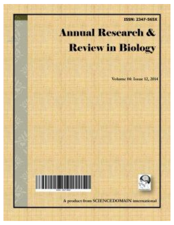

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Genetic Components for Physiological Parameters Estimates in Bread Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration between both authors. Author MP designed the study and wrote the protocol and manuscript. Author MRNR wrote and approved the final manuscript. Both authors read and approved the final manuscript.

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ABSTRACT

Aims: The specific objective of this study was to estimate the genetic components for some physiological parameters to use in breeding programs.

Place and Duration of Study: The present research was conducted in the Experiments Farm at University Putra Malaysia (UPM) during crop season 2010-2011.

Methodology: Eight bread wheat cultivars were used as parents and crosses for a half-diallel among these wheat cultivars were made in the Agriculture and Natural Resources Research Center of Sistan-Iran and genotypes were arranged as a Completely Randomised Block Design at research farms of university Putra Malysia.

Results: The combining ability analysis of variance showed that both general (GCA) and specific combining ability (SCA) variances were highly significant for all the characters except chlorophyll content for SCA, indicating the importance of both additive and non-additive gene effects. Chamran for relative water content and grain yield was the best combiner and the most narrow sense heritability belongs to stomatal conductance.

Conclusion: The eight wheat traits analyzed in this study were under dominance gene effects,

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Chamran with large, positive and significant GCA effects could be used as parent with desirable genes for genetic.

Keywords: Wheat; physiological traits; diallel analysis; gene action.

1. INTRODUCTION

Plant productivity is affected by physiological and agronomic factors and also climatic factors influence the likelihood of developing a particular species for productive purposes, while physiological and agronomic factors determine the productivity level that will be achieved [1,2]. Understanding physiological adaptation for genetic improvement of special traits in plant, has main role in plant breeding [3]. The water index is used to measure the water status of the canopy, including parameters such as stomatal conductance, leaf water potential, relative water content and canopy temperature [2]. Relative water content (RWC) indicates the hydration status of plant tissue, it is expressed in relative terms as a percentage of maximum water content at full turgor [4]. Stomatal aperture and closure regulate the amount of CO2 available at the Rubisco site and therefore limit photosynthesis as a consequence of stress conditions. Stomatal limitations to photosynthesis have been defined as the percentage decrease in light-saturated photosynthesis that is attributable to stomatal conductance [5]. Chlorophyll is an essential factor in the process of photosynthesis. Chlorophyll *a* and *b* are the two main forms of chlorophyll which contribute to the green coloured matter in plants. Chlorophyll *a* is yellowish-green whereas chlorophyll *b* is bluish-green. Chlorophyll *a* donates energy directly to the photosynthetic reaction and all other pigments transfer their absorbed energy to it. Chlorophyll *b* and the carotenoids play a key role in protecting the plant cells against the photochemical reaction induced by the illumination of chlorophyll [6]. Chlorophyll loss is associated with environmental stress and the variation in total chlorophyll / carotenoids ratio may be a good indicator of stress in plants [7]. There are several biometrical methods for evaluating the varieties or strains in terms of their combining ability, hybrid vigour and genetic makeup, diallel and line × tester techniques are in common use. The diallel cross technique as advocated by Hayman [8,9] and Jinks (1954) offers a method especially in self-fertilized crops like wheat to assess the crosses in F1 generation and provides the necessary genetic information on the plant characters. The diallel crossing technique which was developed by Griffing [10] is widely used. Griffing's [10] general and specific combining abilities are mathematically identical to Hayman's additive and dominance components, but breeding program for the development of new varieties depends on precise estimates of genetic variation components for traits of interest, consisting of additive, dominant and non-allelic interaction effects [11]. Also little information available on the genetic architecture of drought-related characters, which may provide practical information to breeders during the development of drought-tolerant wheat varieties [12]. The specific objective of this study was to estimate the genetic parameters in an 8×8 half-diallel bread wheat breeding trial to select promising genotypes to use in crossing block programes.

2. MATERIALS AND METHODS

The present research was conducted in the Experiments Farm at University Putra Malaysia (UPM) during crop season 2010-2011 (latitude 3°02'N, longitude 101°42'E, altitude 32 m), mean annual rainfall is 2140 mm and mean annual temperature 26°C. Eight bread wheat cultivars Table 1 were used as parents and crosses for a half-diallel among these wheat cultivars were made in the Agriculture and Natural Resources Research Center of Sistan-Iran. The parents were chosen based on their broad genetic background and great variations for some physiological parameters that have been evaluated in preliminary and advance experiments in drought stress condition. The 28 F_1 hybrids and their eight parents were sown in plastic pots filled with a soil mixture containing soil/sand/organic matter in a ratio of 1:1:1 and the pot were irrigated after 25% depletion of the soil water. Genotypes were arranged as a completely randomized block design in 3 replications. The chlorophyll content was measured 3 times. Measurements were made on the flag leaf on two seedlings per pot, with a chlorophyll meter, (SPAD-502, Soil Plant Analysis Development (SPAD) Section, Minolta Camera Co, Osaka, Japan). Three readings were taken along the middle section of the leaf, and the mean was used for analysis and values were expressed as SPAD units. Chlorophyll *a* and *b* were estimated by extracting the leaf material in 80% acetone. Absorbances were recorded at 645 and 665 nm for chlorophyll *a* and *b* respectively, and finally total chlorophyll (*a*+*b*) was calculated based on D Arnon [13]. Leaf relative water content (RWC) was estimated according to the method of I Ekanayake, et al. [14]. Leaf material was weighed (two leaves) to determine fresh weight (FW), and placed in distilled water at +4°C for 19 h; thereafter, turgid weight (TW) was recorded. Finally, the samples were dried in an oven at 65-70°C for 48 h and dry weights (DW) were recorded. RWC was calculated as: RWC (%) = [(FW - DW) / (TW - DW)] × 100. Plant height of the main tiller of selected plant was recorded in centimetres from the ground level up to the tip of the spike, excluding awns. Stomatal conductance was measured using an IRGA (Infra-Red Gas Analyzer, LCA-4, Analytical Development Corporation, UK) on the abaxial surface of the mid portion of the flag leaf between 10:00 am and 14:00 pm during the grain filling stage. Two plants from each pot were harvested, and left to dry in the sun. After threshing the samples, the grain yield per plant was recorded on average basis. Mean squares from the analysis of variance showing the effects of additive and dominance components were obtained according to [15]. The dominance component b1 measuring directional dominance; b2 examining the difference between selfs and crosses among parents, and b3 measuring residual dominance variation, i.e. variation not yet accounted for by b1 and b2, were calculated. All data were subjected to analysis of variance. Data obtained from the 28 hybrids of $F_1$and eight parents were subjected to analysis by Griffing's method II, model 1. Analysis of variance was performed on variables by I SAS [16]. The analysis of combining ability was performed using the DIAL98 software [17]. The genetic components were D = Additive variance, H1 = Dominance variance, H2 = Dominance variance, F= Relative frequency of dominant and recessive allels, E = Environment variance, $(H1/D)^{1/2}$ = Average degree of dominance, (kd/kd+kr) = Proportion of dominance genes, uv = the proportion of positive and negative genes.

3. RESULTS AND DISCUSSION

Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value, and in the selection of suitable parents for hybridization. The analysis of variance detected significance at 1% probability for the treatment mean squares in all evaluated traits Table 2. The combining ability analysis of varianceTable3 showed that both general (gca) and specific combining ability (sca) variances were highly significant for all the characters except chlorophyll content for sca, indicating the importance of both additive and non-additive gene effects. These results were in agreement with earlier findings [18]. The significance value for genotypes was expected because the parents were selected based on their high genetic dissimilarity for the traits. In addition, the preponderance of additive genetic variation for plant height and its components in f_1 generation indicated that the parents involved in these crosses could be selected based on their gca values. Gca variance contains additive epistasis, while sca variance contains dominance epistasis [10].

Table 1. Genotype name and pedigree

No	Pedigree/Name	Tolerance status
1	Irena/Babax//Pastor	Tolerant
2	S-78-11	Tolerant
3	Tajan	Susceptible
4	Chamran	Tolerant
5	Hamoon	Semi- tolerant
6	Moghan3	Susceptible
7	Veery/Nacozari	Tolerant
8	Hirmand	Semi- tolerant

The estimates of gca effects are presented in Table 4. The parentshamoon for height, tajan for chlorophyll (*a*), veery/nacozari for chlorophyll (*b*) and (*a*+*b*), irena/babax//pastor for chlorophyll content and stomatal conductance and chamran for rwc and grain yield exhibited significant and high gca values. Thus, for general combining ability these lines can be considered as the most photosynthetically efficient cultivars based on their performance and our results almost are in agreement with the findings of mr naroui rad, et al. [19] in f_2 population of wheat under drought stress condition. Significant sca effects were obtained for different characters and are presented in Table 5. The cross s-78-11×hirmand followed by tajan×moghan3 had highest positive sca effect for plant height. While the cross irena×tajan showed highest positive sca effect for chlorophyll *a*, *b* and *a*+*b*. In general when the total sca score of these crosses is considered, s-78-11×chamran, irena×hamoon, s-78-11×moghan3 and s-78-11×hirmand exhibited the highest sca values for chlorophyll content, stomatal conductance, rwc and grain yield respectively.

Table 2. Analysis of variance for traits (Means squares)

Source of variation	Df	Height	Chl (A)	Chl (*B*)	Chl(*A*+*B*)	Chl (content)	Stomatal conductance	Relative water content	Grain yield
Replication	2	8.12	0.06	0.07	0.17	5.43	464.7	11.41	2.78
Genotype	35	121.4**	0.94**	0.33**	2.11**	49.1**	19363.8**	68.91**	16.65**
Error	70	3.72	0.05	0.09	0.12	6.89	741.7	8.27	1.19

**and ** Significant at 5% and 1% statistical levels; Chl: Chlorophyll*

Table 3. Mean squares for general and specific combining abilities

Source of variation	Df	Height	Chl (*A*)	Chl(*B*)	Chl(*A*+*B*)	Chlorophyll content	Stomatal conductance	Relative water content	Grain yield
Replication	2	8.23	0.12	0.16	0.21	8.33	937.1	3.64	1.87
Gca	7	90**	1.06**	0.37**	2.43**	49.23**	34212.7**	35.06**	9.27**
Sca	28	146.6**	1.13**	0.32**	2.54**	39.03^{NS}	13920.7**	88.42**	5.67**
Error	70	3.75	0.06	0.09	0.13	11.77	548.6	8.79	1.47

**and ** Significant at 5% and 1% statistical levels; Chl: Chlorophyll*

Table 4. Values of general combining ability (gca) of physiological parameters in f_1 generation

Line/Cultivar	Height	Chl(*a*)	Chl(*b*)	Chl(*a*+*b*)	Clorophyll content	Stomatal conductance	Relative water content	Grain yield
Irena/Babax//Pastor	3**	-0.06	-0.15*	-0.2*	3.40*	63.2**	-0.81	0.13
S-78-11	0.89*	-0.21*	-0.17*	-0.39*	-0.46	-4.4	-1.77*	-0.82*
Tajan	-1.0*	0.29**	0.09	0.398	-1.50	35.7**	0.86	-0.54
Chamran	-0.1	-0.34**	-0.17*	-0.50**	0.42	-68.3**	2.07**	0.85*
Hamoon	3.0**	-0.15*	0.02	-0.13	0.53	-37.06**	-1.93*	0.68*
Moghan3	-2.5**	0.28**	0.09	0.36**	-1.87*	-13.8**	0.34	0.57
Veery/Nacozari	-0.3	0.25*	0.20*	0.45**	0.47	-14.6**	0.96	0.18
Hirmand	-2.8**	-.005	0.09	0.03	-0.99	39.3**	0.29	-1.04*
Se (Gi)	0.45	0.05	0.07	0.08	0.8	5.4	0.69	0.28

**and ** Significant at 5% and 1% statistical levels; Chl: Chlorophyll*

Table 5. Values of specific combining ability (SCA) in f_1 generation

Hybrids	Height	Chl(*a*)	Chl(*b*)	Chl(*a+b*)	Chlorophyll Content	Stomatal conductance	Relative water content	Grain yield
IRENA× S-78-11	3.54*	0.54**	0.13	0.678	-4.12	68.03**	-3.37	1.23
IRENA ×TAJAN	-0.85	1.01**	0.63*	1.64**	2.95	-33.86	-2.25	0.29
IRENA× CHAMRAN	2.54	0.14	-0.03	0.11	-2.03	-75.69**	7.13**	0.23
IRENA×HAMOON	6.37**	-0.40*	-0.12	-0.52	1.75	107.98**	-1.20	-1.27
IRENA×MOGHAN3	3.93*	0.40*	0.27	0.67*	3.02	-41.58	-0.14	0.17
IRENA×VEERY	-9.52**	-1.15**	-0.62**	-1.77**	-1.12	-38.41	3.58	-0.44
IRENA×HIRMAND	-6.02**	-0.54**	-0.27	-0.81*	-0.46	13.53	-3.75	-0.21
S-78-11×TAJAN	-9.74**	-0.59**	-0.39	-0.97**	-1.19	-107.19**	-3.03	-2.77*
S-78-11×CHAMRAN	3.32	-0.28*	-0.10	-0.37	7.29*	28.64	-3.58	0.51
S-78-11×HAMOON	-8.85**	0.04	-0.18	-0.15	1.84	57.31**	3.76	-2.33*
S-78-11×MOGHAN3	6.71**	-0.78**	-0.27	-1.05**	-6.29*	-18.58	9.48**	0.45
S-78-11×VEERY	-6.07**	0.54**	0.37	0.92**	0.61	18.25	-2.47	0.51
S-78-11×HIRMAND	11.10**	0.53**	0.44	0.96**	1.86	-46.47*	-0.80	2.40*
TAJAN×CHAMRAN	1.26	-1.05**	-0.43	-1.48**	-4.44	-9.25	-5.20	1.56
TAJAN×HAMOON	2.10	-0.07	0.19	0.13	0.51	24.42	0.80	1.06
TAJAN×MOGHAN3	7.32**	0.29*	-0.14	0.16	-0.68	-21.80	-3.48	1.17
TAJAN×VEERY	6.54**	-0.09	-0.10	-0.19	4.38	94.70**	4.58	-1.10
TAJAN×HIRMAND	-6.63**	0.50**	0.23	0.72*	-1.53	52.98*	8.58**	-0.21
CHAMRAN×HAMOON	-3.52*	0.34*	-0.17	0.53	-1.04	-4.75	3.59	0.01
CHAMRAN×MOGHAN3	-8.29**	0.50**	0.19	0.83*	3.50	-19.63	7.31**	-1.21
CHAMRAN×VEERY	0.93	0.45**	0.32	0.66*	-2.64	16.53	-6.30*	0.17
CHAMRAN×HIRMAND	3.76*	-0.10	0.21	-0.27	-0.65	64.14**	-2.97	-1.27
HAMOON×MOGHAN3	-1.13	-0.05	-0.17	-0.08	-4.78	-35.30	-3.35	-0.05
HAMOON×VEERY	1.76	0.57**	-0.04	0.71*	0.28	-56.13	-2.30	1.34
HAMOON×HIRMAND	3.26	-0.43*	0.14	-0.61	1.43	-93.52**	-1.30	1.23
MOGHAN3×VEERY	1.65	-0.37*	-0.18	-0.42	2.18	46.31*	-3.58	0.45
MOGHAN3×HIRMAND	-10.18**	-0.01	-0.05	-0.10	3.04	90.59**	-6.24*	-0.99
VEERY×HIRMAND	4.71**	0.05	-0.10	0.10	-3.70	-81.25**	6.48*	-0.94
SE.SIJ	1.75	0.22	0.27	0.32	3.11	21.23	2.6	1.09

**and ** Significant at 5% and 1% statistical levels; Chl: Chlorophyll*

From the above discussion it can be obviously concluded that the plant material have shown ample amount of genetic diversity which can be exploited in subsequent generations for varietal development. Table 6 presents the mean squares from the analysis of variance for additive (a) and dominance (b) effects and dominance components (b1, b2 and b3) for the eight traits evaluated. Highly significant gene effects were observed for additive (a), dominance (b) and dominance components b1, b2 and b3 for all traits studied. Dominance components (h1 and h2) were also highly significant and more than additive component for all the traits indicating dominance control Table 7. Additive gene action for specific traits will increase the selection success in a breeding programme [20]. Mr naroui rad, et al. [19] found genetic gain per cycle of selection in preliminary generations to be less for rwc and cell membrane stability to a low narrow sense heritability and dominance effect for traits studied and then Additive gene action for specific traits will increase the selection success in a breeding programme [20].

Table 6. Mean squares from analysis of variance for additive and dominance effects and dominance components for eight traits of wheat

SOV	Df	Height	Chl (*A*)	Chl(*B*)	Chl(*A+B*)	Chl (Content)	St.Con	Rwc	Grain Yield
Replication	2	8.3	0.07	0.11	0.19	10.2	1020.2	9.7	2.4
Additive effect (A)	7	103.3**	0.8**	0.28**	1.74**	58.5**	22851**	36.6**	10.5**
Dominance effect (B)	28	125.5**	0.98**	0.34**	2.21**	43.4**	20462**	74.9**	18.5**
(B1)	1	21.4*	0.31*	1.75**	0.62*	203.6**	43941**	143.8**	21.6**
(B2)	7	80**	0.67**	0.20**	1.51**	33.2*	35797**	26.6**	5.8**
(B3)	20	146**	1.13**	0.32**	2.54**	39**	13920**	88.4**	5.6**
Error	70	3.70	0.06	0.06	0.12	11.99	609.8	8.38	1.20

**and ** Significant at 5% and 1% statistical levels; Chl: Chlorophyll; RWC: Relative water content; St.Con: Stomatal conductance*

Table 7. Genetics parameters of hayman type analysis for Physiological traits in f_1

Genetic components	D	H1	H2	F	E
Height	29.9	178.5**	154.4**	39.8**	1.23**
Chl(*a*)	0.11	1.37**	1.18**	0.17*	0.019**
Chl(*b*)	0.01	0.40**	0.35**	0.02	0.02
Chl(*a+b*)	0.23**	3.10**	2.66**	0.36*	0.04**
Chl (CONTENT)	10.88	49.11**	41.24**	10.4.26	3.9**
ST.Con	7948**	32537**	21504**	15027*	196.8**
RWC	6.61	94.2**	88.08**	8.12	2.81**
Grain Yield	1.96*	17.05**	15.5**	2.05	0.43**

**and ** Significant at 5% and 1% statistical levels, Chl: Chlorophyll; RWC: Relative water content; St.Con: Stomatal conductance*

Continued Table 7.

Genetic components	$(\frac{H1}{D})^{\frac{1}{2}}$	$\frac{KD}{KD+KR}$	UV	H^2(BS)	H^2(NS)
Height	2.44	0.63	0.21	0.97	0.15
Chl(*a*)	3.42	0.60	0.21	0.95	0.17
Chl(*b*)	4.56	0.56	0.22	0.83	0.16
Chl(*a+b*)	3.65	0.60	0.21	0.95	0.17
Chl (Content)	2.14	0.64	0.21	0.76	0.21
ST.Con	2.02	0.73	0.16	0.97	0.26
RWC	3.77	0.58	0.23	0.89	0.08
Grain Yield	2.94	0.58	0.22	0.91	0.14

Chl: chlorophyll; rwc: relative water content; st.con: stomatal conductance

The proportion of positive and negative genes (uv) was unequal, showing different distributions of genes among parents and confirmed by h1 value that was greater than h2 due to which the unbalanced distribution of positive and negative genes was noticed as confirmed by uv. The uv component ranged from 0.16 for stomatal conductance to 0.23 for rwc and proline content. The dominance component (h1) was greater than d and the average degree of dominance at each loci $(h1/d)^{1/2}$ was more than unity, confirming a high level of dominance of the loci affecting these traits. The positive and non-significant value of f revealed that dominant genes were more frequent than recessive genes. Expected environmental variance (e) was significant for all traits except chlorophyll *b* indicating that they were strongly influenced by the environment. Broad-sense heritability, h^2(bs) estimates were never below 76.0% for any of the characters evaluated, but narrow-sense heritability h^2(ns) estimates ranged between 0.08% for relative water content(rwc) and 26% for stomatal conductance but broad-sense heritability for all combinations of f1 progeny is the ratio of the total genetic variance (additive and dominant) to the phenotypic varianc, narrow-sense heritability in some combinations was calculated as the ratio of the additive component of the genetic variance to the phenotypic variance and these result was confirmed by high values of gca and sca for stomatal conductance and relative water content (rwc) respectively. . The ratio (kd/kd+kr) for the traits showed an unequal presence of dominant and recessive genes; there was a slight tendency toward dominant genes, in the case of non-additive gene action for traits, it may be necessary to resort to heterosis breeding [21].

4. CONCLUSION

The eight wheat traits analyzed in this study were under dominance gene effects, Chamran with large, positive and significant GCA effects could be used as parent with desirable genes for genetic improvement of the considered grain yield and relative water content in wheat. Also, from the SCA values of the hybrids, S-78-11×Hirmand appeared to be the best specific combiners for grain yield and height respectively. Though, broad-sense heritability (h^2b) estimates more than 76% for all the traits evaluated, narrow-sense heritability (h^2n) values were less than 22%. Since narrow-sense heritability shows the proportion of a trait that is transmitted from parents to their progenies, all the eight traits investigated cannot be used for any direct breeding program. Improvement for these traits will therefore require a recurrent selection procedure to allow for favorable gene recombination in later generations before a final selection is made.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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