

Estimation of heritability and some genetic parameters for yield and yield-related traits of wheat using Diallel design

Habiballah Soughi^{1*}, Kamal Payghamzadeh¹, Manouchehr Khodarahmi², Mehdi Nazari¹

¹ Horticulture Crops Research Department, Golestan Agricultural and Natural Resources Research and Education Center, AREEO, Gorgan, Iran

² Seed and Plant Improvement Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

ABSTRACT: Wheat is one of the most important edible crops used in several food products. The success of plant breeding programs depends on the availability of parents with desired genetic diversities. In this context, we evaluated the genetic parameters in eight wheat genotypes namely Kohdashet, Morvaread, N-80-19, Darya, UR-82-17, Ehsan, Bacounoura and Atrack as well as their F₁ progenies in term of grain yield and the relevant traits. Randomized complete block design with three replications was used. Data analysis indicated that genotypes and their F₁ hybrids significantly affected grain yield, biological yield, thousand-grain weight, grains per spike, grain weight in spike, plant height, peduncle length and second internode length. The Model I of Griffing's method II was used in SAS software to determine GCA, SCA and other genetic parameters. Among parents, Ehsan cultivar exhibited the highest GCA for grain yield, thousand-grain weight, grain weight in spike, plant height and biological yield. P6×P7 cross was found to have the highest SCA effects on grain yield, thousand-grain weight and plant height. In addition, among examined characteristics, the thousand-grain weight and the peduncle length had the highest broad sense ($h_2=0.98$) and narrow sense heritability ($H_2=0.62$), respectively. These findings indicated that the distinctive crosses engaged in progenitors belongs to high×low GCA; therefore, it is inessential to set crosses with high×high GCA. As a result, potential homozygous lines can be selected from transgressive segregations to increase yield. Such crosses can be applied for exploiting heterosis.

KEYWORDS: General combining ability, Griffing's Diallel approach, hybridization, promising line, specific combining ability

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) plays a pivotal role in providing food products throughout the world. Easy storage, transportation, marketing and processing of this crop has made it one of the strategic crops among cereals [1–3]. Wheat cultivation area has been estimated to be as 221 million hectares thorough the world. There is around 950 million tons demand for wheat [1]. Plant breeding programs have ever given rise to production of new varieties with increased yield or improved physiological properties such as resistance to draught, resistance to

herbicides and so forth. Heterosis is a phenomenon that can be engaged in plant breeding programs to develop new varieties with desired traits of interest. The nature of pollination, the floral biology and the very low natural out-crossing rates in wheat is important for heterosis. In some self-pollinated plants, heterosis appears to be very high because of extremely low out-crossing rates. [4,5]. Manipulation of heterosis and hybridization are important strategies to increase wheat yield [6,7]. Identification of the best parents to take most advantage of heterosis is a

*Corresponding author (✉): hab3asog@gmail.com

Received: 02 December 2019 / Last revised: 28 January 2020

Accepted: 17 February 2020

crucial step in plant breeding programs [8–10]. Breeders use genetic pools to generate new varieties with the traits of interest [9,11]. Information regarding type of gene action in the inheritance of a trait is useful to choose the breeding methods for enhancing wheat characteristics [12,13]. Heritability, general combining ability (GCA) and specific combining ability (SCA) are among the genetic parameters that are considered to select suitable parents for hybridization [4,14]. Environmental and phenotypic parameters are also considered for selection of parents [2]. The choice of breeding procedure for genetic improvement of wheat depend on information of types and amount of genetic components for different traits in the plant materials under investigation [12,15]. Plant breeders frequently use Diallel mating approaches to obtain information of gene action controlling the important traits of plant [16,17]. Diallel analysis providing both early information regarding genetic parameters in the first generation and inheritance of traits among genotypes, helps identify the superior parents for hybrid production [5,9,11]. Diallel approaches have been applied for estimation of genetic parameters for physical traits (such as grain texture and size) [18] and grain yield [6,19] as well as for agronomic traits [20]. Diallel approaches exploited not only for validation of the drought tolerant germplasms [21] but also for understand heritability pattern of quantitative characters [22] and disease resistance (e.g. *Parastagonospora nodorum* and *Rhynchosporium*) [14,23]. Evaluation of genetic parameters of various traits is a necessary step in selecting the best parents for the next breeding programs. The objective of this experiment was to estimating genetic parameters for grain yield and yield attributes of wheat genotypes to be engaged in future breeding programs using Diallel mating design.

MATERIALS AND METHODS

Eight genotypes of spring breed wheat (*Triticum aestivum* L.) namely Kohdashet (P1), Morvaread (P2), N-80-19 (P3), Darya (P4), UR-82-17 (P5), Ehsan (P6), Bacounoura (P7) and Atrack (P8) (Table 1) were selected randomly according to their different performance i.e. yield and agronomic traits. During 2015-2016, the genotypes were sown in 10th December in Araghi-Mahaleh Agricultural and Natural Research Station (36° 53' 19" N 54° 24' 49" E) of Golestan Agricultural and Natural Resources Research and Education Center, Iran. The genotypes were crossed in Diallel fashion excluding

reciprocal (half-Diallel) and F₁'s grains were sown in 5th December based on randomized complete block design with three replications during 2016-2017. All possible 28 F₁ progenies along with their parents were planted in two rows with 2 meters long with inter-row 20 cm spacing and 5 cm intra-row. Agronomic practices were done as recommended. Urea as a nitrogen source (250 kg. ha⁻¹), triple-phosphate (150 kg.ha⁻¹) and potassium sulphate (100 kg.ha⁻¹) applied based on soil test recommendation at the time of sowing time. The urea fertilization was applied three times with a ratio so that one third of urea was applied simultaneously with planting as base fertilizer and the remainder in two stages, at the beginning of the tillering and at the beginning of the stem elongation stages. In each plot, 10 individual plants were tagged randomly before heading time (Zadoks code 43). At the maturity stage (Zadoks code: 92), all the tagged plant were harvested by hand and analyzed for grain yield, biological yield, grain weight per spike, thousand-grain weight, plant height, peduncle length, grains per spike and second internode length [24,25]. The data were expressed as least significant difference (LSD 0.05), and subjected to analysis of variance as described by Steel and colleagues [26] to find out significant differences among parents and hybrids. Genetic parameters were analyzed using SAS ver. 9.4 [27] based on the method described by Griffing and colleagues (model I of method II) of [28]. Also, the Baker ratio [29] was estimated by following equation:

$$Baker\ ratio = \frac{2\sigma_g^2}{2\sigma_g^2 + \sigma_s^2}$$

In which σ_g^2 is variance of general combining ability and σ_s^2 is variance of specific combining ability.

RESULTS AND DISCUSSION

The results of variance analysis for recorded traits are shown in Table 2. In the current work, the total variance was divided into two-distinctive components i.e. parents and genotypes (F₁). These components were found to be significantly different for all traits in parents (Table 2), indicating existence of enough genetic diversity among parents to use them in breeding programs. These findings are in consistence with previous reports [6,12,19], indicating the existence of sufficient magnitude of genetic diversity, which is essential for next breeding programs. However, for the evaluated traits, significant GCA and SCA means squares were observed due to the additive genetic and non-additive gene action of the traits.

Table 1. Pedigree, means of traits and other characters of wheat genotypes used in Diallel crossing

Genotypes No.	Genotypes name*	Pedigree of genotypes	Released year*	Origin	PH (cm)	TGW (gr)	GY (kg.ha ⁻¹)	Characteristics
P1	Kohdashet	TR8010200	2000	CIMMYT	95	45	4850	Late season heat and drought tolerant, early maturing, semi-tolerant to Rust yellow rust
P2	Morvaread	MILAN/SHA7	2009	CIMMYT	93	42	4500	High yielding, mid maturing, semi-tolerant to Rust yellow rust and tolerant to Fusarium head blight
P3	N-80-19	SW89.3064/STAR...	2009	CIMMYT	85	46	4250	High yielding, late maturing and tolerant to Rust yellow rust
P4	Darya	SHA4/CHIL...	2007	CIMMYT	95	45	5400	High yielding, mid maturing, tolerant to Rust yellow rust and Fusarium head blight
P5	UR-82-17	JUP/ALD"S"//ATT"S"/3/...	2007	ICARDA	81	40	4700	Late season heat and drought tolerant, early maturing, sensitive to Rust yellow rust and anti-lodging
P6	Ehsan	SABUF/7/ALTAR...	2016	CIMMYT	99	52	6650	High yielding, late maturing and semi-tolerant and tolerant to Fusarium head blight and Rust yellow rust, respectively
P7	Bacounoura	JUP/BJY//URES	1995	CIMMYT	84	29	3250	Suitable yielding, tolerant to drought stress, early maturing and anti-lodging
P8	Atrack	Kauz"s"	1995	CIMMYT	79	32	3950	Suitable yielding, high tillering, mid maturing, anti-lodging and sensitive to Rust yellow rust

*Genotypes named and released by SPII: Seed and Plant Improvement Institute of Iran; CIMMYT: Centro Internacional de Mejoramiento de Maíz y Trigo; ICARDA: The International Center for Agriculture Research in the Dry Areas; PH: Plant Height; TGW: Thousand Grain Weight; GY: Grain Yield.

Table 2: Mean square values from analysis of variance (ANOVA)

Source of Variation	DF	Grain yield	Biological yield	Thousand grain weight	Grain per spike	Grain weight in spike	Plant height	Peduncle length	Second internode length
Block	2	407.20 ^{ns}	2554 ^{ns}	5.10 ^{ns}	46.90 ^{ns}	0.25 ^{ns}	3.27 ^{ns}	5.8 ^{ns}	0.58 ^{ns}
Genotypes (F ₁)	35	176.40 ^{**}	982 ^{**}	67.90 ^{**}	104.80 ^{**}	0.38 ^{**}	111.10 ^{**}	24.90 ^{**}	5.96 ^{**}
Parents	7	43.20 [*]	296 [*]	177.40 ^{**}	15.80 [*]	0.54 ^{**}	121 ^{**}	32.30 ^{**}	6.15 ^{**}
Residuals	70	48	260.39	4.13	43.06	0.12	16.86	2.31	1.22
GCA	7	35.70 [*]	178.92 ^{**}	73.58 ^{**}	17.76 ^{ns}	0.35 ^{**}	106.11 ^{**}	32.14 ^{**}	6.88 ^{**}
SCA	28	64.56 ^{**}	364.66 ^{**}	9.88 ^{**}	39.21 ^{**}	0.07 [*]	19.77 ^{**}	2.37 ^{**}	0.76 ^{**}
Error	70	16	86.79	1.38	14.39	0.04	5.49	0.77	0.40
Baker Ratio	-	0.53	0.50	0.94	0.48	0.91	0.91	0.96	0.95
% CV	-	25.08	23.59	5.08	10.82	15.17	4.75	4.48	6.22

ns: non-significant, * and ** significant at the 5% and 1% probability level, respectively. GCA: General Combining Ability; SCA: Specific Combining Ability; CV: Coefficient Variation.

Table 3. Estimated Genetic parameters for agronomic traits

Genetic parameters	Grain weight in spike	Second internode length	Biological yield	Grain per spike	Thousand grain weight	Peduncle length	Plant height	Grain yield
σ_g^2	0.03	0.61	0.01	0.01	6.37	2.98	8.36	0.01
σ_s^2	0.03	0.36	277.87	24.82	8.50	1.60	14.27	48.56
VA	0.01	2.45	0.01	0.01	25.50	11.91	34.53	0.01
VD	0.13	1.45	1111.49	99.29	34.00	6.41	57.10	194.25
H2	0.85	0.91	0.93	0.87	0.98	0.96	0.94	0.92
h2	0.38	0.57	0.01	0.01	0.42	0.62	0.35	0.01
DR	1.58	1.07	0.001	0.001	1.63	1.04	1.82	0.001
BR	0.67	0.77	0.001	0.001	0.60	0.79	0.54	0.001
σ_g^2/σ_s^2	1.00	1.69	0.001	0.001	0.75	1.86	0.58	0.001

σ_g^2 : General combining ability variance; σ_s^2 : specific combining ability variance; VA: additive variance; VD: dominance variance; H2: broad sense heritability; h2: narrow sense heritability; DR: dominance ratio; BR: Baker ratio; σ_g^2/σ_s^2 : type of gene action.

The analysis of combining ability variation (Table 3) showed high GCA for plant height, thousand-grain weight and peduncle length; meanwhile, other traits have lower GCA. For all the traits except grain weight in spike, peduncle length and second internode length, the variance of SCA was higher than that of GCA (Table 3). Higher SCA was observed for biological yield, grain yield, grain per spike, plant height and thousand-grain weight. Higher dominance ratio, lower σ_g^2/σ_s^2 and Baker ratio variance

for grain yield, biological yield, thousand grain weight, plant height and grain per spike represents preponderance of non-additive action of genes showing the existence of preponderance dominant gene action and vice versa. These findings indicated that both additive and non-additive gene effects are most important in the current genotypes. Non-additively controlled gene action was found to be more prominent than additive gene action for most of the traits (Table 3). These findings are also

Table 4: General Combining Ability for evaluated traits in parents

Parents	Grain weight in spike	Second internode length	Biological yield	Grain per spike	Thousand grain weight	Peduncle length	Plant height	Grain yield
P1	-0.14**	-0.31 ^{ns}	-4.53 ^{ns}	0.65 ^{ns}	0.84**	1.32**	1.08 ^{ns}	-2.14 ^{ns}
P2	-0.05 ^{ns}	1.00**	-3.45 ^{ns}	-1.96 ^{ns}	0.01 ^{ns}	2.48**	1.28 ^{ns}	-1.21 ^{ns}
P3	0.25**	-0.73**	-2.88 ^{ns}	0.78 ^{ns}	1.94**	-0.12 ^{ns}	-0.61 ^{ns}	-0.76 ^{ns}
P4	0.11 ^{ns}	0.50**	1.84 ^{ns}	0.43 ^{ns}	0.51**	-0.48 ^{ns}	1.62**	0.02 ^{ns}
P5	-0.12*	-0.21 ^{ns}	-0.13 ^{ns}	-0.31 ^{ns}	-1.83**	-1.25**	-3.52**	0.55 ^{ns}
P6	0.27**	0.87**	8.21**	-1.91 ^{ns}	4.84**	1.09**	5.16**	3.98**
P7	-0.18**	0.30 ^{ns}	3.03 ^{ns}	0.46 ^{ns}	-3.29**	-0.35 ^{ns}	0.39 ^{ns}	0.81 ^{ns}
P8	-0.13**	-1.42**	-2.10 ^{ns}	1.84 ^{ns}	-3.02**	-3.39**	-5.41**	-1.25 ^{ns}
SE _(gi)	0.06	0.19	2.75	1.12	0.35	0.26	0.69	1.18

Ns: non-significant, * and ** significant at the 5% and 1% probability level, respectively.

consistent with previous published reports [6,19,30–34]. Higher SCA has already been reported for yield and yield-related traits [35]. Akhtar and Chowdhary [36] indicated that non-additive gene effects were more important than additive gene actions for grain yield in wheat. While other researchers reported contrary results [12,37–39]. Therefore, suggesting that hybridization method is a useful breeding program for improving those traits which controlling by non-additive gene actions.

Heritability estimation using archived data indicated that, peduncle length, second internode length and thousand-grain yield are inherited to the next generation with the probability more than 42%. All the studied traits had more than 87% of broad sense heritability in which thousand-grain weight had higher broad sense heritability than others. A similar trend has been reported for grain yield and thousand-grain weight [40,41], while the results obtained by other researches for yield-related traits was against of our results [34,42].

We found some very low narrow sense heritability degrees for the characters examined in the study (Table 3), indicating that additive variance is not great enough in the population and therefore the selection process should be postponed to be done in the next generations. Hence, short stature and high yielding varieties can be developed by controlling genes responsible for peduncle length, second internode length, grain weight in spike, plant height and thousand-grain weight.

General combining ability was used to determine the best parents for achieving suitable transgressive segregates. In plant breeding methods, the estimation of general and specific combining potential is a prerequisite for selection of promising parents. Both Ehsan and Morvarid were found to have suitable GCA to be used as a parent in

hybridization program. By comparison, Parent 6 (Ehsan) expressed higher positive and significant GCA for grain yield, biological yield, thousand grain weight, plant height and grain weight in spike than others. (Table 4). These genotypes can be used in breeding programs as a donor, which may provide a better population in advanced generation. Hence, if the aim of wheat breeding is improving the grain yield, using Ehsan cultivar would profitable. Positive effect of GCA for abovementioned traits has been reported in numerous studies [6,19,31,33,43–45]. The higher GCA for biological yield, plant height, grain weight in spike and thousand-grain weight, caused the greater GCA for yield. The correlation of traits; furthermore, showed that biological yield, plant height and grain weight in spike correlated significantly with grain yield (Table 6). These findings are consistent with previously issued reports [19,46]. Therefore, for the mentioned traits, these cultivars may serve as favorable parents in breeding programs. Higher GCA effects is almost due to additive or additive×additive gene interactions [28]. Most of the genotypes showed negative or weak GCA for grain yield, but indicated strong GCA for yield components and agronomic traits. For example, Morvarid cultivar showed the higher GCA for second internode length and peduncle length and Ehsan cultivar indicated the higher GCA for grain weight in spike, biological yield, thousand-grain weight and plant height. Therefore, these cultivars can be engaged for generation of dynamic population with significant number of favorable genes.

Of 28 combinatorial crosses, twenty for grain weight per spike, five for biological yield, three for thousand-grain weight, four for grain per spike, two for second internode

Table 5: Specific combining ability for evaluated traits in wheat hybrids

Hybrids	Grain weight in spike	Biological yield	Thousand grain weight	Grain per spike	Second internode length	Peduncle length	Grain yield	Plant height
P1×P2	0.17 ^{ns}	-11.5 ^{ns}	-4.14 ^{**}	-2.64 ^{ns}	-0.53 ^{ns}	-1.29 ^{ns}	-5.21 ^{ns}	-12.5 ^{**}
P1×P3	0.57 ^{**}	-11.3 ^{ns}	-1.74 ^{ns}	4.42 ^{ns}	-0.66 ^{ns}	-1.95 ^{**}	-5.79 ^{ns}	-1.28 ^{ns}
P1×P4	0.42 [*]	4.1 ^{ns}	-6.64 ^{**}	8.44 ^{**}	1.07 ^{ns}	1.04 ^{ns}	2.92 ^{ns}	1.56 ^{ns}
P1×P5	-0.11 ^{ns}	23.6 ^{**}	-3.64 ^{**}	2.65 ^{ns}	-1.22 [*]	0.25 ^{ns}	8.58 ^{**}	-3.66 ^{ns}
P1×P6	0.46 ^{**}	-2.0 ^{ns}	0.36 ^{ns}	-2.21 ^{ns}	0.70 ^{ns}	-1.34 ^{ns}	-0.76 ^{ns}	-1.69 ^{ns}
P1×P7	0.14 ^{ns}	23.4 ^{**}	3.16^{**}	-0.46 ^{ns}	0.31 ^{ns}	2.42 ^{**}	8.33 [*]	5.36 ^{**}
P1×P8	-0.08 ^{ns}	-3.8 ^{ns}	1.89 ^{ns}	12.69^{**}	0.47 ^{ns}	-1.06 ^{ns}	-0.79 ^{ns}	1.62 ^{ns}
P2×P3	0.85^{**}	13.1 ^{ns}	0.76 ^{ns}	9.83 ^{**}	1.39^{**}	3.12^{**}	4.41 ^{ns}	5.76 ^{**}
P2×P4	0.46 ^{**}	13.0 ^{ns}	-0.14 ^{ns}	1.25 ^{ns}	0.82 ^{ns}	0.88 ^{ns}	3.57 ^{ns}	1.42 ^{ns}
P2×P5	0.76 ^{**}	26.9^{**}	1.53 ^{ns}	5.72 ^{ns}	1.30 [*]	1.25 ^{ns}	11.55 ^{**}	6.59 ^{**}
P2×P6	0.40 [*]	-10.8 ^{ns}	-1.47 ^{ns}	1.13 ^{ns}	0.48 ^{ns}	-0.36 ^{ns}	-4.86 ^{ns}	-1.22 ^{ns}
P2×P7	0.15 ^{ns}	7.8 ^{ns}	-1.00 ^{ns}	-5.52 ^{ns}	-1.44 ^{**}	-0.55 ^{ns}	3.79 ^{ns}	-5.88 ^{**}
P2×P8	0.41 [*]	-0.4 ^{ns}	-0.94 ^{ns}	-2.78 ^{ns}	-0.80 ^{ns}	-2.66 ^{**}	1.62 ^{ns}	-2.55 ⁿ
P3×P4	0.70 ^{**}	-8.5 ^{ns}	1.26 ^{ns}	4.97 ^{ns}	-0.71 ^{ns}	0.15 ^{ns}	-5.42 ^{ns}	-0.38 ^{ns}
P3×P5	0.23 ^{ns}	3.8 ^{ns}	-3.40 ^{**}	1.11 ^{ns}	-0.90 ^{ns}	0.19 ^{ns}	0.86 ^{ns}	-2.71 ^{ns}
P3×P6	0.44 ^{**}	12.6 ^{ns}	-2.74 ^{**}	1.52 ^{ns}	0.42 ^{ns}	-0.89 ^{ns}	10.60 ^{**}	0.29 ^{ns}
P3×P7	0.43 ^{**}	22.3 ^{**}	-0.60 ^{ns}	2.01 ^{ns}	0.20 ^{ns}	-1.85 ^{**}	8.84 ^{**}	-1.29 ^{ns}
P3×P8	0.43 ^{**}	7.2 ^{ns}	0.80 ^{ns}	-0.04 ^{ns}	0.59 ^{ns}	1.59 [*]	4.72 ^{ns}	-0.54 ^{ns}
P4×P5	0.62 ^{**}	14.0 ^{ns}	1.03 ^{ns}	3.13 ^{ns}	-0.03 ^{ns}	-0.95 ^{ns}	7.76 [*]	-0.84 ^{ns}
P4×P6	0.17 ^{ns}	-2.1 ^{ns}	-3.30 ^{**}	-2.19 ^{ns}	-1.08 ^{ns}	-1.73 [*]	-3.58 ^{ns}	-6.33 ^{**}
P4×P7	0.54 ^{**}	7.6 ^{ns}	0.83 ^{ns}	1.89 ^{ns}	1.02 ^{ns}	0.74 ^{ns}	0.84 ^{ns}	-0.72 ^{ns}
P4×P8	0.39 [*]	16.7 ^{ns}	-1.10 ^{ns}	0.25 ^{ns}	0.25 ^{ns}	0.41 ^{ns}	6.22 ^{ns}	-2.95 ^{ns}
P5×P6	0.34 ^{ns}	9.3 ^{ns}	-2.64 ^{**}	-2.85 ^{ns}	0.93 ^{ns}	1.74 [*]	2.15 ^{ns}	0.51 ^{ns}
P5×P7	0.54 ^{**}	-15.4 ^{ns}	0.49 ^{ns}	2.63 ^{ns}	1.03 ^{ns}	-1.25 ^{ns}	-8.56 ^{**}	-0.15 ^{ns}
P5×P8	0.61 ^{**}	-1.1 ^{ns}	-2.77 ^{**}	-0.67 ^{ns}	0.06 ^{ns}	-1.05 ^{ns}	-2.72 ^{ns}	-3.53 ^{ns}
P6×P7	0.84 ^{**}	23.9 ^{**}	3.16^{**}	8.77 ^{**}	0.69 ^{ns}	1.83 [*]	13.17^{**}	7.50^{**}
P6×P8	0.68 ^{**}	8.3 ^{ns}	1.24 ^{ns}	2.73 ^{ns}	-0.46 ^{ns}	1.77 [*]	3.08 ^{ns}	2.01 ^{ns}
P7×P8	0.70 ^{**}	16.4 ^{ns}	2.70 ^{**}	2.55 ^{ns}	0.32 ^{ns}	-2.03 ^{**}	6.01 ^{ns}	-2.45 ^{ns}
SE _(sij)	0.18	8.45	1.06	3.43	0.57	0.79	3.63	2.12

Ns: non-significant, * and ** significant at the 5% and 1% probability level, respectively.

length, five for peduncle length, seven for grain yield and four for plant height were found to have positive significant SCA effects (Table 5). Some cross combinations showed significant SCA effects for grain yield and number of its attributes. For instance, P6×P7 (Ehsan×Bacounora) cross, which had the highest SCA effects for grain yield, had a highly significant SCA for thousand-grain weight and plant height, as well. P2×P3 (Morvarid×N-80-19) cross had the highest SCA effects for grain weight in spike and second internode length as well as peduncle length. Crosses P1×P7 (Kohdasht×Bacounora), P1×P8 (Kohdasht×Atrack) and

P2×P5 (Morvarid×UR-82-17) showed positive and highly significant SCA for thousand-grain weight, grain per spike and biological yield, respectively. The heterotic crosses involved parents belongs to high×low general combiners, which may be due to favorable additive effects of the good general combiner parent and epistatic effects of poor general combiner, which fulfils the favorable plant attribute. At least one of the parents contributing to SCA effects was shown to be a good general combiner for those traits. So, selection among transgressive segregates of these crosses can lead to genetic improvement [47]. Therefore, pure lines are likely

Table 6: Pearson coefficients of correlation between eight agro-morphological traits in weight

Traits	Traits No.	1	2	3	4	5	6	7	8
Grain yield	1	1							
Biological yield	2	0.94**	1						
Thousand grain weight	3	0.11 ^{ns}	0.07 ^{ns}	1					
Grain per spike	4	0.34**	0.42**	-0.15 ^{ns}	1				
Grain weight in spike	5	0.38**	0.42**	0.53**	0.44**	1			
Plant height	6	0.22*	0.21*	0.62**	0.08 ^{ns}	0.43**	1		
Peduncle length	7	0.14 ^{ns}	0.14 ^{ns}	0.37**	-0.06 ^{ns}	0.15 ^{ns}	0.64**	1	
Second internode length	8	0.27**	0.29**	0.27**	0.13 ^{ns}	0.35**	0.64**	0.54**	1

Ns: non-significant, * and ** significant at the 5% and 1% probability level, respectively.

to be developed from a population in which additive gene action exists even if SCA effects were insignificant. [48]. Some parents involved in crosses were shown to be good general combiners, despite being poor specific combiners. Parents with high GCA effects do not necessarily have high SCA effects, indicating that SCA may negatively affects grain filling, maturity and plant height [49,50]. These findings shows that it is unnecessary to have high×high general combiners to get the best recombinants, as reported earlier [6,19,51]. Genotypes with high GCA are the most promising parents for crossing to have a SCA effects. The major portion of such variances is flexible for the given traits in the crosses mentioned above. Similar findings have been reported for grain yield and agro-morphological and quality traits in bread wheat [19,52–54]. Traits with high non-additive genes are difficult to be improve and fix by simple pedigree breeding methods in the early generation. Thus, retaining heterozygosity in early segregating generations in selected breeding materials is necessary to maximize gain yield. Therefore, a few selection cycles followed by pedigree breeding method will be effective and useful for enhancement of yields and yield related components in the genotypes.

Traits correlation

Traits coefficient correlations are presented in Table 6. Grain yield highly correlated with biological yield, grain per spike, grain weight in spike, plant height and second internode length, indicating that grain yield directly depends on related yield components. However, biological yield highly and positively correlated with grain yield, grain per spike, grain weight in spike, plant height and second internode length. Thousand-grain weight significantly correlated grain weight in spike, plant height, peduncle length and second internode

length. In addition, grain per spike have a high relationship with grain yield, biological yield and grain weight in spike. Generally, all studied traits have different types of correlation (null, positive or negative) with each other (Table 6), indicating they are influencing grain yield directly and indirectly except thousand-grain weight and peduncle length. Hence, even though quantitative traits indicated extremely negative, positive or null correlation with grain yield in segregating population, it was still possible to observe different kind of correlation in the next generations due to segregation property. Those differences may be associated with population structure, as each population has its own gene and genetic frequency, traits heritability and genetic variance and correlation [55]. To improve yield and other quantitative traits simultaneously, parent that could generates breeding populations with a positive correlation between these target traits are necessary [55]. Therefore, selection of negatively or null correlated traits with yield as an indirect selection index, will yield usefulness results.

CONCLUSION

Parents with high GCA, that give rise to progenies with the higher SCA are suitable for improving grain yield in bread wheat. Ehsan cultivar expressed higher GCA for grain yield, biological yield, thousand-grain weight and plant height as well as grain weight in spike. Morvaread cultivar has a high GCA for second internode length and peduncle length. P6×P7 (Ehsan×Bacounora) cross has the highest SCA for grain yield, thousand-grain weight and plant height. P2×P3 (Morvarid×N-80-19) cross has a high SCA effects for grain weight in spike and second internode length as well as peduncle length. Thus, parental genotypes with good GCA and SCA should be involved in multiple crosses to make tangible

improvement of yield and its components in spring wheat. Moreover, the involvement of both types of gene actions opens a new chapter of discussion. As a dominant type of gene action was prominent for yield-related traits, the selection of paternal and maternal lines proved best specific combiners should utilize for yield enhancement in the next generation. While the heritability and genetic gain for these traits indicated a broader spectrum of acclimatization of yield-related traits in the next generation as non-additive gene action was prominent.

ACKNOWLEDGEMENTS

We thank the Agricultural and Natural Resources Research and Education Center of Golestan and the Seed and Plant Improvement Institute (SPII) for providing genetic materials and facilities for conducting the current experiment (Project ID: 0-03-03-94208).

REFERENCES

- [1] Thomas, N. 2018. Stability analysis for quantitative and physiological traits related to terminal heat tolerance in wheat (*Triticum aestivum* L.). Sam Higginbottom University Of Agriculture, Technology And Sciences, PhD. thesis. 213 p.
- [2] Kutlu, I. 2018. Heritability of end-use quality and biofortification characteristics in Line×Tester bread wheat (*Triticum aestivum* L.) cross. Appl. Ecol. Environ. Res., 16 (5), 7305–7326.
- [3] Dashti, H. Bihamta, M.R. Shirani, H. and Majidi, M.M. 2012. Genetic analysis of salt tolerance in vegetative stage in wheat (*Triticum aestivum*). Plant Omics, 5 (1), 19.
- [4] Rigatti, A. Pelegrin, A.J. De Meier, C. Lunkes, A. Klein, L.A. Silva, A.D.B.A.F. Bellé, E.P. Silva, A.D.B.A.F. Marchioro, V.S. Souza, V.Q. De de Pelegrin, A.J. Meier, C. Lunkes, A. Klein, L.A. da Silva, A.F. Bellé, E.P. Silva, A.D.B.A.F. Marchioro, V.S. and de Souza, V.Q. 2018. Combination capacity and association among traits of grain yield in wheat (*Triticum aestivum* L.): a review. J. Agric. Sci., 10 (5), 179.
- [5] Parveen, N. Kanwal, A. Amin, E. Shahzadi, F. Aleem, S. Tahir, M. Younas, A. Aslam, R. Aslam, N. Ghafoor, I. and Makhdoom, M. 2018. Assessment of heritable variation and best combining genotypes for grain yield and its attributes in bread wheat. Am. J. Plant Sci., 9 (08), 1688–1698.
- [6] Farooq, M.U. Ishaq, I. Maqbool, R. Aslam, I. Naqvi, S.M.T.A. and Mustafa, S. 2019. Growing degree days during the late reproductive phase determine spike density and cognate yield traits. AIMS Agric. Food, 4 (1), 56–72.
- [7] Yao, J. Zhao, D. Chen, X. Zhang, Y. and Wang, J. 2018. Use of genomic selection and breeding simulation in cross prediction for improvement of yield and quality in wheat (*Triticum aestivum* L.). Crop J., 6 (4), 353–365.
- [8] Parashar, N. 2019. Combining ability analysis in barley (*Hordeum vulgare* L.) Under high temperature stress. Sri Karan Narendra Agriculture University, PhD. thesis. 204 p.
- [9] Shaukat, S. Khan, A.S. Hussain, M. Kashif, M. and Ahmed, N. 2018. Selection of superior parents and cross combinations for quality traits in bread wheat (*Triticum aestivum* L.) under normal and heat stressed conditions. Pakistan J. Agric. Sci., 55 (4).
- [10] Arshad, Y. and Zahravi, M. 2017. Study of genetic diversity in bread wheat germplasm using nitrogen uptake and nitrogen use efficiency characteristics. Iran. J. Genet. Plant Breed., 6 (2), 48–59.
- [11] Patel, H.N. 2018. Identification of heterotic combinations for grain yield and quality traits in bread wheat (*Triticum aestivum* L.). Int. J. Pure Appl. Biosci., 6 (4), 107–115.
- [12] Abbasi, S. and Mohammadi-Nejad, G. 2017. Genetic Analysis and QTLs Identification of Some Agronomic Traits in Bread Wheat (*Triticum aestivum* L.) under Drought Stress. J. Plant Mol. Breed., 5 (1), 1–9.
- [13] Khattab, S.A.M. Shaheen, A.M.A. and Afiah, S.A.N. 2001. Genetic behavior of some metric traits in four bread wheat crosses under normal and saline conditions. J. Agric. Sci. Mansoura Univ, 26 (1), 217–229.
- [14] Jalata, Z. Mekbib, F. Lakew, B. and Ahmed, S. 2018. Investigating parent combining ability and gene interactions via diallel analysis against scald resistance in barley. J. Appl. Sci., 18 (3), 129–137.
- [15] Ojaghi, J. and Akhundova, E. 2010. Genetic analysis for yield and its components in doubled haploid wheat. Afr. J. Agric. Res, 5 (4), 306–315.
- [16] Zeeshan, M. Arshad, W. Khan, M.I. Ali, S. Nawaz, A. Batool, A. Tariq, M. Akram, M.I. and Ali, M.A. 2018. Breeding for pre-harvest sprouting resistance in bread wheat under rainfed conditions. Front. Agric. Sci. Eng., 5 (2), 253–261.
- [17] Kumar, A. 2018. Genetic characterization for economic and biochemical traits in bread wheat (*Triticum aestivum* L.) genotypes over the generation. Int. J. Genet., 10 (6), 975–2862.
- [18] Ahmed, H.G.M.-D. Khan, A.S. Kashif, M. and Khan, S. 2018. Genetic analysis of yield and physical traits of spring wheat grain. J. Natl. Sci. Found. Sri Lanka, 46 (1), 23–30.
- [19] Arya, V.K. Kumar, P. Singh, J. Kumar, L. and Sharma,

- A.K. 2018. Genetic analysis of some yield and quality traits in bread wheat (*Triticum aestivum* L.). Wheat Barley Res., 10 (1), 25–32.
- [20] Ferrari, E. Picca, A. Domínguez, R. and Paccapelo, H. 2018. Heterosis and combining ability for yield and other agronomic traits in Triticale. Open Agric., 3 (1), 38–45.
- [21] Chaudhary, N. 2018. Characterization and validation of bread wheat (*Triticum aestivum* L.) germplasm for drought tolerance and its introgression into adapted genotypes.
- [22] Fellahi, Z.E.A. Hannachi, A. Bouzerzour, H. Benbelkacem, A. Iftikhar, R. Hussain, S.B. and Ullah, S. 2015. Inheritance pattern of metric characters affecting grain yield in two bread wheat (*Triticum aestivum* L.) crosses under rainfed conditions. Jordan J. Biol. Sci., 147 (3380), 1–7.
- [23] Jones, O.C. 2018. Genomic selection for glume blotch resistance and milling and baking quality traits in soft red winter wheat. University of Illinois at Urbana-Champaign, MSc thesis. 88 p.
- [24] Zadoks, J.C. Chang, T.T. and Konzak, C.F. 1974. A decimal code for the growth stages of cereals. Weed Res., 14 (6), 415–421.
- [25] Bell, M.A. and Fischer, R.A. 1994. Guide to plant and crop sampling: Measurements and observations for agronomic and physiological research in small grain cereals. Mexico. CIMMYT. Series: CIMMYT Wheat Special Report (WPSR), CIMMYT.
- [26] Steel, R.G.D. and Torrie, J.H. 1980. Principles and procedures of statistics. A biometrical approaches. pp. 633. McGraw Hill, Books Inc., New York, USA., McGraw-Hill Kogakusha, Ltd.
- [27] SAS 2017. Statistical Analysis Systems (SAS). SAS Version 9.4. SAS Institute Inc., Cary, USA., SAS Institute.
- [28] Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci., 9 (4), 463–493.
- [29] Baker, R.J. 1978. Issues in Diallel analysis. Crop Sci., 18 (533), 536.
- [30] Leilah, A.A.A. Abdel-Moneam, M.A. and Leilah, A.A.A. 2018. Combining ability for yield and its attributes in barley under stressed and non-stressed nitrogen fertilization environments. Int. J. Adv. Res. Biol. Sci., 5 (3), 37–50.
- [31] Adel, M.M. and Ali, E.A. 2013. Gene action and combining ability in a six parent diallel cross of wheat. Asian J. Crop Sci., 5 (1), 14–23.
- [32] Çifci, E.A. and Yagdi, K. 2010. The research of the combining ability of agronomic traits of bread wheat in F1 and F2 generations. J. Agric. Fac. Uludag Univ., 24 (2), 85–92.
- [33] Ammar, A. Irshad, A. Liaqat, S. Ahmad, R.I. Qayyum, A. Mahmood, S. Noor, E. Aziz, M.K. Asim, A. and Manzoor, S.A. 2014. Combining ability studies for yield components in wheat (*Triticum aestivum*). J. Food, Agric. Environ., 12 (2), 383–386.
- [34] Fellahi, Z.E.A. Hannachi, A. Bouzerzour, H. and Boutekrabt, A. 2013. Line × tester mating design analysis for grain yield and yield related traits in bread wheat (*Triticum aestivum* L.). Int. J. Agron., 9 p.
- [35] Siddique, M. Ali, S. Malik, M.F.A. Awan, S.I. and Jang, F. 2004. Combining ability estimates for yield and yield components inspring wheat. Sarhad J. Agric., 20 (4), 485–487.
- [36] Akhtar, N. and Chowdhry, M.A. 2006. Genetic analysis of yield and some other quantitative traits in bread wheat. Int. J. Agric. Biol., 4, 523–527.
- [37] Ahmad, F. Khan, S. Ahmad, S.Q. Khan, H. Khan, A. and Muhammad, F. 2011. Genetic analysis of some quantitative traits in bread wheat across environments. African J. Agric. Res., 6 (3), 686–692.
- [38] Jain, S.K. and Sastry, E.V.D. 2012. Heterosis and combining ability for grain yield and its contributing traits in bread wheat (*Triticum aestivum* L.). J. Agric. Allied Sci., 1 (1), 17–22.
- [39] Kamboj, M.C. Naveen, C. and Yadava, R.K. 2000. Genetic analysis of yield and its components in bread wheat (*Triticum aestivum* L.). Ann. Agri Bio Res., 5 (1), 41–43.
- [40] Farooq, M.U. Cheema, A.A. Ishaq, I. and Zhu, J. 2018. Correlation and genetic component studies for peduncle length affecting grain yield in wheat. Int. J. Adv. Appl. Sci., 5 (10), 67–75.
- [41] Farooq, M. Khan, A. Ishaq, I. Cheema, A. Afzal, M. Ali, A. and Zhu, J. 2018. Growing degree days during the late reproductive phase determine spike density and cognate yield traits. Agronomy, 8 (10), 217.
- [42] Hussain, B. Khan, A.S. and Farid, M.Z. 2014. Inheritance of plant height, yield and yield related traits in bread wheat. Int. J. Mod. Agric., 3, 74–80.
- [43] Baloch, M.J. Mallano, I.A. Baloch, A.W. Jatoi, W.A. and Veesar, N.F. 2011. Efficient methods of choosing potential parents and hybrids: Line Tester analysis of spring wheat (*Triticum aestivum* L.) cultivars. Pak. J. Sci. Ind. Res., 54 (3), 117–121.
- [44] Malik, M.F.A. Awan, S.I. and Ali, S. 2005. Genetic behavior and analysis of quantitative traits in five wheat genotypes. J. Agric. Soc. Sci., 1 (4), 313–315.
- [45] Jatav, M. Jatav, S.K. and Kandalkar, V.S. 2014. Combining ability and heterosis analysis of morpho-

- physiological characters in wheat. *Annu. Plant Soil Res.*, 16, 79–83.
- [46] Ali, I.H. and Al-Falahy, M.A.H. 2011. Analysis of partial diallel cross for yield and its components in durum wheat. *Bull. Fac. Agric. Cairo Univ.*, 62, 145–152.
- [47] Seboka, H. Ayana, A. and Zelleke, H. 2009. Combining ability analysis for bread wheat (*Triticum aestivum* L.). *East African J. Sci.*, 3 (1), 87–94.
- [48] Tiwari, D.K. Pandey, P. Giri, S.P. and Dwivedi, J.L. 2011. Prediction of gene action, heterosis and combining ability to identify superior rice hybrids. *Int. J. Bot.*, 7 (2), 126–144.
- [49] Javaid, A. Masood, S. and Minhas, N.M. 2001. Analysis of combining ability in wheat (*Triticum aestivum* L.) using F2 generation. *Pakistan J. Biol. Sci.*, 4 (11), 1303–1305.
- [50] Topal, A. Aydın, C. Akgün, N. and Babaoglu, M. 2004. Diallel cross analysis in durum wheat (*Triticum durum* Desf.): identification of best parents for some kernel physical features. *F. Crop. Res.*, 87 (1), 1–12.
- [51] Kulshreshtha, N. and Singh, K.N. 2011. Combining ability studies in wheat (*Triticum aestivum* L.) for genetic improvement under salt stress. *J. Wheat Res.*, 3 (2), 22–26.
- [52] Singh, M.K. Sharma, P.K. Tyagi, B.S. and Singh, G. 2014. Combining ability analysis for yield and protein content in bread wheat (*Triticum aestivum*). *Indian J. Agric. Sci.*, 84 (3), 328–336.
- [53] Kumar, A. Harshwardhan, H. Kumar, A. and Prasad, B. 2015. Combining ability and gene interaction study for yield, its attributing traits and quality in common wheat. *J. Appl. Nat. Sci.*, 7 (2), 927–934.
- [54] Kumar, J. Singh, S.K. and Singh, L. 2016. Estimates of general and specific combining ability for grain yield and other physiological characters in bread wheat under late sown condition. *Res. Environ. Life Sci.*, 9 (7), 784–789.
- [55] Yao, J. Zhao, D. Chen, X. Zhang, Y. and Wang, J. 2018. Use of genomic selection and breeding simulation in cross prediction for improvement of yield and quality in wheat (*Triticum aestivum* L.). *Crop J.*, 6, 353–365.

ارزیابی وراثت‌پذیری و برخی پارامترهای ژنتیکی برای صفات عملکرد و اجزای عملکرد گندم با استفاده از طرح دی‌آلل

حبیب اله سوقی^{۱*}، کمال پیغام‌زاده^۱، منوچهر خدارحمی^۲، مهدی نظری^۱

^۱ بخش تحقیقات علوم زراعی-باغی، مرکز تحقیقات و آموزش کشاورزی و منابع طبیعی استان گلستان، سازمان تحقیقات، آموزش و ترویج کشاورزی، گرگان، ایران
^۲ مؤسسه تحقیقات اصلاح و تهیه نهال و بذر، سازمان تحقیقات، آموزش و ترویج کشاورزی، تهران، ایران

*نویسنده مسئول: hab3asog@gmail.com

چکیده

گندم یکی از مهمترین گونه‌های خوراکی است که در تولیدات غذایی متعددی مورد استفاده قرار می‌گیرد. با افزایش رشد جمعیت جهانی نیاز به این منبع غذایی نیز رو به افزایش است. برنامه‌های اصلاح گیاهی، که به طور طبیعی منجر به ایجاد تنوع ژنتیکی می‌شود برای تولید گیاهان هیبرید با عملکرد بالا یا خصوصیات فیزیولوژیکی بهبود یافته بکار می‌رود تا عملکرد بیشتری تحت محیط‌های کشت مساوی حاصل گردد. موفقیت برنامه‌های اصلاح گیاهی به دسترسی والدین با تنوع ژنتیکی مناسب بستگی دارد. برای این منظور، پارامترهای ژنتیکی مرتبط با عملکرد و صفات مرتبط در ۸ ژنوتیپ گندم با نام‌های کوه‌دشت (P1)، مروارید (P1)، (P3) N-80-19، دریا (P4)، UR-82-17 (P5)، احسان (P6)، باکونورا (P7)، اترک (P8) و نتاج F₁ آنها مورد بررسی قرار گرفت. در این آزمایش طرح بلوک‌های کامل تصادفی با سه تکرار بکار برده شد. تجزیه داده‌ها نشان داد که ژنوتیپ‌ها و هیبریدهای F₁ آنها عملکرد دانه، عملکرد بیولوژیک، وزن هزار دانه، تعداد دانه در سنبله، وزن دانه در سنبله، ارتفاع گیاه، طول پدانکل و طول دومین میانگره را به طور معنی‌داری تحت تاثیر قرار داد. برای به دست آوردن GCA، SCA و پارامترهای ژنتیکی دیگر مدل دوم روش اول گریفینگ در نرم افزار SAS مورد استفاده قرار گرفت. در میان والدین، رقم احسان برای عملکرد دانه، وزن هزار دانه، وزن دانه در سنبله، ارتفاع گیاه و عملکرد بیولوژیک بیشترین مقدار GCA را داشت. تلاقی P₆ × P₇ دارای بیشترین ترکیب‌پذیری خصوصی برای صفات عملکرد دانه، وزن هزار دانه و ارتفاع گیاه داشت. بعلاوه، در میان صفات مورد بررسی وزن هزار دانه و طول پدانکل به ترتیب دارای بیشترین وراثت‌پذیری عمومی ($h^2=0.98$) و وراثت‌پذیری خصوصی ($H^2=0.62$) بودند. این نتایج نشان می‌دهد که تلاقی‌های منحصر به فرد دارای والدینی با ترکیب‌پذیری عمومی زیاد × کم هستند، در نتیجه در تلاقی‌ها بکارگیری والدین با قدرت ترکیب‌پذیری زیاد × زیاد ضروری نیست. در نتیجه، برای افزایش عملکرد می‌توان لاین‌های هموزیگوس بالقوه را از نسل‌های در حال تفکیک انتخاب کرد و از این نوع تلاقی می‌توان در کاربرد پدیده هتروزیس استفاده کرد.

کلمات کلیدی: قابلیت ترکیب‌پذیری عمومی، قابلیت ترکیب‌پذیری خصوصی، لاین‌های امیدبخش، روش دای‌آلل گریفینگ