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Coinheritance Studies of Yield and Yield Related Traits in Wheat (*Triticum Aestivum* L.) Preliminary Lines

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ABSTRACT

A field trial was performed to explore the genetic diversity and coheritability among the 64 bread wheat genotypes. These lines/genotypes were analyzed for days to heading, days to maturity, plant height, flag leaf area, spikelet Spike-1, grain per spike, thousand-grain weight, and grain yield. Based on the mean performance, the best genotype for early maturity was CCRIA1-10, CCRIA1-1, and CCRIA1-11. Likewise, for the flag leaf area, desirable genotypes were CCRIA1-16 and CCRIA1-27, and for grain spike-1, CCRIA1-28 and CCRIA1-22. In addition, the best genotypes for 1000-grain weight were CCRIA1-64 and CCRIA1-37. The highest genotypic and phenotypic coefficients of variation (PCV = 1054.40%, GCV = 446.68%) were recorded for grain yield, followed by grain spike-1 (PCV = 125.29 and GCV = 123.39). The highest heritability (0.97) was indicated by spike weight and grains spike-1 (0.97), while plant height (0.58), 1000 grain weight (0.44), and flag leaf area (0.31) showed moderate heritability. The lowest heritability estimates were recorded for the length of the peduncle (0.01), length of spikes (0.13), grain yield (0.18), days to heading, and spikelet spike-1 (0.25). High coheritability was observed among day to maturity and spike weight (0.99), on the contrary, minimum coheritability was observed for the flag leaf area with heading (0.12). The most desired inheriting pairs were spikelet spike-1 with grains spike-1 (0.97), weight of spike with spikelet spike-1 (0.92), and flag leaf area with spike weight (0.86), spike length with grains spike-1, spike weight with grains spike-1 and flag leaf area with grains spike-1.

INTRODUCTION

One of the widely cultivated varieties of wheat is bread wheat (*Triticum aestivum* L) [1], which is allohexaploid, having six sets of chromosomes from different species. Wheat is a cereal grain that is commonly farmed for its seeds worldwide, is the world's third-largest cereal food crop, is the most productive, and has the most planted area of any cereal crop globally [2]. Over 95% of the wheat produced worldwide is bread wheat, planted on over 218.22 million hectares worldwide, with a

predicted total yield of 765.53 million tons in the 2018-2019 cropping season [3]. Compared to other grain crops, wheat has a protein level of 14%. It provides about 20% of the world's population's nutritional sources in addition to being a major source of carbohydrates and calories, wheat is also a rich source of several other nutrients, including dietary fibers, proteins, vitamins (especially B vitamins), and phytochemicals that are vital to overall health [4].



In Pakistan, wheat provides 1.8% of the GDP and 7.8% of the value of agriculture; there are more than 22 million acres dedicated to its production. The amount of wheat produced decreased by 3.9 percent between 2021 and 2022, from 27.464 million tons to 26.394 million tons. Wheat contributed 10% of agricultural value added and 2.1% of GDP (MINFA, 2014-15). One of the government's top initiatives is a program to increase wheat self-sufficiency.

The productivity of an area's agriculture is significantly impacted by climatic factors. The significant limiting factors that have an important influence on the growth of the plants are soil moisture and water accessibility. Water is typically provided to plants through irrigation or rainfall (rainfed). In both irrigated and non-irrigated areas of Pakistan, wheat is grown as the main cereal crop [5]. The demand for food products manufactured from wheat is due to factors such as the world's population, per capita income, and changing trends of food consumption. However, the annual productivity growth in wheat during the Green Revolution and the years that followed has been largely attributed to advances in plant breeding tools and techniques, generally through traditional procedures and agronomical approaches.

Genetic diversity plays a critical role in increasing crop production in wheat breeding programs, while lack of variety limits plant improvement choices. The complex polygenic trait of yield is regulated by multiple factors. Several genetic features that are essential to improving yield have a direct or indirect impact on the genetic

architecture of economic yield. In wheat genetics, the study of combined inheritance of several traits is known as coinheritance, which is a vital approach in wheat genetics. Heritability and genetic progress are complementary features, according to [6]. Thus, the current study objectives were to estimate genetic diversity, yield heritability, and coheritability.

MATERIAL AND METHODS

Experimental material consists of 64 (62 advance wheat lines + 2 wheat checks) sown in an alpha lattice design using two replicates at the Cereal Crop Research Institute (CCRI), Pirsabak, and Nowshera for morpho-physiological characteristics evaluation and screening during rabi season 2022–23. Every tested genotype was an experimental plot with four rows, each two meters long and 25 cm apart from the others. The evaluation of genetic diversity and morpho-physiological impact was directed by the study of several wheat traits. Eight parameters were determined during the current study: days to heading, days to maturity, plant height, flag leaf area, spikelet Spike⁻¹, grain per spike, thousand-grain weight, and grain yield.

Statistical Analysis

Data analysis was performed using Steel and Torri's (1980) suggested methodology. The least significant difference (LSD) test was used to separate the means. Using the TNAU STAT program, ANOVA, ANCOVA, and co-heritability among traits were calculated.

Table 1

ANOVA outline for 64 genotypes in 8 × 8 Alpha Lattice design. (REPS=Replication, RCB=Randomized complete block, EMS=Error mean square, MS=Mean square, F value=Fisher value)

Source of Variance	Degree of freedom	MS	F-Value
REPS	(r-1) = 1	RMS	RMS/EMS
Genotypes (unadjusted)	(g-1) = 63	G _{unadj} .MS	G _{unadj} .MS/ EMS
Blocks within Reps/ Block	r(b-1) = 14	B _{w/n} RMS	B _{w/n} RMS/ EMS
Genotypes (adjusted)	(g-1) = 63	G _{adj} .MS	G _{adj} .MS/ EMS
RCB	(g-1) = 63	--	
Intra block error	(b ² -1) (b-1) = 49	EMS	
Total	(gr-1) = 128	--	

Table 2

Analysis of covariance. (Where, RMP = Replication means the product, GMP= Genotypes mean product, and EMP= Error mean product)

Source of Variance	Degree of freedom	Cross Product	Mean Product	Effective F-test
Replication	(r-1) = 1	RCP	RMP=RCP/Rdf	RMP/ EMP
Genotypes	(g-1) = 63	GCP	GMP= GCP/Gdf	GMP/ EMP
Error	(g-1) (r-1) = 63	ECP	EMP= ECP/Edf	----

Total	(gr-1) = 127
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Replication Cross Product (RCP) = (Replication total (X_1, X_2)/g)-Correction Factor

Genotype Cross Product (GCP) = (Genotype total (X_1, X_2)/r)-Correction Factor

Total Cross Product (TCP) = (Total observation (X_1, X_2))-Correction Factor

Error Cross Product (ECP) = TCP-RCP-GCP

Where, X_1 = Trait 1 X_2 = Trait 2

Co-variances estimation for estimating co-heritability among traits:

Genetic Covariance = $\sigma_g (X_1X_2) = (GMP-EMP)/r$
Environmental/Error Covariance = σ_e

(X_1X_2) = EMP

Phenotypic Covariance = $\sigma_p (X_1X_2) = \sigma_g (X_1X_2) + \sigma_e (X_1X_2)$

Co-heritability = $Co-h^2 (X_1X_2) = \sigma_g(X_1X_2) / \sigma_p(X)$

RESULTS AND DISCUSSION

To evaluate genotype variability, heritability, and coinheritance, 64 advanced wheat lines were used. Data were gathered for days to heading (DH), days to maturity (DM), plant height (PH), flag leaf area (FLA), peduncle length (PL), spike length (SL), spike weight (SW), grains spike⁻¹ (GS), thousand-grain weight (TGW), spikelet spike⁻¹ (SPS) and grain yield (GY).

The number of heading days among advance lines of spring wheat varied from 109 to 127 days. The least significant difference at 5% among tested wheat genotypes for heading interval was 8 days. The same findings were also reported by [7] who found that the heading interval of the examined wheat genotypes varied significantly. phenotypic coefficient of variation and genotypic coefficient of variation were found for days to heading (42.08) and (21.20).

The average number of maturity days for advanced wheat genotypes was 163.0 days, with a range of 159 to 166 days. The least significant difference was 5% among the tested wheat genotypes for days to maturity. Our results are also confirmed by [8] as they observed significant variation among 64 bread wheat genotypes. The phenotypic coefficient of variation and genotypic coefficient of variation were found for days to maturity (12.76) and (7.00).

Genotypes for plant height are highly significant and were noted with a 5.7% coefficient. The least significant difference at 5% among tested genotypes for plant height was 12.0 cm. Our results were confirmatory with [9] as they showed a high significant variance for plant height by using a randomized complete block design with three replications. phenotypic coefficient of variation and genotypic coefficient of variation was found for plant height was (89.94) and (68.46).

Flag leaf area showed highly significant differences with a Coefficient of variation was 16.2%). Thus, the flag leaf area ranged from 19.1 to 36.8 cm² with an average of 27.1 cm². Similar results about genetic variation of flag leaf area in wheat were also revealed by [10] for 24 tested wheat genotypes. The least significant difference for flag leaf area at 5% was 8.8 cm². phenotypic coefficient of variation and genotypic coefficient of variation for flag leaf area were found (101.16) and (101.16). Same result was also observed by [18].

The coefficient of variation for spike length was 11.0%. The wheat genotypes average spike length was 10.8 cm, with a variation of 8.3 cm to 12.8 cm among the genotypes. Current findings for spike length were also supported by ([11]. phenotypic coefficient of variation and genotypic coefficient of variation for spike length were found (38.86) and (14.18).

average spikelets spike⁻¹ was 19.4 recorded, while spikelets spike⁻¹ varied in number from 14 to 24 among wheat advance lines. The least significant difference at 5% for spikelets spike⁻¹ was 3.7. These results are in accord with those obtained by [11] who found spikelets spike⁻¹ with highly significant differences among genotypes. phenotypic coefficient of variation and genotypic coefficient of variation for spikelets spike⁻¹ was found (47.77) and (23.94).

Among wheat genotypes spike weight ranged from 0.4 to 4.2 g with 1.4 g average weight. The same results were also reported by [8] who evaluated 64 wheat genotypes during the 2021 main cropping season. The least significant difference in spike weight was 0.3 g. phenotypic coefficient of variation and genotypic coefficient of variation spike weight were found (58.66) and (57.65).

The coefficient of variation was 3.2% for grains spike⁻¹. Grain spike⁻¹ among wheat genotypes ranged from 28.7 to 68.5, with 50.3 average grains. The findings of [12] for grains spike⁻¹ are similar to the present findings which evaluated 60 genotypes of wheat during Rabi 2017-18 by using a Randomized Complete Block Design. The least significant differences for grains spike⁻¹ were 3.3%. phenotypic coefficient of variation and genotypic coefficient of variation grains spike⁻¹ were found (125.39) and (123.29).

The weight of a thousand grains in the wheat advance lines varied from 35.0 to 49.8 g, with an average of 42.1g. The least significant difference at 5% for thousand-grain weight was, Same result was recorded by [18]. [13] results showed highly significant variance and non-significant variation among genotypes for 1000-grain weight. The phenotypic coefficient of variation and genotypic coefficient of variation for 1000-grain weight was 70.85.

The coefficient of variation was 19.9% for grain yield. Grain yield varied among wheat genotypes, ranging from 1410 to 3080 Kg ha⁻¹, with an average of 2316.60 Kg ha⁻¹. The least significant difference at 5% for grain production was 923.8 Kg ha⁻¹. The findings of [14] who assessed 64 bread wheat genotypes for 16 parameters.

Heritability

As a result, a character-effective selection is aided by high heritability. According to our results, the spike weight and grains, spike⁻¹ showed substantial heritability estimates (0.97), while plant height (0.58), 1000 grain weight (0.44) and flag leaf area (0.31) showed moderate heritability (Table. 4). The lowest heritability estimates were recorded for peduncle length (0.01), spike length (0.13), grain yield (0.18), days to heading (0.25), spikelet spike⁻¹ (0.25) and days to maturity (0.30) presented in Table 4. Heritability high estimates for days to maturity, days to heading, and days to plant height were observed by [15]. A similar finding has been recorded by [16] for yield of grain via assessing bread wheat genotypes in 2015. Singh *et al.* showed similar results for high heritability for grains spike⁻¹ relating 44 genotypes.

Coheritability

According to our result co-heritability for heading interval was ranged from 0.12 to 0.99 among

studied traits. The findings [12] also showed a negative correlation association for heading. Similarly, [7] observed a negative association between. In the case of maturity, coheritability ranged from 0.04 to 0.96. Maximum coheritability of maturity was recorded with spikelet spike⁻¹ (0.96). Similarly, a positive connection was also shown by [8] between days to maturity and spikelet spike⁻¹, who evaluated 46 bread wheat advanced lines at two experimental sites in 2018.

Our results revealed that coinheritance for plant height ranged from 0.25 to 0.99. Maximum coheritability for plant height was observed with a peduncle length of (0.99) Furthermore, [11] evaluated 36 lines of wheat with three replications using RCBD design and reported that plant height and spikelets spike⁻¹ are positively correlated. Our results follow the previous observation of [8] which showed a maximum correlation between plant height and grains spike⁻¹ who evaluated ten wheat genotypes during 2014-15.

Peduncle length showed coinheritance ranging from 0.31 to 0.99 among studied traits according to table 4.6. Peduncle length showed maximum coheritability with grains spike⁻¹ (0.99). While [13] results showed a positive correlation among peduncle length, spike length, and spikelet per spike who used randomized full block design to study 17 advanced breeding lines at the University of Sargodha.

Coheritability for spike length varied between 0.06 to 0.98 among studied traits. Maximum coinheritance of spike length was recorded with grains spike⁻¹ (0.98) Similarly, the correlation between spike length and grains spike⁻¹

Spike weight showed coheritability ranged from (0.13) to (0.98). Maximum coinheritance was estimated for grains spike⁻¹(0.98) followed by spikelets spike⁻¹ (0.92). These findings follow the results of [7] who evaluated 90 wheat genotypes in a 9 × 10 alpha-lattice design in 2020 and found spike weight is positively correlated with grains spike⁻¹ and spikelet spike⁻¹.

Spikelets spike⁻¹ showed coheritability ranging from (0.27) to (0.97). The maximum coheritability was noted for grains spike⁻¹ (0.97). Our results correspond with those of [12] which showed maximum correlation for spikelet spike⁻¹ with grains spike⁻¹, who evaluated 60 genotypes of wheat during Rabi 2017-18.

GPS showed maximum coheritability for Grain yield (0.31) and minimum coheritability for thousand-grain weight (0.23). Additionally, [12] revealed a non-significant correlation between grains spike⁻¹ with grain yield plot⁻¹ and a negative significant correlation of grains spike⁻¹ with 100-

grain weight for 10 genotypes during 2014-15.

Thousand-grain weight shows coheritability with grain yield in contrast [13] results revealed a negative correlation between 1000-grain weight and days to maturity.

Table 3

Mean squares for yield and yield-related traits at CCRI during 2022-23

Source of Variance	Df	Heading Days	Maturity days	Plant height	Flag leaf area	Peduncle length	Spike length	Spikelets spike-1	Spike weight	Grains spike-1	1000-grain Weight	Grain Yield
REPS	1	55.13 ^{ns}	27.20*	13.13 ^{ns}	186.23**	20.06 ^{ns}	0.17 ^{ns}	8.86 ^{ns}	0.04 ^{ns}	13.13*	36.66 ^{ns}	6771200.00**
Treatment (unadjusted)	63	25.36*	3.48**	131.69**	36.52**	15.32 ^{ns}	1.85 ^{ns}	5.42**	0.88**	159.60**	30.15**	306563.29**
Blocks within Reps/ Block	14	6.54	4.64	23.51	29.06	9.37	1.57	1.91	0.01	4.13	9.33	383739.29
Treatment (adjusted)	63	26.44*	3.43**	133.12**	36.22**	15.63 ^{ns}	1.84 ^{ns}	5.53*	0.96**	155.42**	30.41**	303322.73**
RCB	63	13.69	2.46	32.80	21.44	13.90	1.45	3.00	0.01	2.96	11.30	231145.24
Intra block error	49	15.73	1.84	35.46	19.26	15.19	1.41	3.31	0.02	2.62	11.86	187546.94
Coefficient of Variation	--	3.3	0.8	5.7	16.2	11.3	11.0	9.4	9.1	3.2	8.2	19.9

RCB=Randomized complete block, **, * = significant at 1% and 5%, ns = non-significant

Table 4

Estimation of genotypic, phenotypic variances, and heritability for various traits in 64 wheat genotypes.

Traits	Vg	Ve	Vp	GCV	PCV	Heritability
Days to heading	5.4	15.7	21.1	21.20	42.08	0.25
Days to maturity	0.8	1.8	2.6	7.00	12.76	0.30
Plant height	48.8	35.5	84.3	68.46	89.94	0.58
Flag leaf area	8.5	19.3	27.7	55.92	101.16	0.31
Peduncle length	0.2	15.2	15.4	7.97	66.87	0.01
Spike length	0.2	1.4	1.6	14.18	38.86	0.13
Spikelet spike ⁻¹	1.1	3.3	4.4	23.94	47.77	0.25
Spike Weight	0.47	0.02	0.49	57.65	58.66	0.97
Grains spike ⁻¹	76.4	2.6	79.0	123.29	125.39	0.97
Thousand Grain Weigh	9.28	11.86	21.14	46.93	70.85	0.44
Grain Yield	46221.7	211327.0	257548.7	446.68	1054.40	0.18

Vp = Phenotypic Variance, Vg = Genotypic Variance, PCV (per cent) = Phenotypic coefficient of Variation, GCV (per cent) = Genotypic coefficient of Variation, ECV (per cent) = Environment coefficient of Variation

Table 5

Coheritability estimation of various traits in 64 wheat genotype

	DH	DM	PH	FLA	PDL	SL	SPKW	SPKS	GPS	TGW	GY
DH	--	0.61	0.80	0.12	0.60	0.30	0.99	0.54	0.96	0.66	0.18
DM	--	--	0.26	0.23	0.50	0.45	0.67	0.96	0.77	0.44	0.04
PH	--	--	--	0.95	0.99	0.94	0.81	0.25	0.98	0.63	0.33
FLA	--	--	--	--	0.69	0.80	0.86	0.30	0.98	0.03	0.22
PDL	--	--	--	--	--	0.85	0.95	0.32	0.99	0.35	0.31
SL	--	--	--	--	--	--	0.55	0.15	0.98	0.08	0.06

SPW	--	--	--	--	--	--	--	0.92	0.98	0.61	0.13
SPKS	--	--	--	--	--	--	--	--	0.97	0.51	0.27
GPS	--	--	--	--	--	--	--	--	--	0.23	0.31
TGW	--	--	--	--	--	--	--	--	--	--	0.35
GY	--	--	--	--	--	--	--	--	--	--	--

CONCLUSION

Analysis of variances revealed significant genetic variability among the genotypes for all traits. The genotypes CCRIA1-10, CCRIA1-1, and CCRIA1-11 were the best for early maturity based on mean performance. Likewise, for flag leaf area desirable, genotypes were CCRIA1-16 and CCRIA1-27, and for grains spike⁻¹ CCRIA1-28 and CCRIA1-22. In addition, the best genotypes for 1000 grain weight were CCRIA1-64 and CCRIA1-37. Likewise, genotypes for grain production, CCRIA1-13, and CCRIA1-29 yielded the maximum. Grain yield

was associated with higher values of GCV and PCV, followed by grain spike⁻¹. The highest heritability was indicated by spike weight followed by grains spike⁻¹. High coheritability was observed among day to maturity and spike weight (0.99). Maximum desirable coinheriting pairs were flag leaf area with grains spike⁻¹, spike length with grains spike⁻¹, and spike weight with grains spike⁻¹ (0.98), spikelet spike⁻¹ with grains spike⁻¹, spike weight with spikelet spike⁻¹ flags leaf area with spike weight.

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