



Original Article

Combining Ability, Gene Action, Yield, and Quality in Half-Diallel Bread Wheat

Fatih Karim Hama Ali*¹, Sherwan Ismael Tawfiq², Dliir Amin Sabir³

¹Food Science and Quality Control Department, Bakrajo Technical Institute, Sulaimani Polytechnic University, Sulaymaniyah, Iraq.

²Deptment of Biotechnology Crop Science College of Agriculture Eng. Science, University of Sulaimani, Sulaymaniyah, Iraq.

³Deptment of food science Quality Control Science College of Agri. Engin. Science, University of Sulaimani, Sulaymaniyah, Iraq.

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ABSTRACT

The study conducted to improve bread wheat genotypes with high grain yield, yield related traits, and quality. A half diallel mating design involving seven bread wheat parents (Maroof, Aras, Hsad, Alaa, Tamuz-2, Adana and Sabr Beg) and their 21 progenies were used to study the combining ability in bread wheat. Seven bread wheat (*Triticum aestivum* L.) parents and 21 F₁ crosses were evaluated using half-diallel analysis under RCBD with three replications. The parent Tamuz-2 emerged as the best general combiner for several yield attributes, whereas the cross 1x5 exhibited maximum for spike weight plant⁻¹, biological yield, and protein content. Cross 5x2 recorded maximum for grain weight spike⁻¹ and thousand grain weight, besides recording maximum grain yield. There is strong genetic diversity in many of these attributes. Though the additive and non-additive actions were significant, the latter predominated in many of the attributes. Suitable parent and cross combinations have been identified to be useful in future breeding work. The Analysis of variance reveal that the general combining ability (GCA) of the parents was significant for days to heading and spike length and highly significant for plant height, spike weight, grain number spike⁻¹, grain weight spike⁻¹, thousand grain weight, harvest index, biological weight plant⁻¹, protein content, and grain yield plant⁻¹, while the specific combining ability (SCA) effects of the crosses were highly significant for almost all of the traits. In particular, for the sike length, ($h_{b,s}^2$)=0.503 and ($h_{n,s}^2$)= 0.154; for grain yield plant⁻¹, ($h_{b,s}^2$)= 0.950 and ($h_{n,s}^2$)= 0.464. The high value of $h_{b,s}^2$ for biological yield per plant (0.981) pointed to the strong genetic influence, while the smaller ($h_{n,s}^2$) (0.474) indicated smaller additive variance, reducing selection efficiency.

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Keywords: Bread wheat, (general combining ability), (specific combining ability), yield and protein content.

1 Introduction

Bread wheat (*Triticum aestivum* L.) is a most important food crop that provides billions of calories and proteins. It helps playing a vital role in global food security. The world's population is expected to reach 10 billion by 2050, which would boost the need for wheat. This will be affected by shifting tastes for wheat-based foods. As a result, agricultural scientists and breeders need to come up with new ways to breed and grow wheat in order to increase yields ^[1,2]. Enhancing grain output and the several agronomic traits that accompany it is the primary objective of wheat breeding efforts; however, they also have other objectives. Kernel weight, plant height, drought resistance, and disease resistance are the most important characteristics, and these are becoming increasingly important as a result of climate change

and new pathogens. Breeders challenge to improve these traits to create wheat types that can withstand biotic and abiotic challenges and yield ^[3].

In bread wheat, the sum of squares is often split into parts for General Combining Ability (GCA) and Specific Combining Ability (SCA) when the variation for combining ability is analyzed. Studies demonstrate that both GCA and SCA effects are typically extremely significant, the findings of the study indicate that genotypic variation is highly significant in identifying the desirable traits of wheat. The notable impacts of both GCA and SCA demonstrate that particular genotype combinations and overall genotype performance are crucial for trait improvement. This knowledge can aid with breeding strategies by helping you choose the best genotypes and look into helpful hybrid combinations that can make wheat better ^[4,5]. Half-diallel Mating design is popular in breeding of wheat to examine parental line performance and crosses. The way is an efficient means of examining the combining ability and the control of the

* Corresponding author

E-mail address fatih.karim@spu.edu.iq (Instructor).

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genetic characteristics of yield and other associated traits. This method provides insights into gene functionality and aids in identifying optimal parental pairings that can yield varieties with enhanced features [16].

The study highlights the importance of gene effect, both additive and non-additive, in the development of yield and other related characteristics in bread wheat. An understanding of these genetic processes will help breeders to optimize parental choice and make efficient breeding programs to produce high performing and robust varieties of wheat [7].

The objective of the present study was to enhance genotypes of bread wheat breeds in terms of their high yield, traits related to yield, and quality through a half-diallel mating design which compared the combining ability of seven parents with 21 F₁ offspring. The study has also determined the important genetic characteristics affecting the yield and the adaptation status, and thus can be applied to guide practical breeding programs in wheat to produce productive, resilient, and more nutritionally enhanced types of wheat to ensure food security.

2 Materials and Methods

A half-diallel non-reciprocal mating scheme was used to produce 21 F₁ hybrids in the 2022-2023 seasons in which controlled emasculation and hand pollination of seven parental genotypes of bread wheat (*Triticum aestivum* L.) were performed. (Table 1) was used to get parental genotypes at the Directorate of central research in Iraq. This produced F₁ seeds, which were further developed to F₁ generation and tested in the 2023-2024 growing season at the College of Agriculture production farm, about 2 km outside the Sulaymaniyah center. The experiment was constituted in the randomized complete block design (RCBD) consisting of three replications. Plots were made up of three-meter-long rows, separated by a distance of 30 cm and 10 cm between plants. Agronomic procedures, such as plowing, application of compost, and weeding were effectively applied all through the experimental time. Estimation of general combining ability (GCA) and specific combining ability (SCA) effects on yield and yield-related traits was done using a half-diallel analysis of the following model: Statistical model for General Combining Ability (GCA) and Specific Combining Ability (SCA) in diallel cross analysis (Griffing, 1956). The governing equations and their corresponding boundary conditions are given as follows [8, 9].

Statistical model (Griffing, Method II) [7].

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e_{ij} \quad (i < j) \quad (1)$$

Where:

Y_{ij} = Observed performance of the hybrid (cross between the i th and j th parents.

μ = Overall mean of all genotypes.

g_i = General combining ability effect of the i th parent.

g_j = General combining ability effect of the j th parent.

s_{ij} = Specific combining ability effect of the cross $i \times j$.

e_{ij} = experimental error.

General Combining Ability variance; [9]:

$$\sigma_{GCA}^2 = \frac{MS_{GCA} - MS_e}{r(p+2)} \quad (2)$$

Specific Combining Ability variance; [9]:

$$\sigma_{SCA}^2 = \sigma_D^2 = \frac{MS_{SCA} - MS_e}{r} \quad (3)$$

Where:

σ_D^2 : Non-additive (dominance and epistasis) genetic variance.

Additive genetic variance (σ_A^2); [9]:

$$\sigma_A^2 = 2\sigma_{GCA}^2 \quad (4)$$

Where:

σ_A^2 : Additive genetic variance.

Genetic effects in diallel crosses. [9].

$$Y_{ij} = \mu + GCA_i + GCA_j + SCA_{ij} + e_{ij} \quad (5)$$

(5)

Where: Y_{ij} = performance of cross $i \times j$

$GCA_i + GCA_j$ = general combining ability effects.

SCA_{ij} = specific combining ability (non additive).

e_{ij} = error.

The average degree of dominance ($\bar{a}$); [8]:

$$\bar{a} = \sqrt{\frac{2\sigma_D^2}{\sigma_A^2}} = \sqrt{\frac{2\sigma_{SCA}^2}{2\sigma_{GCA}^2}} = \sqrt{\frac{\sigma_{SCA}^2}{\sigma_{GCA}^2}} \quad (6)$$

Heritability in broad-sense ($h_{b.s}^2$); [8]:

$$h_{b.s}^2 = \frac{\sigma_G^2}{\sigma_P^2} = \frac{\sigma_A^2 + \sigma_D^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2} = \frac{2\sigma_{GCA}^2 + \sigma_{SCA}^2}{2\sigma_{GCA}^2 + \sigma_{SCA}^2 + \sigma_e^2} \quad (7)$$

Heritability in narrow-sense heritability ($h_{n.s}^2$); [8]:

$$h_{n.s}^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_D^2 + \sigma_e^2} = \frac{2\sigma_{GCA}^2}{2\sigma_{GCA}^2 + \sigma_{SCA}^2 + \sigma_e^2} \quad (8)$$

Where:

$h_{b.s}^2$: Heritability in broad sense.

$h_{n.s}^2$: Heritability in narrow sense.

σ_{GCA}^2 : The variance of general combining ability.

σ_{SCA}^2 : The variance of specific combining ability.

σ_e^2 : The variance of experimental error (i.e., environmental variance)

σ_G^2 : Total genetic variance

σ_P^2 : Phenotypic variance (genetic and environmental variance)

To collect data, five plants were randomly sampled in each plot making fifteen plants per genotype. Data recorded were days to 50% heading, days to 50% maturity, plant height, number of tillers, spike length, spike weight, number of grains per spike, grain weight per spike, 1000-gram weight, harvest index, biological yield per plant, protein content and grain yield per plant. The lines of parents and F₁ hybrids were analyzed by analysis of variance (ANOVA), Twenty-one bread wheat hybrids were generated from a seven-parent half-diallel crossing matrix (Table 2).

The monthly minimum, maximum, and average temperatures (°C), alongside the total monthly rainfall (mm) recorded during the wheat growing season, are presented in (Table 3). The

statistical analyses were performed using XLSTAT version 2019.2.2, statistical and data analysis solution developed by Addinsoft.

Table 1: Seven Bread Wheat parental genotypes and their pedigree used in the study.

Number	Variety Name	Pedigree
1	Maroof	NAKAN/21MTNTK × TMM11ATNDA-2
2	Aras	SONORA 64× LERMA ROJO 64) × SENTACLENA
3	Hsad	AKI115N3A9T9CC1H/5K9A91H1TAABMT
4	Alaa	SEE1TMEA × 10
5	Tamuz-2	SABR BEG/MAXIBAC (RAD.)
6	Adana	118//S2/57-S2-SR7-S2
7	Sabr Beg	Local Variety

Table 2: Twenty-one Bread Wheat hybrids produced from seven genotypes using half-diallel cross.

No.	Hybrids	Diallel Crosses and Parental No.
1	Maaroof × Aras	1×2
2	Maaroof × Hsad	1×3
3	Maaroof × Alaa	1×4
4	Maaroof × Tamuz-2	1×5
5	Maaroof × Adana	1×6
6	Maaroof × Sabr Beg	1×7
7	Aras × Hsad	2×3
8	Aras × Alaa	2×4
9	Aras × Tamuz 2	2×5
10	Aras × Adana	2×6
11	Aras × Sabr Beg	2×7
12	Hsad × Alaa	3×4
13	Hsad × Tamuz 2	3×5
14	Hsad × Adana	3×6
15	Hsad × Sabr Beg	3×7
16	Alaa × Tamuz 2	4×5
17	Alaa × Adana	4×6
18	Alaa × Sabr Beg	4×7
19	Tamuz 2 × Adana	5×6
20	Tamuz 2 × Sabr Beg	5×7
21	Adana × Sabr Beg	6×7

Table 3: Qlyasan Location Monthly Weather Data season 2023-2024.

Months	Mini. Temp. (°C)	Max. Temp. (°C)	Avg. Temp. (°C)	Rainfall (mm)
October	16.2	27.7	21.9	9.3
November	10.7	20.1	15.4	78.9
December	6.9	16.4	11.7	59.1

January	5.4	13.4	9.4	97.7
February	5.0	13.1	9.1	196.5
March	7.7	17.5	12.6	144.6
April	15.8	27.2	21.5	38.6
May	16.3	27.8	22.1	99.6
Total rainfall				724.3

(Sulaimani Directorate of Meteorology and Seismology).

3 Results and Discussion

The analysis of variance in (Table 4) demonstrated that the mean square of the genotypes was significant for most of the evaluated traits, including days to %50 heading, plant height, number of tillers/plant, spike length, weight of spike/plant, number of grains/spikes, weight of grains/spike, 1000 grain weight, harvest index, biological yield/plant, protein content and grain yield/plant. In contrast days to %50 maturity showed only significant effect, The general combining ability (GCA) effects exhibited significant differences for several traits, reflecting the importance of additive gene action. GCA mean squares were highly significant for plant height, weight of spike, number of grains per spike, weight of grains per spike, 1000–grain weight, harvest index, biological yield per plant, protein content, and grain yield per plant. Meanwhile, days to 50% heading and spike length showed significant GCA effects, whereas days to 50% maturity and number of tillers per plant were non-significant, indicating a

relatively limited contribution of additive genetic effects for these traits ^[10].

Regarding specific combining ability (SCA), the mean squares were highly significant for days to 50% heading, plant height, weight of spike, number of grains per spike, weight of grains per spike, 1000–grain weight, Harvest Index, biological yield per plant, protein content, and grain yield per plant. while days to 50% maturity and number of tillers per plant spike length were non-significant ^[11,12].

These findings indicate that both additive (GCA) and non-additive (SCA) gene actions play important roles in controlling most yield and yield-related traits in bread wheat. The significant variability among genotypes and the combining ability effects suggest the presence of promising parental lines and cross combinations that can be effectively utilized in future wheat breeding programs aimed at improving yield potential and grain quality ^[13].

Table 4: Mean squares of variance analysis of traits.

S.O.V	d.f	DH	DM	PH	NT	SL	WS	NGS	WGS	TGW	H. I	BY	PC	GY
Block	2	1.190 *	10.750**	18.746n.s	0.126 n.s	4.761 **	11.668n.s	25.107n.s	0.005 n.s	1.887 n.s	1.15n.s	3.643 n.s	0.005 n.s	0.197 n.s
Gen.	27	2.372 **	2.737 *	141.691**	0.766 **	1.712 **	67.788**	415.277**	0.595 **	52.143**	31.831**	193.134**	0.782 **	29.827**
GCA	6	0.814 *	2.410 n.s	74.960**	0.300 n.s	1.234 *	47.595**	281.352**	0.489 **	24.597**	19.843**	121.322**	0.373 **	24.366**
SCA	21	0.784 **	0.484 n.s	39.308**	0.243 n.s	0.381 n.s	15.453**	97.590**	0.115 **	15.319**	7.972**	48.108**	0.229 **	5.821 **
Exp. Error	54	0.302	0.343	11.639	0.139	0.462	3.908	9.860	0.018	1.483	2.068	1.421	0.008	0.583

DH- Days to 50% heading, DM- Days to 50% maturity, PH- Plant height (cm), NT-Number of tillers, SL- Spike length(cm), WS- WS(g), NGS-NGS, WGS-weight of grains per spike(g), TGW-1000 grain weight, HI- Harvest index; BY- Biological yield per plant (g), PC protein content, GY- Grain yield per plant (g), *, ** significant at 5% and 1% levels, respectively.

The results shown in (Table 5) reveal a variety of agronomic attributes among distinct parental lines, highlighting both their genetic variability and potential for yield increase the same information was recorded by ^[4]. Days to heading, days to maturity, plant height, number of tillers, spike length, spike weight, number of grains per plant, 1000-grain weight, harvest index, protein content, and grain yield are among the important characteristics evaluated. Days to Heading, shown by a minimum day to heading of 106.333days and maximum biological of 31.885g for parent 2, can be useful for reducing the impact of late-season problems like heat or drought Findings analogous to the present study were reported by ^[1,14]. Parent 5 and parent 7 in

contrast, exhibited a maximum of 109.00 days, supporting the research results of ^[15]. Plant height Parent 5 had the tallest plants, measuring 100.67 cm. taller varieties are better for eliminating weeds and capturing sunlight, and their deeper root systems often make them more resistant to dry conditions Results corroborate those obtained by ^[16]. On the other hand, parent 6 was the shortest at 90.067 cm for plant height. The shorter types exhibit greater resistance to lodging and enhanced nutrient utilization, resulting in increased grain yields and facilitating mechanized harvesting Consistent findings were observed by ^[17]. Parent 3, with an average of 6.75 tillers, had the fewest tillers. This suggests that the plant had little branching, perhaps impacting its production capacity. Conversely, parent 4 had the highest number of tillers,

totaling 8.17, indicating superior productivity, a finding consistent with previous results ^[18].

Spike Length and Spike Weight, when it comes to yield, spike length is extremely significant. Parent 5 had the longest spikes at 12.67 cm, while Parent 4 had the shortest ones at 9.958 cm. Extended spikes can improve grain yield but may bend under excessive stress previously recorded by ^[3,19]. For spike weight, parent 5 again had the highest measurement at 42.01 g, and parent 7 had the lowest at 25.42 g. A high spike weight signifies improved nutrient absorption and enhanced plant vigor, which are associated with greater yield potential ^[20].

Total of grains per spike. Parent 4 had the maximum number of grains per spike at 75.667, and parent 2 had a lowest number at 46.00 grains. The significant number in parent 4 shows that it can develop well and has good conditions for growth, however the small quantity in parent 2 indicates that it is incapable of developing well and has weaker growth, indicating that it can produce less ^[21]. The greatest amount of grain per spike was 2.763g from parent 5, and the lowest was 1.223g from parent 7. Parent 4 had the highest 1000-grain weight at 45.877g, and parent 7 had the smallest amount of 1000-grain weight at 33.573g. A greater 1000-grain weight is linked to bigger, well-filled grains, which have significance for getting an effective yield. The fewer weight, on the other hand, suggests that pressures could be impacting grain fill ^[22]. Parent 7 had the highest value of protein with 13.500, while parent 6 had the lowest value with 11.663, The protein level has a big effect on the quality of the grain. Parent 5 had the greatest harvest index, at 32.923, and parent 6 had the lowest, at 19.836 in agreement with the findings of ^[23].

According to the results parent 5 had the highest grain production, which was an amazing 19.81g/plant. This means that it did better than other parents in many crucial areas for successful wheat

breeding. Similar trends were documented by ^[24]. This study highlights the significance of genetic diversity among parental lines and their prospective contributions to enhancing yield and quality traits in wheat. Future research may focus on the interrelationships among these elements to optimize breeding strategies effectively. This study analyzed 21 hybrids, uncovering substantial prospects for enhancing traits vital for future breeding initiatives focused on identifying new genotypes with superior quality and yield. The hybrid (1×2) had the lowest values for important traits like the number of tillers per spike (6.417), the length of the spike (9.833 cm), and the number of grains per spike (36.667). The cross (1×3), on the other hand, contained the least amount of protein, at 11.800%. Hybrid (1×5) had highest values for plant height and grain yield with 118.667 and 18.520 respectively. Cross (1×6), on the contrary hand, needed the longest for maturity (109 days) and had the lowest value for spike weight (26.833 g), weight of grain per spike weight (1.283 g), 1000-grain weight (31.683 g), and grain yield (8.007 g). furthermore, hybrid (2×3) recorded the least days to heading (106 days), but cross (2×4) demonstrated the largest protein content (13.667%) and the shortest days to maturity (151 days). Hybrid (2×5) also had the greatest weights for 1000-grain weight (49.430 g) and weight of grain per spike (3.077 g). Cross (3×6) had the lowest plant height with (94.200 cm) and crosse (3×7) had the lowest harvest index with (21.216), whereas cross (4×7) had the highest numbers of tillers per plant (8.417) and maximum value for biological yield per plant with (47.313) g. Finally, hybrid (5×6) had the longest spike length (12.583 cm) and the greatest number grains per spike (82.000), but hybrid (5×7) and hybrid (6×7) had a long time to maturity with (154.667 days). The highest harvest index was recorded by cross (6×7) with (31.422). The results show that these hybrids may differ in important agricultural features and have a lot of potential. This supports future breeding efforts to enhance the efficiency of crops In line with the present findings, previous studies by ^[1,25,26].

Table 5: Mean of the studied characters for parents and their F₁.

Crosses	DH	DM	PH	NT	SL	WS	NGS	WGS	TGW	H. I	BY	PC	GY
1×2	106.667	151.667	106.600	6.417	9.833	28.260	36.667	1.517	38.010	24.340	26.904	12.400	9.450
1×3	107.000	151.667	115.333	8.000	11.375	29.687	45.333	2.037	42.400	24.690	31.648	11.800	10.523
1×4	106.583	153.667	102.133	7.583	11.417	36.060	52.000	2.530	41.897	29.168	29.081	12.967	14.427
1×5	107.333	153.000	118.667	7.750	11.708	41.510	54.333	1.950	38.240	29.477	33.678	12.500	18.520
1×6	109.000	153.000	108.867	7.417	11.542	26.833	55.333	1.283	31.683	20.842	27.436	12.300	8.007
1×7	106.667	153.667	104.800	7.583	10.500	37.893	44.333	1.553	32.683	25.216	24.238	12.400	13.693
2×3	106.000	153.667	99.267	6.667	10.708	29.713	54.333	2.130	41.233	27.301	27.898	12.400	10.880
2×4	107.333	151.000	110.667	6.583	11.375	36.353	42.000	2.357	38.440	22.490	26.627	13.667	12.867
2×5	106.333	152.667	101.133	7.250	11.792	35.430	72.000	3.077	49.430	29.329	30.843	12.733	14.657
2×6	106.333	153.667	105.133	7.917	10.583	27.033	49.333	1.907	44.083	23.022	33.406	12.000	9.510
2×7	106.000	153.000	103.600	7.583	10.792	35.940	58.333	2.120	43.783	29.661	28.417	13.100	15.063
3×4	106.667	154.333	100.467	7.167	10.583	34.117	54.000	2.433	43.053	27.162	29.554	12.200	13.410
3×5	107.000	152.667	97.933	6.917	10.125	29.867	54.333	1.863	40.990	25.742	29.095	12.667	10.280
3×6	107.667	153.333	94.200	6.917	10.250	33.910	54.333	1.877	37.517	27.775	24.820	12.133	12.880
3×7	107.667	153.333	104.533	7.167	10.000	28.630	54.667	1.633	38.323	21.216	27.850	12.267	8.987
4×5	107.000	153.667	107.933	7.250	11.917	39.430	74.667	2.313	48.220	29.281	22.193	12.833	16.887
4×6	107.333	153.333	106.133	6.667	10.542	33.843	61.000	2.033	40.627	26.473	22.109	13.200	13.267
4×7	108.000	154.333	109.267	8.417	11.625	35.760	59.333	2.097	43.447	29.982	47.313	12.367	16.000

5×6	108.667	152.667	101.067	7.000	12.583	39.633	82.000	2.247	38.693	27.436	32.800	12.733	17.087
5×7	106.333	154.667	103.667	6.750	11.667	32.363	76.667	2.680	43.010	30.926	32.386	12.300	14.253
6×7	107.333	154.667	101.867	6.917	11.250	31.953	39.333	2.000	42.830	31.422	27.503	13.167	13.340
1	107.333	154.667	99.600	7.250	11.208	28.867	69.000	2.123	41.547	26.781	26.729	12.100	10.233
2	106.333	153.000	100.400	7.083	10.167	30.740	46.000	2.220	42.467	26.791	31.885	12.733	11.277
3	107.667	154.667	93.667	6.750	11.000	28.860	49.667	1.297	37.827	25.507	28.396	12.100	10.223
4	106.667	154.667	90.800	8.167	9.958	29.903	75.667	2.353	45.877	26.879	30.042	11.700	10.930
5	109.000	154.000	100.667	7.500	12.667	42.013	66.667	2.763	37.910	32.923	31.778	12.633	19.810
6	107.667	153.667	90.067	7.333	10.750	25.987	52.000	1.870	43.300	19.836	31.675	11.633	9.183
7	109.000	153.667	91.400	7.000	11.208	25.420	54.667	1.223	33.573	25.512	28.788	13.500	8.323
LSD p≤0.05)	0.899	1.182	4.164	0.828	1.113	3.236	5.140	0.220	1.993	2.354	1.750	0.150	1.250

Heterosis values for F₁ hybrids of some yield traits

(Table 6) shows the data analysis for heterosis value cross (1×6) shows the highest positive heterosis value for days of maturity at 1.395, while recorded the minimum negative value for each trait (weight of grains per spike, 1000 grain weight and Grain yield per plant with -35.726, -25.316 and -17.528 respectively, the same results were obtained by^[1]. while the lowest negative value for days to heading was recorded by 5×7 at -2.466. Cross (6×7) recorded the highest positive heterosis value for days of maturity with (0.651), while the lowest negative heterosis value recorded by (1×3) for days to maturity with (-1.940). Hybrid (4×7) recorded the highest positive heterosis for Plant height at 19.941 and cross (2×5) recorded the lowest positive for Plant height at 0.597 this result indicating a significant increase that could boost biomass and yield but may heighten lodging risk, requiring dwarfing gene integration. Its lowest positive heterosis suggests a more moderate height gain, offering stability and adaptability, making it a versatile option for breeders to target either taller, high-yielding types or balanced. Cross (1×3) recorded the highest heterosis value for Number of tillers with 14.286. Hybrid (1×7) obtained the highest positive heterosis value for weight of spike and biological yield per plant with (39.605 and 51.763)

respectively. Cross (2×4) obtained the highest positive heterosis value for Spike length and protein content with 13.043 and 11.869 while, recorded the lowest negative heterosis value for harvest index with -16.190. For 1000 grain weight cross (2×5) recorded the highest positive heterosis value with 22.996 while recorded the lowest heterosis value with 0.597 for Plant height the similar results recorded by^[3]. Cross (3×5) noted the lowest negative heterosis value for Spike length and weight of spike with -14.437 and -15.718. Hybrid (4×6) recorded the lowest negative heterosis value for Number of tillers with -13.978. For Plant height and Grain yield per plant, the highest positive heterosis value were recorded by (4×7) with 19.941 and 66.205 for plant height and grain yield. Cross (5×6) recorded the highest heterosis value for number of grains per spike with 38.202. hybrid 5×7 recorded the highest positive heterosis value for weight of grains per spike with 34.448, while recorded the lowest negative heterosis for days of heading and protein content with -2.446 and -5.867 similar results were obtained by^[17]. Hybrid (6×7) recorded the highest positive heterosis value for Days to maturity and harvest index with 0.651 and 38.580.

Table 6: Heterosis values for F₁ hybrids of some yield traits.

Crosses	DH	DM	PH	NT	SL	WS	NGS	WGS	TGW	H. I	BY	PC	GY
1×2	-0.156	-1.408	6.600	-10.465	-7.992	-5.178	-36.232	-30.161	-9.514	-9.133	-3.490	-0.134	-12.134
1×3	-0.465	-1.940	19.352	14.286	2.439	2.853	-23.596	19.103	6.837	-5.563	8.800	-2.479	2.884
1×4	-0.623	-0.647	7.283	-1.622	7.874	22.716	-28.111	13.031	-4.152	8.713	25.605	8.964	36.336
1×5	-0.770	-0.864	18.509	5.085	-1.920	17.128	-19.902	-20.191	-3.746	-1.256	27.536	1.078	23.289
1×6	1.395	-0.757	14.798	1.714	5.123	-2.163	-8.540	-35.726	-25.316	-10.582	-9.097	3.652	-17.528
1×7	-1.387	-0.324	9.738	6.433	-6.320	39.605	-28.302	-7.171	-12.984	-3.560	51.763	-3.125	47.584
2×3	-0.935	-0.108	2.302	-3.614	1.181	-0.291	13.589	21.137	2.707	4.405	-3.124	-0.134	1.209
2×4	0.782	-1.842	15.760	-13.661	13.043	19.892	-30.959	3.061	-12.976	-16.190	38.219	11.869	15.881
2×5	-1.238	-0.543	0.597	-0.571	3.285	-2.602	27.811	23.478	22.996	-1.768	-2.639	0.394	-5.704
2×6	-0.623	0.217	10.396	9.827	1.195	-4.689	0.680	-6.764	2.798	-1.251	-6.843	-1.505	-7.038
2×7	-1.548	-0.217	8.029	7.692	0.975	27.991	15.894	23.136	15.159	13.418	34.306	-0.127	53.707
3×4	-0.467	-0.216	8.927	-3.911	0.994	16.115	-13.830	33.333	2.871	3.699	22.500	2.521	26.789
3×5	-1.231	-1.080	0.789	-2.924	-14.437	-15.718	-6.590	-8.210	8.243	-11.889	-20.492	2.426	-31.543
3×6	0.0001	-0.541	2.540	-1.775	-5.747	23.654	6.885	18.526	-7.511	22.509	7.517	2.247	32.738

3×7	-0.615	-0.541	12.968	4.242	-9.944	5.490	4.792	29.630	7.348	-16.832	15.273	-4.167	-3.091
4×5	-0.773	-0.432	12.744	-7.447	5.341	9.655	4.918	-9.577	15.102	-2.075	14.357	5.479	9.868
4×6	0.156	-0.541	17.361	-13.978	1.811	21.107	-4.439	-3.710	-8.885	13.340	18.486	13.143	31.919
4×7	0.155	0.108	19.941	10.989	9.843	29.276	-8.951	17.241	9.369	14.453	43.965	-1.852	66.205
5×6	0.308	-0.758	5.977	-5.618	7.473	16.569	38.202	-3.022	-4.708	4.006	16.885	4.945	17.866
5×7	-2.446	0.542	7.949	-6.897	-2.269	-4.014	26.374	34.448	20.336	5.847	-1.505	-5.867	1.327
6×7	-0.923	0.651	12.270	-3.488	2.467	24.316	-26.250	29.310	11.430	38.580	6.423	4.775	52.399

(Table 7) showed that all traits exhibited an average degree of dominance greater than unity, ranging from 1.377 for spike length to 3.734 for number of tillers. The level of

dominance of grain yield per plant was 1.447 but the biological yield (BY) and protein content was 1.883 and 2.345 respectively. The results provide strong evidence of over-dominance gene expression, which has shown the importance of non-additive effects and supported the usage of recurrent selection or hybrid-focused breeding methods to enhance yield. The broad-sense heritability ($h^2_{b.s}$) estimates were broadly high with a range of 0.981 to 0.503 indicating biological yield to spike length. High $h^2_{b.s}$ values for yield-related traits such as Grain yield per plant (0.950), 1000 grain weight (0.932), for number of grains per spike

(0.941), and protein content (0.973) indicate that genetic factors largely control phenotypic expression.

In contrast, narrow-sense heritability ($h^2_{n.s}$) estimates were comparatively low to moderate, with values ranging from 0.085 for Number of tillers to 0.474 for biological yield per plant. Grain yield per plant exhibited a moderate $h^2_{n.s}$ value of 0.464, suggesting that although genetic control is strong, only a limited proportion of the total variance is due to additive effects. The large difference between $h^2_{b.s}$ and $h^2_{n.s}$ across traits further confirms the substantial contribution of dominance and epistatic interactions. This means the trait involves more gene interactions, so breeding strategies like hybridization creating hybrids to exploit heterosis or "hybrid vigor" are more effective for improvement [27,28].

Table 7: Estimation of some genetic parameters for the studied characters.

Genetic Parameters	DH	DM	PH	NT	SL	WS	NGS	WGS	TGW	H. I	BY	PC	GY
MSe'	0.101	0.174	3.969	0.085	0.154	1.303	3.287	0.006	0.494	0.689	0.474	0.003	0.194
σ^2_{gca}	0.047	0.031	1.567	0.004	0.040	1.715	10.299	0.018	0.893	0.709	4.476	0.014	0.895
$\sigma^2_{sca} = \sigma^2_D$	0.176	0.238	14.512	0.059	0.076	4.717	31.434	0.036	4.942	2.428	15.878	0.075	1.876
$\frac{\sigma^2_{gca}}{\sigma^2_{sca}}$	0.264	0.129	0.108	0.072	0.528	0.363	0.328	0.493	0.181	0.292	0.282	0.182	0.477
σ^2_A	0.093	0.061	3.134	0.008	0.080	3.429	20.597	0.036	1.785	1.419	8.952	0.027	1.791
$\bar{a}$	1.945	2.781	3.043	3.734	1.377	1.659	1.747	1.425	2.353	1.850	1.883	2.345	1.447
$h^2_{b.s}$	0.728	0.632	0.816	0.442	0.503	0.862	0.941	0.923	0.932	0.848	0.981	0.973	0.950
$\sqrt{h^2_{n.s}}$	0.101	0.130	0.145	0.085	0.154	0.363	0.372	0.458	0.247	0.313	0.474	0.260	0.464

Conclusion

The combining ability test of the F_1 generation of bread wheat showed that there was extensive genetic diversity in breeding parents as well as between parents and crosses in terms of yield, yield characteristics and protein level as the half-diallel method proved to be useful. Extensive segregation was indicated by great variation in genotype, which offered good chances of effective selection. None of the models could be excluded since both GCA and SCA played important roles in expressing traits, which showed additive and dominance effects. The importance of non-additive gene action was confirmed by the greater role of SCA on large yield traits. A number of F_1 hybrids were better than parents, which means that there was transgressive segregation. The better parents and crosses were identified that can serve as a valuable material to the future wheat improvement, and the selection of the advanced generation is suggested to create the genotypes with high yields and qualities.

References

- [1] Reynolds, M.P., Borlaug, N.E. Impacts of breeding on international collaborative wheat improvement. *J. Agric. Sci.* **144**, 3–17, doi:10.1017/S0021859606005867, (2006b).
- [2] Krishnappa, G., Tyagi, B.S., Gupta, V., Gupta, A., Venkatesh, K., Kamble, U.R., R. S., Singh, G., Singh, G.P. Wheat breeding. In *Fundamentals of field crop breeding*. Springer Nature Singapore, Singapore, doi:10.1007/978-981-16-9257-4_2, (2022).
- [3] Khobra, R., Sareen, S., Meena, B.K., Kumar, A., Tiwari, V., Singh, G.P. Exploring the traits for lodging tolerance in wheat genotypes: a review. *Physiol. Mol. Biol. Plants* **25**, 589–600, doi:10.1007/s12298-018-0629-x, (2019).
- [4] El Hanafi, S., Bendaou, N., Kehel, Z., Sanchez-Garcia, M., Tadesse, W. Phenotypic evaluation of elite spring bread wheat genotypes for hybrid potential traits. *Euphytica* **216**, 168, doi:10.1007/s10681-020-02695-7, (2020).
- [5] Philipp, N., Weichert, H., Bohra, U., Weschke, W., Schulthess, A.W., Weber, H. Grain number and grain yield distribution along the spike remain stable despite breeding for high yield in winter wheat. *PLoS ONE* **13**, e0205452, doi: 10.1371/journal.pone.0205452, (2018).

- [6] Hassan, M.K., Al-Jubouri, J.M.A. Genetic analysis of combining ability and genetic parameters of half diallel crosses of bread wheat (*Triticum aestivum* L.). *IOP Conf. Ser.: Earth Environ. Sci.* **1262**, 052038, doi:10.1088/1755-1315/1262/5/052038, (2023).
- [7] Ahmad, A., Gupta, R.K. Identification of heterotic cross combinations for grain yield and associated traits in bread wheat (*Triticum aestivum* L.). *Agric. Res. J.* **61**, 311–317, doi:10.5958/2395-146X.2024.00040.1, (2024).
- [8] Falconer, D.S. *Introduction to quantitative genetics*. Pearson Education India, India, (1996).
- [9] Griffing, B. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* **9**, 463–493, doi:10.1071/B19560463, (1956).
- [10] Mohammadi, R. Breeding for increased drought tolerance in wheat: a review. *Crop Pasture Sci.* **69**, 223–241, doi:10.1071/CP17387, (2018).
- [11] Rharrabti, Y., Villegas, D., Garcia del Moral, L.F., Aparicio, N., Elhani, S., Royo, C. Environmental and genetic determination of protein content and grain yield in durum wheat under Mediterranean conditions. *Plant Breed.* **120**, 381–388, doi:10.1046/j.1439-0523.2001.00628.x, (2001).
- [12] Singh, C., Yadav, S., Khare, V., Gupta, V., Kamble, U.R., Gupta, O.P., Kumar, R., Saini, P., Bairwa, R.K., Khobra, R., Sheoran, S., Kumar, S., Kurhade, A.K., Mishra, C.N., Gupta, A., Tyagi, B.S., Ahlawat, O.P., Singh, G., Tiwari, R. Unraveling the secrets of early-maturity and short-duration bread wheat in unpredictable environments. *Plants* **13**, 2855, doi:10.3390/plants13202855, (2024).
- [13] Reynolds, M., Foulkes, M.J., Slafer, G.A., Berry, P., Parry, M.A.J., Snape, J.W., Angus, W.J. Raising yield potential in wheat. *J. Exp. Bot.* **60**, 1899–1918, doi:10.1093/jxb/erp016, (2009).
- [14] Moghaddam, M., Ehdaie, B., Waines, J.G. Genetic variation and interrelationships of agronomic characters in landraces of bread wheat from southeastern Iran. *Euphytica* **95**, 361–369, doi:10.1023/A:1003045616631, (1997).
- [15] Pretini, N., Alonso, M.P., Vanzetti, L.S., Pontaroli, A.C., González, F.G. The physiology and genetics behind fruiting efficiency: a promising spike trait to improve wheat yield potential. *J. Exp. Bot.* **72**, 3987–4004, doi:10.1093/jxb/erab080, (2021).
- [16] Mohammadi, M., Mirlohi, A., Majidi, M.M., Soleimani Kartalaei, E. Emmer wheat as a source for trait improvement in durum wheat: a study of general and specific combining ability. *Euphytica* **217**, 64, doi:10.1007/s10681-021-02796-x, (2021).
- [17] Khan, H., Krishnappa, G., Kumar, S., Mishra, C.N., Parkash, O., Rathore, A., Das, R.R., Yadav, R., Krishna, H., Bishnoi, O.P., Sohu, V.S., Sendhil, R., Yadav, S.S., Singh, G., Singh, G.P. Genetic gains in grain yield in wheat (*Triticum aestivum* L.) cultivars developed from 1965 to 2020 for irrigated production conditions of northwestern plains zone of India. *Cereal Res. Commun.* **51**, 437–446, doi:10.1007/s42976-022-00293-y, (2023).
- [18] Reynolds, M., Foulkes, J., Furbank, R., Griffiths, S., King, J., Murchie, E., Parry, M., Slafer, G. Achieving yield gains in wheat. *Plant Cell Environ.* **35**, 1799–1823, doi:10.1111/j.1365-3040.2012.02588.x, (2012).
- [19] Fouad, H., Mohamed, M., Salim, M., Mohiy, M., Abd El-Mageed, M. Half diallel analysis and heat stress tolerance indices for grain yield in bread wheat. *J. Plant Prod.* **13**, 763–773, doi:10.21608/jpp.2022.161348.1168, (2022).
- [20] Pour-Aboughadareh, A., Kianersi, F., Pocza, P., Moradkhani, H. Potential of wild relatives of wheat: ideal genetic resources for future breeding programs. *Agronomy* **11**, 1656, doi:10.3390/agronomy11081656, (2021).
- [21] Patel, P.U., Patel, B.C., Sidapara, M.P., Sharma, D.D. Combining ability and gene action studies for yield and its component traits in bread wheat (*Triticum aestivum* L.). *Int. J. Curr. Microbiol. Appl. Sci.* **9**, 2463–2469, doi:10.20546/ijcmas.2020.905.282, (2020).
- [22] Kumar, P., Nagar, S.S., Singh, C., Gupta, V., Singh, G., Tyagi, B. Assessment of heterosis and inbreeding depression for agro-morphological traits in bread wheat. *Wheat Barley Res.* **11**, doi:10.25174/2249-4065/2019/89648, (2019).
- [23] Tadesse, W., Sanchez-Garcia, M., Assefa, S.G., Amri, A., Bishaw, Z., Ogbonnaya, F.C., Baum, M. Genetic gains in wheat breeding and its role in feeding the world. *Crop Breed. Genet. Genom.* **1**, e190005, doi:10.20900/cbagg20190005, (2019).
- [24] Hossain, A., Skalicky, M., Brestic, M., Maitra, S., Ashraf Alam, M., Syed, M.A., Hossain, J., Sarkar, S., Saha, S., Bhadra, P., Shankar, T., Bhatt, R., Kumar Chaki, A., EL Sabagh, A., Islam, T. Consequences and mitigation strategies of abiotic stresses in wheat (*Triticum aestivum* L.) under the changing climate. *Agronomy* **11**, 241, doi:10.3390/agronomy11020241, (2021).
- [25] Al-Mafarji, T.R.Th., Al-Jubouri, J.M.A. Combining ability and gene action of half diallel crosses in bread wheat (*Triticum aestivum* L.). *IOP Conf. Ser.: Earth Environ. Sci.* **1262**, 052027, doi:10.1088/1755-1315/1262/5/052027, (2023).
- [26] Sulaiman, F.S., Aziz, J.M., Ismail, N.B. Genetic study of some drought tolerance indicators in the first generation of durum wheat (*Triticum durum* Desf.). *Passer J. Basic Appl. Sci.* **5**, 362–370, doi:10.24271/PSR.2023.395923.1323 (2023).
- [27] Ahmad, A., Gupta, R.K. Combining ability for yield and yield-associated traits in wheat (*Triticum aestivum* L.). *Electron. J. Plant Breed.* **15**, 526–531, doi:10.37992/2024.1502.041, (2024).
- [28] Krystkowiak, K., Adamski, T., Surma, M., Kaczmarek, Z. Relationship between phenotypic and genetic diversity of parental genotypes and the specific combining ability and heterosis effects in wheat (*Triticum aestivum* L.). *Euphytica* **165**, 419–434, doi:10.1007/s10681-008-9761-y, (2009).