carbohydrates	0.17	0.8	4.5**
CAT	0.08	0.05	3.4**
APX	0.03	0.01	1.8**
GPX	0.02	0.09	3.6**
Grain yield	0.18	1.25	5.7**

Adequacy test of additive dominance-model for traits * Significant at $P \leq 0.05$, ** $P \leq 0.01$

From the graphical analysis of diallel, according to Fig. 1, can be concluded that for all traits there is overdominant gene action. With regard to the distribution of data around theregression line, 'Roushan', 'shahpasand' and 'Kalheydari' cultivars have the most dominant genes in the sum of all the traits. In contrust 'Excaliber', 'Kavir' and 'Shiraz' have the most recessive genes in total of all traits and other parents are intermediate (Fig.1).



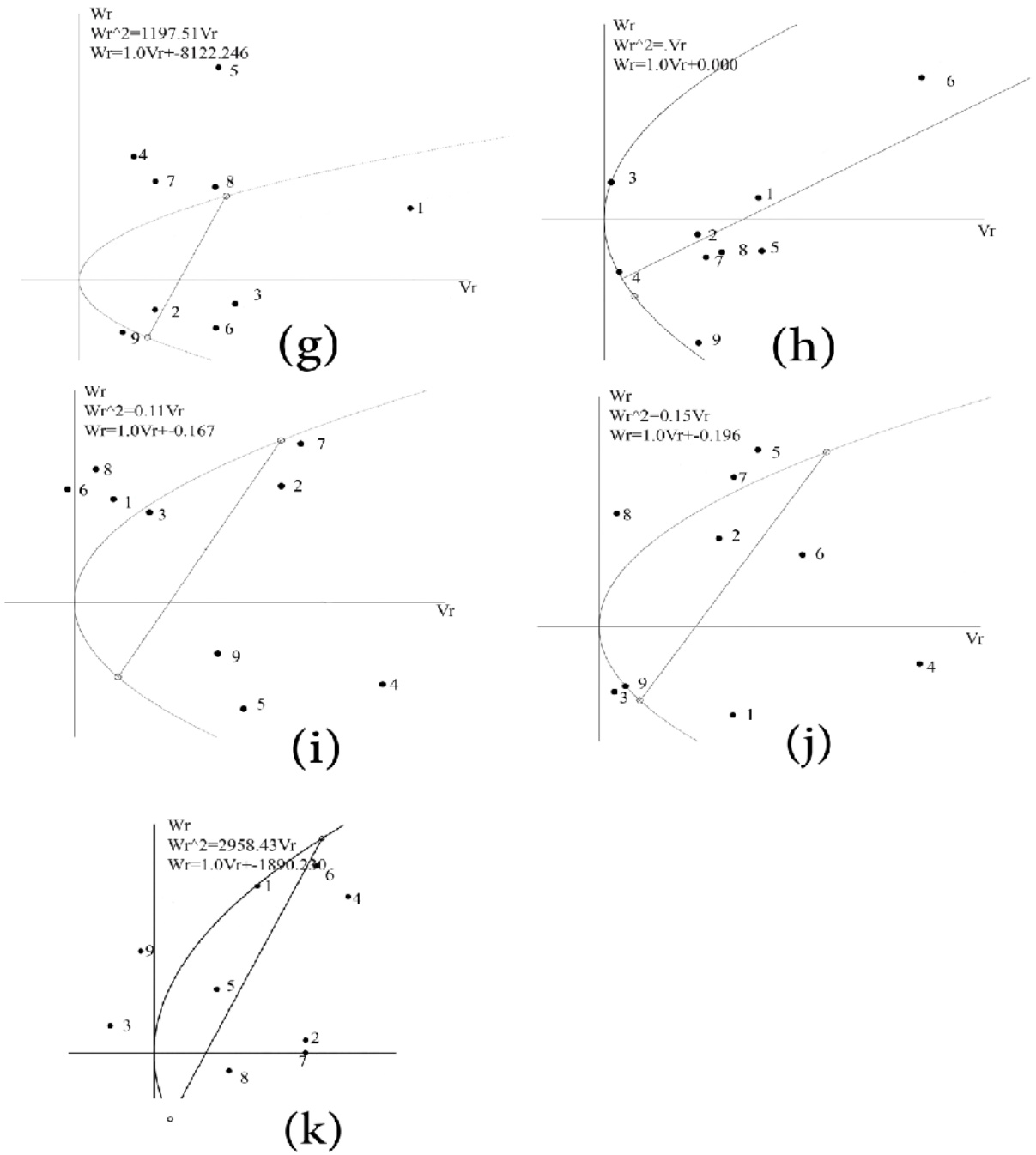


Fig. 1. Covariance between parental and F2 progeny(Wr) plotted against the variance of all F2 hybrids in each parental array (Vr) for traits measured in a 9×9 diallel mating design. Letters and numbers denote traits and parental types respectively: a: chla, b: chlb, c: chlT, d: car, e: protein, f: proline, g: carbohydrate, h: CAT, i: APX, j: GPX, k: grain yield, 1. Mahdavi 2. Azar2 3. Roshan 4. Ghods 5. Kavir 6. Excaliber 7. Kalheydari 8. shiraz 9. shahpasand

DISCUSSION

Development of wheat cultivars with consistent yield under diverse environments has been an important goal of Wheat breeding. As described earlier, the genetic differences were significant for all the traits and comparison of treatments mean according to Multiple Rang Dun-can's test was varied among cultivars, therefore there can be done diallel genetic analysis.

Similar findings for grain yield and related traits in different cultivars of wheat were re-ported by Ambreen *et al.* (2002) and Adel *et al.* (2012). GCA and SCA variances are associated with the additive and non-additive gene effects, respectively. Gained genetic improvement from selection for a trait (selection response) depends upon the type of gene action. In this research, dominance gene effects for the most evaluated traits were the more important than additive effects. Among the components of genetic variation, additive gene effects are the most important components, as these effects have the highest response to selection (Falconer & Mackay, 1996). Hence, the most evaluated traits in this research were controlled with non-additive effects, therefore it is suggested hybridization method and management of generated population after crosses for breeding program in these traits. The Baker ratio (1978) in this re-search, was to some extent moderate, that indicates for the most studied traits, selection method is not desirable and allowing selection by phenotype for superior genotypes in breeding pro-grams is not suitable. A lower GCA/SCA ratio in studied traits, indicates that phenotypic selection identifies superior genotypes less efficiently. The preponderance of dominance over additive variances for traits, indicated that variation can be exploited through heteros is breeding (Ogata *et al*, 2003). Obtained results in this research, is confirmed the results of Alhamdani *et al.* (2010), Adel *et al*. (2012), Chawdhary *et al.* (1999), Inamullah *et al*. (2006). Based on Hey-man and Jinks (1956,57) analysis, significant differences for genetic components, additive (a) and dominant (b) for all studied traits, indicated the efficient creation of genetic variability. The breeding value of a line is a function of the additive gene action. All the most traits were con-trolled with non additive effects, which was evident from the significant and higher value of H1 and H2 than the additive variance (D). The values of H1 and H_2 were unequal in all the studied traits, that indicates unequal distribution of dominant alleles. F value indicated that the-relative frequency of dominant and recessive alleles in the parents was negative for Chlb and APX, which showed the importance of recessive alleles in these characters. However, positive values of F in the rest of the traits showed the important role of dominant genes in the parents, that is correspond with Alhamdani *et al*. (2010).The additive dominance model revealed fitness of the data used for Chla, Chlb, ChlT and Car but was not fit for the other traits. Significant Wr+Vr statistic is an indication of a dominant effect, that is corresponded with Alhamdani *et al*. (2010). The partially adequate model for these characters might be due to the presence of non-allelic interaction, linkage, and non-independent distribution of the genes in the parents as suggested by Mather and Jinks (1982). However, several partial adequacies of the simple genetic model to the data set nevertheless analyzed the diallel cross data in wheat (Hussain,1991). Degree of dominance was more than one for all the traits. Hence, over-dominance type of gene action was predominated for these traits, which was confirmed from the regression line cutting the Wr axis bellow the origin. Preponderance of over dominance in these traits revealed the importance of fixed generation selection, which would be helpful in future breeding endeavors. Over dominance for these traits was also reported by Inamullah *et al.* (2006) and Adel *et al.* (2012). The relatively low broad sense heritability indicated a more environmental influence in the expression of these traits and were not transferable to the offspring progenies. The narrow sense heritability estimates were moderately low for all the traits, suggesting that they can not be readily modified by selection procedures. Additionally, these F_2 populations can't be used for pure line selection in early generations. These results are in conformity with those of Eid *et al.* (2009) and Ahmed *et al*. (2007).

CONCLUSION

Totally due to the amount of moderate - to - low broad sense heritability, relatively low Baker ratio and narrow sense heritability concluded that for the physiological traits in this research selection in advanced generations after arrival to homozigosity and genetically fixed should be done. For breeding of these traits, Bulk, Bulk seed discent and Double haploeid method suggested.

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