



Genetic Analysis of Grain Yield and Plant Height in full diallel Crosses of Bread Wheat

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ABSTRACT: A full diallel cross study comprising of five bread wheat (*Triticum aestivum* L.) cultivars was carried out with parents and F2 progeny to determine combining ability, gene action, and correlations for grain yield, plant height and their components under irrigated and water deficient stress. Estimates of the genetic components of variation as well as ratio of GCA/SCA showed that all the characters were predominantly controlled by additive gene action. The results revealed insensitivity of both kinds of gene effects to the environmental variations. Partitioning the GCA and SCA effect to male and female showed that maternal effect case over estimate in value of general and specific combining ability. The estimates of general combining ability pointed out that the best general combiners for the plant height and its components were dwarf mutant (As-48) which appeared to appreciate parent for reduce plant height and also increase spike length in wheat breeding program. Our results revealed that selection for plant height and its components would be effective in early generation. The dwarf mutant (AS-48) might be helpful for wheat breeders to develop new varieties with semi-dwarf and lodging resistance.

Key words: Combining ability, Mutant line, Plant height, Terminal water deficient, Wheat

INTRODUCTION

Drought is one of the major environmental challenges in crop productions to worldwide today, and recent global climate change has made this situation more serious. Thus, improvement of wheat production for drought tolerance is a major objective in plant breeding programs (Farshadfar *et al.* 2012). Plant height at maturity is considered as a factor in plant response to drought stress. Drought resistance and dwarfism are important traits for wheat breeding. Dwarfism genes have been introduced in the last 50 years and is now commonly used in breeding programs around the world (Edwards *et al.* 1976).

Maluszynski and Szarejko (2003) reported at least 13 mutations for semidwarfness, that induced by chemical or physical mutagens in wheat. However, only two of them have high breeding value and brought significant economic impact. Both these dwarfing genes reduce significantly stem internode length while having no direct effects on spike morphology. Wheat breeding programs mostly involve hybridization, evaluation and selection of desirable genotypes. In addition, the assessment of combining ability and determine gene action are elementary tools for selection of ideal genotypes. According to Baker (1978), the combining

ability is a better biometrical tool to circumvent the plant breeding program. Diallel mating Design has been extensively used to analyze the combining ability effects of wheat genotypes and also to provide information regarding genetic mechanism controlling grain yield and other traits (Khan *et al.* 2007). The diallel analysis also provides a unique opportunity to test a number of lines in all possible combinations. The knowledge of genetic structure and mode of inheritance of different characters helps breeder to select suitable breeding methodology for the development of drought tolerance genotypes (Farshadfar *et al.* 2012). Significant estimates of general and specific combining ability variances for yield and yield related traits have been reported in the literature. The effects of general combining ability (GCA) were highly significant for number of grains per spike, 1000 kernel weight and grain yield while specific combining ability (SCA) effects were highly significant for all the studied traits (Ahmadi *et al.* 2003). Saeed *et al.* (2010) by diallel cross of six wheat genotypes in irrigated and water stress conditions indicated that mean squares due to general combining ability, specific combining ability and reciprocals were highly significant for all of the studied characters except spike density and 1000-grain yield under both of the environmental conditions.

Both additive (fixable) and non-additive (non-fixable) components of genetic variance were involved in governing the inheritance of almost all the quantitative and quality traits (Joshi *et al.* 2002; Joshi *et al.* 2004; Khan *et al.* 2007). Khan *et al.* (2007) reported the additive gene effects for plant height, plant biomass, Number of grain/spike and grain yield /plant. According to their reports number of tiller/ plant and 1000 grain weight controlled by non-additive gene effects.

Farshadfar *et al.* (2013) demonstrated highly significant GCA and SCA for plant height and peduncle length. Several researchers demonstrated that additive effects of gene play an important role in controlling traits for plant height (Fick and O. 1973; Edwards *et al.* 1976; Gorjanoviã and Kraljeviã-Balaliã 2007; Khan *et al.* 2007; Saeed *et al.* 2010; Yao *et al.* 2011). In most of the diallel studies of wheat, plant height, spike length and peduncle length seemed to be controlled by the partial dominance with additive gene effects.

Masood and Kornstad (2000) by using several generation for combing ability analysis in wheat demonstrated that overall the estimates of GCA effects in F1 to F5 generation were quite consistent for all traits

evaluated, so that crosses could be studied for combining ability in F2 or F3 instead of F1 generation when seed is limited. Bhullar *et al.* (1979) and Mihalgiv (1980) reported similar finding. Gill *et al.* (1984) reported that the result over various generation were not comply with simple additive- dominance model. According their results F2 generation were in better agreement with those from F3, F4 and F5 when compared to result from F1.

The objectives of the present investigation were to study (i) specific and general combining abilities, as well as (ii) the genetic properties of plant height in wheat under normal and terminal water deficient stress conditions.

MATERIALS AND METHODS

Five wheat cultivars (Brown Bolani, White Bolani, Kealk, Tajan and AS-48) were selected (Table 1) to prepare F1 hybrid based on full diallel mating design. Ten F1 seed from each 20 crosses were planted and self-pollinated under greenhouse condition in 2012 to produce F2 seeds.

Table 1: Origin and pedigree of wheat cultivars used as parental genotypes for prepared diallel crosses.

Cultivars	Origin	Plant height	Pedigree
Brown Bolani	South east of Iran	106.1	Land race of Sistan province
White Bolani	South east of Iran	103.03	Land race of Sistan province
Kealk	South east of Iran	91.6	Land race of Sistan province
Tajan	CYMMIT	80.4	Bow’S’/Nkt’S’
AS-48	Azadi Cv.	50.8	Mutant induced by Gamma ray

The experiment was carried out 2013-2014 at research farm of nuclear agricultural research school (35o 49’N, 50o44’E, altitude 1251 m above sea level). The experiment was performed based on randomized complete block design with three replication in two environment (normal and terminal water deficient).The seeds of F2 progenies and their parents were sown in 4 row 1.5m length and 30 cm apart in early November of 2013. Irrigated plots were watered normal at flowering and grain filling periods. The second environment plots received no water other than rainfall when 60% of plots went to flowering stage.

Five plants in parental rows and 10 once from each F2 plots randomly taken for traits measurements. Data from Plant height(PH), inter nod 2 Length (NL2) and inter nod 3 Length (NL3), Peduncle length (PL), spike length(SL), Grain yield per plant (GY), Total biomass (TB), harvest index (HI), Number of spikelet/spike (NSP), number of grain/spike (GN) and thousand grain weight (1000GW) were recorded.

Diallel analysis were conducted according to Griffing method two model one (Griffing 1956) using the SAS program (Zhang *et al.* 2005). Analysis of variance was performed using general liner model (GLM) procedure in SAS (ver.9.3). To estimate general and specific combing ability effects for each parent when it is used as a female or a male in its hybrid combination the GCA and SCA effects partitioned according to Mahgoub (2011) as follows:

$$g_{fi} = \frac{1}{2}(X_{io}) - \frac{1}{P^2}(X_{oo}) \quad \text{and} \quad g_{mi} = \frac{1}{2}(X_{oi}) - \frac{1}{P^2}(X_{oo})$$

Where g_{fi} is the deviation of general combining ability of i^{th} parent when it is used as a female and g_{mi} is the deviation of i^{th} parent when it is used as a male.

Specific combing ability is partitioned to estimate SCA effects for cross s_{ij} and for its reciprocal s_{ji} as follows:

$$s_{ij} = X_{ij} - \frac{1}{2P} (X_{i0} + X_{oi} + X_{jo} + X_{oj}) + \frac{1}{P^2} X_{oo}$$

$$s_{ji} = X_{ji} - \frac{1}{2P} (X_{i0} + X_{oi} + X_{jo} + X_{oj}) + \frac{1}{P^2} X_{oo}$$

Where s_{ij} and s_{ji} the deviation of specific combining ability.

Additive and dominant genetic variance estimated by following equation:

$$V_{gca} = \frac{(1+F)}{4} V_a \quad V_{sca} = \frac{(1+F)^2}{2} V_d$$

Where F is Inbreeding Coefficient, which in F2 generation is equal to 0.5. Average degree of dominance estimated by equation: $\frac{2 \times \sigma^2 D / \sigma^2 A}{(\sigma^2 A)}$: additive variance and $\sigma^2 D$ (dominant variance)

The data were tested for normal distribution of frequency using Kolmogorov-Smirnov test in SPSS software (ver.22).

RESULTS AND DISCUSSION

The combined analysis of variance reveal that highly significant difference ($p < 0.01$) among genotypes in all studied traits (Table 2). Environments (Normal and water deficient stress) showed highly significant difference for all traits except Number of grain per spike (GN). Genotype \times environment interaction was not significant for all of the measured traits except for GN that showed significant difference at $p < 0.05$. In other word the genotypes shown same reaction under both environment. Phenotypic expression of quantitative traits is highly influenced by environmental fluctuations. Genotype \times environment interaction, depending upon their nature and magnitude, leads to bias in the estimates of gene effects. It is, therefore, necessary to assess the sensitivity of estimates of gene effects under variable environmental conditions so as to ensure better prediction and gain under selection.

The pooled analysis of variance for combining ability reveal that general combining ability (GCA) were highly significant ($p < 0.01$) for all traits (Table 2). Thus, additive gene effect figured important in controlling inheritance of all the studied characters. Specific combining ability (SCA) were highly significant ($p < 0.01$) for PH, PL, GY and significant ($p < 0.05$) for NL2, NL3, GN and 1000GW. Most of the traits controlled by dominant gene effect, although, SL, HI, TB, NSP, just under control additive gene effects. Reciprocal effect was significant just for GY.

The GCA/SCA ratio in all studied traits indicated that GCA effects were predominant and played a more important role than the SCA effects in exercising genetic control. These result in agreement with earlier finding. However, in contrast with Hasnain *et al.* (2006) and Bogale *et al.* (2011) about higher importance of non-additive gene actions for the genetic control of PH, and PL.

Non-significant difference were recorded for interaction GCA \times environments, SCA \times environments as well as REC \times environment in all the traits except GCA \times environments for NL3 at ($p < 0.01$) and GN ($p < 0.05$). It

seems that gene function of studied characters was same in normal and water deficient. Thereby indicating the insensitivity of both kinds of gene effects (additive and non-additive) to the environmental variations. However, relatively higher magnitude of GCA \times environments interactions as compared to SCA \times environments interactions suggested a higher sensitivity of GCA to environments than that of SCA.

In self-pollinated crops such as wheat, heterozygosity is expected to decline by a half with advancing generation of selfing (Masood and Kornstad 2000). When a particular trait responds to additive type of gene action, in the absence of selection, the mean of segregating population is expected to approach the mean of parents. Ultimately the variance due to SCA in subsequent selfed generation should be non-significant. The presence of significant SCA estimates in F2 after generation of selfing could indicate the relative importance of epistasis. Genes, which contribute to additive \times additive epistasis, can be fixed. Thus, they influence the variance among lines in the later generation. Masood and Kornstad (2000) revealed that the significant SCA in the later generation due to these interactions. Therefore, probably non-additive gene effect such as additive \times additive epistasis has an effect in controlling PH, PL and GY. According to non-significant SCA, for SL, HI and NSP, additive gene effect has more important role in genetic control of these traits. Although PH, NL2, NL3, PL, GN and 1000GW showed significant SCA, but according to high value of GCA/SCA ratio and also high narrow heritability (Table 3), we could concluded that additive gene effect has more important role on controlling most of the studied traits in this research. In this way, selection for these traits in early generation would be effective in developing the semi-dwarf cultivars in wheat breeding program and pedigree method of selection can be used for the improvement of these characters.

Therefore plant height, and its related compound could be selected in early generation. The present findings coincident with pervious finding (Joshi *et al.* 2002; Joshi *et al.* 2004; Yao *et al.* 2011; Farshadfar *et al.* 2013) of which also showed that additive genetic variance as the main component of genetic variance of various economic traits in bread wheat. According to estimates of the average degree of dominance, GY, HI, TB, PL and NSP under over-dominance control, SL and 1000GW under dominance control and NL2, NL3, PH control by partials dominance.

The highest positive general combining ability (Table 4) for PH (6.73), NL2 (1.53) and NL3 (2.18) exhibited by genotype Brown Bolani and the highest GCA Value for Pl exhibited by Kelak.

Table 2: Combined analysis of variance for effect of genotype and environment (normal and water deficient stress) and their Interaction.

		Mean Square										
	DF	PH	NL2	NL3	PL	SL	GY	TB	HI	NSp	GN	1000 GW
Env	1	3543.37**	172.58**	281.29**	84.01*	34.86**	4257.43**	38051.39**	104.058*	57.150**	24.056 ^{ns}	595.15**
Rep./Env.	4	199.36	17.5	26.77	39.4	1.16	55.6	489.8	91.103	3.61	60.14	1.94
Gen.	24	821.18**	36.45**	81.86**	92.9**	2.78**	168.364**	801.8*	54.59*	15.57*	318.64**	66.78**
GCA	4	3740.32**	173.9**	432.39**	365.3**	11.39**	330.277**	1993.81**	130.48**	41.49**	1538.4**	273.74**
SCA	10	352.82**	11.59*	16.78*	59.69**	1.59 ^{ns}	153.788**	488.3 ^{ns}	40.41 ^{ns}	7.98 ^{ns}	98.41*	31.83*
REC	10	123.34 ^{ns}	6.32 ^{ns}	6.75 ^{ns}	17.15 ^{ns}	0.51 ^{ns}	118.175*	638.6 ^{ns}	38.41 ^{ns}	12.79 ^{ns}	50.96 ^{ns}	18.95 ^{ns}
MAT	4	147.6 ^{ns}	6.88 ^{ns}	6.77 ^{ns}	33.8 ^{ns}	0.84 ^{ns}	58.387 ^{ns}	529.9 ^{ns}	5.067 ^{ns}	10.65 ^{ns}	51.18 ^{ns}	21.36 ^{ns}
NMAT	6	107.17 ^{ns}	5.59 ^{ns}	6.74 ^{ns}	6.44 ^{ns}	0.288 ^{ns}	158.034**	710.99 ^{ns}	60.63*	14.22 ^{ns}	50.81 ^{ns}	17.34 ^{ns}
Gen.× Env	24	104.17 ^{ns}	5.6 ^{ns}	10.91 ^{ns}	12.66 ^{ns}	0.288 ^{ns}	80.01 ^{ns}	614.88 ^{ns}	27.73 ^{ns}	74.05 ^{ns}	67.58*	13.87 ^{ns}
GCA×Env	4	304.32 ^{ns}	12.18 ^{ns}	28.19**	31.64 ^{ns}	0.07 ^{ns}	98.684 ^{ns}	547.04 ^{ns}	3.55 ^{ns}	0.773 ^{ns}	17.54 ^{ns}	18.12 ^{ns}
SCA×Env	10	58.87 ^{ns}	4.69 ^{ns}	8.56 ^{ns}	64.46 ^{ns}	0.3 ^{ns}	70.416 ^{ns}	635.37 ^{ns}	32.99 ^{ns}	0.77 ^{ns}	67.31 ^{ns}	4.42 ^{ns}
REC×Env	10	69.43 ^{ns}	3.89 ^{ns}	6.36 ^{ns}	11.39 ^{ns}	0.36 ^{ns}	82.141 ^{ns}	621.54 ^{ns}	32.137 ^{ns}	10.73 ^{ns}	87.88*	21.64 ^{ns}
Error	96	102.35	5.33	7.15	13.66	0.42	51.6073	452.63	21.04	8.2	41.75	13.24
GCA/SCA	-	10.60	15.004	25.76	6.12	7.16	2.148	4.08	3.23	5.2	15.63	8.6
CV	-	11.39	18.68	12.54	11.09	5.47	22.62	24.11	12.3	13.66	10.38	7.95

PH: Plant Height; NL2: Inter Nod 2 Length; NL3: Inter Nod 3 Length; PL: Peduncle length; SL: Spike length; GY: grain yield per plant; TB: Total Biomass; HI: harvest index; NSP : No. of spikelet per spike; GN: No. of grain per spike; 1000GW : 1000 Grain weight; Env: Environment effect, Gen: Genotype, GCA: General Combining Ability, SCA :Specific Combining Ability, REC: Recurrent Crosses, MAT: Maternal effect, NMAT:Non Maternal** and * respectively significant at 1% and 5% probability level; ns : non-significant

Table 3: Heritability and average degree of dominance of studied traits.

Traits	h^2_n	h^2_b	\bar{d}
GY	0.23	0.62	2.43
TB	0.44	0.66	1.33
HI	0.37	0.66	1.70
NSP	0.52	0.70	1.11
GN	0.79	0.89	0.68
1000GW	0.66	0.83	0.95
PH	0.71	0.86	0.86
NL2	0.78	0.89	0.69
NL3	0.86	0.93	0.52
PL	0.57	0.79	1.19
SL	0.61	0.81	1.08

h^2_n : narrow heritability, h^2_b : broad heritability
 \bar{d} : Average Degree of dominance

Table 4: Estimate of general combining ability effects for studied genotypes.

Genotype		Brown Bolani	White Bolani	Tajan	Kealk	AS-48
Traits						
Y	g _i	0.06 ^{ns}	-0.51 [*]	0.78 ^{**}	3.08 ^{**}	-3.42 ^{**}
	gf _i	0.88 ^{**}	0.74 ^{**}	0.30 ^{ns}	2.61 ^{**}	-4.53 ^{**}
	gm _i	-0.75 ^{**}	-1.75 ^{**}	1.27 ^{**}	3.54 ^{**}	-2.30 ^{**}
	BV	0.127	-1.015	1.567	6.153	-6.833
TB	g _i	2.81 ^{ns}	3.33 ^{ns}	-3.3 ^{ns}	5.60 [*]	-8.49 ^{**}
	gf _i	4.34 [*]	7.80 ^{**}	-4.67 [*]	2.83 ^{ns}	-10.30 ^{**}
	gm _i	1.29 ^{ns}	-1.15 ^{ns}	-1.8 ^{ns}	8.37 ^{**}	-6.67 ^{**}
	BV	5.63	6.65	-6.51	11.20	-16.97
HI	g _i	-1.75 ^{**}	-1.92 ^{**}	2.78 ^{**}	1.32 [*]	-0.42 ^{ns}
	gf _i	-3.30 ^{**}	-0.25 ^{ns}	2.79 ^{**}	1.53 ^{**}	-0.78 ^{ns}
	gm _i	-0.20 ^{ns}	-3.60 ^{**}	2.76 ^{**}	1.10 [*]	-0.06 ^{ns}
	BV	-3.50	-3.84	5.55	2.63	-0.84
NSP	g _i	-0.71 [*]	-0.63 ^{ns}	0.12 ^{ns}	-0.13 ^{ns}	1.35 ^{**}
	gf _i	-0.96 ^{**}	-0.57 ^{ns}	0.49 ^{ns}	-0.71 [*]	1.76 ^{**}
	gm _i	-0.45 ^{ns}	-0.70 [*]	-0.25 ^{ns}	0.46 ^{ns}	0.95 ^{**}
	BV	-1.41	-1.27	0.23	-0.26	2.71
GN	g _i	-4.37 ^{**}	-3.92 ^{**}	1.84 [*]	-1.46 [*]	7.91 ^{**}
	gf _i	-4.25 ^{**}	-2.53 ^{**}	1.02 ^{ns}	-1.28 ^{ns}	7.04 ^{**}
	gm _i	-4.49 ^{**}	-5.31 ^{**}	2.65 ^{**}	-1.63 [*]	8.78 ^{**}
	BV	-8.74	-7.83	3.67	-2.92	15.82
1000 GW	g _i	0.79 ^{ns}	2.04 ^{**}	-2.27 ^{**}	1.74 ^{**}	-2.30 ^{**}
	gf _i	0.41 ^{ns}	2.87 ^{**}	-1.84 ^{**}	1.38 ^{**}	-2.82 ^{**}
	gm _i	1.17 [*]	1.21 ^{**}	-2.70 ^{**}	2.10 ^{**}	-1.78 ^{**}
	BV	1.59	4.07	-4.54	3.48	-4.60
PH	g _i	6.73 ^{**}	6.34 ^{**}	-4.53 ^{**}	3.04 ^{**}	-11.58 ^{**}
	gf _i	9.19 ^{**}	6.64 ^{**}	-4.59 ^{**}	1.52 ^{ns}	-12.75 ^{**}
	gm _i	4.27 ^{**}	6.04 ^{**}	-4.47 ^{**}	4.57 ^{**}	-10.41 ^{**}
	BV	13.46	12.68	-9.06	6.08	-23.17
NL2	g _i	1.53 ^{**}	1.31 ^{**}	-0.88 ^{**}	0.57 [*]	-2.54 ^{**}
	gf _i	2.07 ^{**}	1.36 ^{**}	-0.95 ^{**}	0.20 ^{ns}	-2.68 ^{**}
	gm _i	0.99 ^{**}	1.27 ^{**}	-0.82 ^{**}	0.95 ^{**}	-2.39 ^{**}
	BV	3.06	2.62	-1.76	1.15	-5.07
NL3	g _i	2.18 ^{**}	1.59 ^{**}	-0.69 [*]	1.33 ^{**}	-4.40 ^{**}
	gf _i	2.64 ^{**}	1.65 ^{**}	-0.63 [*]	0.87 ^{**}	-4.53 ^{**}
	gm _i	1.71 ^{**}	1.52 ^{**}	-0.75 ^{**}	1.79 ^{**}	-4.26 ^{**}
	BV	4.35	3.17	-1.38	2.66	-8.80
PL	g _i	1.79 ^{**}	0.27 ^{ns}	-1.33 ^{**}	2.72 ^{**}	-3.45 ^{**}
	gf _i	2.93 ^{**}	-0.06 ^{ns}	-1.11 ^{**}	1.88 ^{**}	-3.63 ^{**}
	gm _i	0.64 ^{ns}	0.61 ^{ns}	-1.54 ^{**}	3.56 ^{**}	-3.27 ^{**}
	BV	3.57	0.55	-2.66	5.44	-6.90
SL	g _i	-0.20 ^{**}	-0.21 ^{**}	0.00 ^{ns}	-0.35 ^{**}	0.75 ^{**}
	gf _i	-0.05 ^{ns}	-0.28 ^{**}	0.04 ^{ns}	-0.5 ^{**}	0.81 ^{**}
	gm _i	-0.34 ^{**}	-0.13 ^{ns}	-0.04 ^{ns}	-0.19 ^{**}	0.69 ^{**}
	BV	-0.39	-0.41	0.00	-0.69	1.50

g_i :GCA ; gf_i :GCA female; gm_i : GCA male; BV : Breeding Value,** and * respectively significant at 1% and 5% probability levels; ns : non-significant

The least negative GCA effect for PH (-11.58), NL2 (-2.54), NL3 (-4.4) and PL (-3.45) exhibited by dwarf mutant (AS-48). Dwarf mutant showed the highest positive GCA for Number of grain per spike (7.91) and spike length (0.75). Bolani Brown and Kelak respectively for GN (-4.37) and SL (-0.35) exhibited the least negative value of this traits. Dwarf mutant (AS-48) showed the least negative GCA for GY (-3.42) and 1000GW (-2.3). While the Kealk showed the highest GCA for yield and its related compound. Therefore, dwarf mutant can be effective for reducing plant height and also effective for improvement and increasing Number of grain per spike and spike length.

Partitioning of GCA effects into the maternal and paternal combining abilities showed that the dwarf mutant can be use in both form of parent for reducing plant height and also increasing the number of grains per spike and spike length in case of dwarf mutant maternal GCA in all traits except GN were more than paternal GCA, Mahgoub (2011) showed that estimated GCA effects according to Griffing's method is equal to the average of GCA effects of each parent, after partitioning, when it is used as a male and a female in its hybrid combinations. In addition, the average of the difference between female and male GCA effects would provide precise estimation of the maternal effect. This would prove that the maternal effect provides precise estimation to the favorable alleles, which is mainly additive. According above mentioned reason, if

dwarf mutant used as female in crosses, additive gene effect could be use more than when it used as male in crosses. Mahgoub (2011) showed that estimated GCA effects according to Griffing's method is equal to the average of GCA effects of each parent, after partitioning, when it is used as a male and a female in its hybrid combinations. In addition, the average of the difference between female and male GCA effects would provide precise estimation of the maternal effect. The estimates of specific combining ability (SCA) showed the highest positive and significant SCA for PH (6.66), PL(3.27) and high SCA for GY(3.26) and HI(2.98) were exhibited in cross Brown Bolani × AS-48 (Table 5). However, SCA didn't significant or showed low value, when AS-48 participate as female in above mentioned crosses. Other satisfy combinations, which showed significant SCA effects for GY(4.86, 4.67) were respectively cross AS-48× white Bolani and White Bolani×AS-48. It means that these genotype revealed high SCA in both form of combinations. Whereas combinations of Tajan×AS-48 and its revers crosses, showed the least negative SCA for GY respectively (-5.65,-3.37).

The result showed that dwarf mutant (AS-48) overall have good general and specific combining ability. Therefore it is appropriate for reducing height breeding program of bread wheat. Partitioning of general and specific combining ability effects would provide additional information about each parent.

Table 5: Estimates of specific combining ability and reciprocal effects for different characters in 5 × 5 diallel cross of bread wheat.

Traits	GY	TB	HI	NSP	GN	PH	NL2	NL3	PL	SL	1000GW
Genotype	SCA										
1×2	1.87**	8.93 ^{ns}	-4.90**	-0.35 ^{ns}	0.37 ^{ns}	-1.68 ^{ns}	-0.40 ^{ns}	-0.44 ^{ns}	-0.90 ^{ns}	-0.10 ^{ns}	0.65 ^{ns}
1×3	-1.94**	-4.04 ^{ns}	0.56 ^{ns}	-0.43 ^{ns}	-1.42 ^{ns}	1.91 ^{ns}	1.02 ^{ns}	1.87*	1.21 ^{ns}	-0.01 ^{ns}	0.32 ^{ns}
1×4	-1.00 ^{ns}	-6.13 ^{ns}	1.20 ^{ns}	-0.33 ^{ns}	2.06 ^{ns}	-2.67 ^{ns}	-0.68 ^{ns}	-1.52*	1.40 ^{ns}	0.15 ^{ns}	1.06 ^{ns}
1×5	4.86**	4.68 ^{ns}	3.08**	1.94*	2.50 ^{ns}	5.40 ^{ns}	0.84 ^{ns}	1.05 ^{ns}	1.64 ^{ns}	0.38 ^{ns}	0.01 ^{ns}
2×3	0.59 ^{ns}	-0.02 ^{ns}	0.73 ^{ns}	0.25 ^{ns}	0.84 ^{ns}	3.84 ^{ns}	0.78 ^{ns}	1.75*	0.60 ^{ns}	-0.16 ^{ns}	0.85 ^{ns}
2×4	-2.45**	-7.46 ^{ns}	0.44 ^{ns}	0.08 ^{ns}	-1.78 ^{ns}	-0.91 ^{ns}	-0.02 ^{ns}	-0.61 ^{ns}	-1.06 ^{ns}	-0.11 ^{ns}	-2.15 ^{ns}
2×5	3.26**	0.89 ^{ns}	2.98*	-0.38 ^{ns}	0.32 ^{ns}	6.66*	1.20 ^{ns}	1.95*	3.27**	0.26 ^{ns}	1.15 ^{ns}
3×4	0.96 ^{ns}	3.12 ^{ns}	-1.40 ^{ns}	0.98 ^{ns}	2.05 ^{ns}	3.05 ^{ns}	0.88 ^{ns}	0.81 ^{ns}	0.69 ^{ns}	0.02 ^{ns}	-1.87 ^{ns}
3×5	-5.65**	-6.61 ^{ns}	-3.31**	-0.52 ^{ns}	-3.64 ^{ns}	-3.27 ^{ns}	-0.71 ^{ns}	-1.08 ^{ns}	-1.38 ^{ns}	0.03 ^{ns}	1.76 ^{ns}
4×5	2.18**	8.60 ^{ns}	0.30 ^{ns}	-0.17 ^{ns}	3.90 ^{ns}	4.64 ^{ns}	1.07 ^{ns}	1.13 ^{ns}	1.69 ^{ns}	0.44*	-0.26 ^{ns}
	RECs										
2×1	1.59*	1.32 ^{ns}	-7.15**	-0.01 ^{ns}	-1.54 ^{ns}	3.14 ^{ns}	0.73 ^{ns}	1.17 ^{ns}	2.01 ^{ns}	0.12 ^{ns}	-0.74 ^{ns}
3×1	-0.12 ^{ns}	1.10 ^{ns}	-0.60 ^{ns}	0.59 ^{ns}	-0.07 ^{ns}	5.72 ^{ns}	1.25 ^{ns}	2.40**	0.91 ^{ns}	0.17 ^{ns}	0.56 ^{ns}
4×1	-2.07**	-2.99 ^{ns}	-1.34 ^{ns}	0.31 ^{ns}	0.02 ^{ns}	-0.80 ^{ns}	-0.23 ^{ns}	-0.29 ^{ns}	1.31 ^{ns}	0.33 ^{ns}	-0.99 ^{ns}
5×1	4.67**	8.19 ^{ns}	1.34 ^{ns}	-2.16*	2.20 ^{ns}	4.23 ^{ns}	0.58 ^{ns}	0.62 ^{ns}	1.50 ^{ns}	0.11 ^{ns}	-0.73 ^{ns}
3×2	-0.44 ^{ns}	-2.58 ^{ns}	0.83 ^{ns}	-0.55 ^{ns}	-0.31 ^{ns}	-0.23 ^{ns}	-0.11 ^{ns}	-0.72 ^{ns}	-0.41 ^{ns}	-0.29 ^{ns}	0.08 ^{ns}
4×2	6.92**	18.51**	1.04 ^{ns}	0.81 ^{ns}	3.96 ^{ns}	2.55 ^{ns}	1.01 ^{ns}	0.54 ^{ns}	1.37 ^{ns}	0.29 ^{ns}	2.28 ^{ns}
5×2	1.33*	7.78 ^{ns}	-0.64 ^{ns}	0.05 ^{ns}	1.77 ^{ns}	2.31 ^{ns}	0.15 ^{ns}	0.75 ^{ns}	-0.64 ^{ns}	-0.29 ^{ns}	1.05 ^{ns}
4×3	0.40 ^{ns}	-2.48 ^{ns}	2.73 ^{ns}	2.11*	-2.33 ^{ns}	5.44 ^{ns}	1.46*	2.57**	1.72 ^{ns}	0.10 ^{ns}	0.17 ^{ns}
5×3	-3.37**	-6.07 ^{ns}	-2.42 ^{ns}	-0.22 ^{ns}	-2.14 ^{ns}	-0.24 ^{ns}	0.00 ^{ns}	-0.60 ^{ns}	-0.15 ^{ns}	-0.04 ^{ns}	2.64 ^{ns}
5×4	2.93**	-0.80 ^{ns}	3.52**	0.30 ^{ns}	2.52 ^{ns}	-0.44 ^{ns}	-0.06 ^{ns}	-0.62 ^{ns}	0.19 ^{ns}	-0.08 ^{ns}	-0.36 ^{ns}

1: Brown Bolani, 2: White Bolani, 3:Tajan , 4:Kealk , 5: AS-48

The SCA effects calculated according to Griffing's method is the average of SCA effects of each cross and its reciprocal. The average of the difference between SCA effects of each cross and its reciprocal is equal to the reciprocal effect. Partition plant height SCA effect into male and female showed that when genotypes were

participated as a female in cross combination have better performance than when they used as male in hybrid combination (Table 6). So it can be concluded that cytoplasmic factors were the reason for high value of SCA in parents when they used as female. This result in agreement of (Mahgoub 2011).

Table 6: Partitioned SCA effect to maternal and paternal effect, Griffing method (Upper) and to Mahgoub method (lower) for plant height.

Male \ Female		Brown Bolani	White Bolani	Tajan	Kealk	AS-48
		Brown Bolani	-	-1.68	1.91	-2.67
White Bolani	3.14	-	3.84	-0.91	6.66	
Tajan	5.72	3.84	-	3.05	-3.27	
Kealk	-0.8	4.23	3.62	-	4.64	
AS-48	4.23	2.31	5.44	-0.44	-	
	1.64	-	4.07	-3.45	4.35	
	7.63	3.62	-	-2.38	-3.03	
	-3.46	9.63	5.44	-	5.08	
	9.63	8.67	8.49	4.20	-	

Table 7: Correlation coefficient between traits based on mean of two environment (normal and water deficient stress).

Traits	GY	HI	TB	NSP	GN	PH	NL2	NL3	PL	SL
HI	0.3*	1								
TB	0.88**	-0.16 ^{ns}	1							
NSP	.11 ^{ns}	0.07 ^{ns}	0.07 ^{ns}	1						
GN	0.02 ^{ns}	0.18 ^{ns}	0.09 ^{ns}	0.51**	1					
PH	0.51**	0.08 ^{ns}	0.59**	-0.17 ^{ns}	-0.59**	1				
NL2	0.45**	-0.13 ^{ns}	-0.55**	-0.16 ^{ns}	-0.65**	0.96**	1			
NL3	0.5**	-0.05 ^{ns}	-0.56**	-0.22 ^{ns}	-0.67**	0.96**	0.96**	1		
PL	0.48**	0.12 ^{ns}	-0.44**	-0.14 ^{ns}	-0.43**	0.84**	0.78**	0.85**	1	
SL	0.31**	-0.03 ^{ns}	-0.31*	0.6**	0.6**	-0.12 ^{ns}	-0.17 ^{ns}	0.26 ^{ns}	-0.14 ^{ns}	1
1000Gw	0.5**	-0.16 ^{ns}	0.61**	-0.11	-0.48**	0.64**	0.63**	0.63**	0.53**	-0.04 ^{ns}

Correlation coefficient between measured traits were presented in Table 7. Plant height, NL2, NL3, PL, SL, TB and 1000GW positively and significantly correlated with GY. The strong positive correlations among the traits should provide wheat breeders with insights on possible selection for one trait in others. From the results of correlation analysis, it could be concluded that the plant height can be decreased by selecting progenies with low NL2, NL3, and PL.

The main effect of dwarfing genes is transferring assimilate into the spike in growth stage and as resulting increase in the number of fertile florets per spike, that the most effective ingredient of yield, number of grains per spikelet, is increased (Gupta NK *et al.* 2001). Plant height with GN showed negative significant correlations and non-significant correlation with NSP. In other words dwarf plant have more grain per spike.

Negative correlation of PH and GN in agreement with Sio-se *et al.* (2006) which showed the negative relationship of plant height with GN in wheat cultivars. Van Ginkel *et al.* (1988) found that grains/spike was criteria for high grain yield only under irrigated conditions and it was negatively correlated with grain yield under late season drought condition.

Plant height and its related compound (NL2, NL3 and PL) showed positive and highly significant ($P < 0.01$). Spike length and plant height was independent. According to table 7 GY have positive and highly significant correlation with HI, TB, SL and 1000GW. Bogale *et al.* (2011) reported a significant and positive correlation between plant height and peduncle length. Peduncle length has been suggested as a useful indicator of yield capacity in dry environments. The significant and positive correlation observed between PL and GY in the present study. This result suggested that PL and PH could be a good indicator of grain yield for breeding purpose these findings are disagreement with Khamssi and Najaphy (2012) and in conformity with previous reports that showed peduncle length as an indirect selection criterion in wheat under drought stress (Kaya *et al.* 2002; Bogale *et al.* 2011). In other cases, such relationship has been found inverse (Briggs and Aytenfisu 1980), or no relation (Villegas *et al.* 2006) depending on the environment. Favorable conditions for growth may permit an expansion of the last internodes as well as a higher yield (Gupta NK *et al.* 2001).

CONCLUSION

Overall, significant genetic variation were observed for plant height and its compound that investigated in this research. Significant GCA for all the traits implies the role of additive gene action in genetic control of these traits. Significant SCA in some traits, such as yield and plant height, manifest the effects of non-additive genes in controlling these traits. However, the ratios of GCA/SCA imply the higher contribution of additive gene effects to the inheritance of all the characters. The preponderance of additive gene action in explaining genetic variations in plant height and its compound indicates the possibility for their genetic improvement through accumulating favorable alleles from dwarf mutant (AS-48) with highly negative GCA values for PH, NL2, NL3 and PL and highly positive value for SL and GN in the target genotypes using conventional breeding methods. Our results indicated insensitivity of both kinds of gene effects to the environmental variations, therefore, same breeding method could be used in Normal and terminal water deficient stress for reduce plant height. Grain number per spike and peduncle length could be used as reliable criteria for

selection of bread wheat genotypes for water stress tolerance.

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