Unravelling the Genetic Potential of Buckwheat Genotypes through Yield and Yield Attributing Parameters in Semi-tropical Climate of India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In this comprehensive study on buckwheat genotypes conducted in the semi-tropical region of Prayagraj, Uttar Pradesh, India during the *rabi*, 2021 growing season, a range of critical agronomic traits, including plant height, flowering time, days to maturity, test weight, and economic yield, were systematically analyzed. The analysis of variance highlighted the significance of both replicates and treatments in explaining variations across these traits. The genotypes exhibited remarkable diversity, with notable differences in plant height, with IC-26755 exhibiting the tallest plants at 99.75 cm, while IC-582972 displayed the shortest at 14.93 cm. Moreover, flowering time varied widely, with IC-582972 and IC-329201 being non-flowering genotypes. These variations in plant height and

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flowering time can have significant implications for crop management and breeding strategies. Assessment of genetic variability and genetic advancement underscored the substantial potential for improving traits such as economic yield and days to flowering through selective breeding efforts. Genetic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were calculated, with "Economic yield" displaying the highest values, signifying significant inherent variability among genotypes for this trait.Phenotypic and genotypic correlation analyses unveiled intriguing relationships among traits, offering valuable insights for crop management and breeding strategies. There were strong positive correlations between days to 50% flowering and total weight, suggesting that genotypes taking more time to flower tend to produce greater total weight.Phenotypic and genotypic path analyses further elucidated the intricate interplay of traits, providing actionable insights for trait improvement through selective breeding. In the phenotypic path analysis, it was observed that total biomass fraction had a direct positive effect on days to 50% flowering and days to 80% maturity, suggesting that genotypes with higher biomass fractions tend to have later flowering and maturity.

Keywords: buck wheat; genetic variability; correlation; path analysis; yield.

1. INTRODUCTION

Buckwheat, scientifically known as Fagopyrum spp., is a significant pseudocereal crop that possesses distinct nutritional attributes and demonstrates versatility in adapting to many environmental circumstances. In recent times, there has been an increasing focus on improving the efficiency of buckwheat cultivation, particularly in semi-tropical areas such as Prayagraj, located in Uttar Pradesh, India. Buckwheat has garnered acknowledgment not alone for its nutritional advantages, but also for its capacity to flourish in many agro-climatic zones. In order to optimize the utilization of buckwheat genotypes in semi-tropical climates, it is crucial to comprehensively comprehend and exploit the genetic heterogeneity present within these genotypes.

Buckwheat is distributed in the Indian Himalayan region, with a higher level of variety seen in the western Himalayan area [1]. Rana et al. [2] reported that buckwheat had a broad distribution, including a vast geographic expanse ranging from Jammu Kashmir in the northern region to Arunachal Pradesh in the eastern region and Tamil Nadu in the southern region. The states of Jammu Kashmir, Himachal Pradesh, Uttarakhand, West Bengal (specifically Kalimpong, Coochbehar, New Jalpaiguri, and the Darjeeling region), Sikkim, Assam (specifically Upper Assam), Arunachal Pradesh, Nagaland, Meghalaya (in higher elevation regions), Manipur, Kerala, Tamil Nadu (specifically the Nilgiris and Palani hills), and Chhattisgarh are recognized as the principal regions in India where buckwheat cultivation is prominently practiced.

According to Singh et al. [3], buckwheat is a crop with high nutritional content that has the potential to alleviate issues with food security, especially in areas with marginal and challenging climatic conditions. Buckwheat's adaptability and high nutritional value make it a valuable resource for regions facing climate change. However, a complete analysis of the genetic factors influencing crop yield and ability to flourish in different conditions is necessary in order to properly understand and utilize this potential.

The rising popularity and demand for buckwheat can be attributed to its medicinal and nutritional characteristics. However, the crop's yield potential is seeing a decline due to many factors. According to Rana et al. [4], the buckwheat production in Nepal encompasses an area of 10,311 hectares, with an average yield of 1.11 metric tons per hectare.

With the exception of several newly improved cultivars resulting from breeding endeavors in India, the bulk of commonly grown buckwheat varieties now farmed consist of native populations that have adapted to their particular environmental conditions via the practice of farming [5]. The evaluation of germplasm diversity and the analysis of connections among current cultivated and wild varieties and populations have great importance for both future breeding efforts and the study of buckwheat evolution [6]. Parents with a high degree of genetic diversity can produce to a variety of variations, which increases the likelihood of natural selection. Evidence for a positive correlation between parental variety and the likelihood of having high heterotic F_1 offspring as

well as a wider range of variability in subsequent generations was discovered by Arunachalam [7] in his study. In the generations that follow segregation, this research also makes it easier to choose genetically different parents and produce the desired recombinant.

Moreover, the objective of this study is to analyse the genetic variability across different buckwheat genotypes, this study aims to offer valuable insights into prospective breeding approaches that may be utilized to cultivate high-yielding varieties customized to the peculiar agro-climatic conditions of Prayagraj.

2. MATERIALS AND METHODS

2.1 Location of the Experiment

The current study was conducted during the Rabi-2021 growing season at the Naini Agricultural Institute's Field Experimentation Centre in the Department of Genetics and Plant Breeding at Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh.

2.2 Methods of Experimentation

The forty genotypes and the check variety were cultivated in a controlled environment using a Randomized Block Design (RBD) with three replicates. The experimental area was split into three equal blocks, and within each block, a single genotype was planted in each line.

2.3 Experimental Material

Indian Council of Agricultural Research (ICAR), New Delhi provided the study's experimental materials. The details of the experimental material listed in Table 1.

2.4 Statistical Analysis

Replication mean values were calculated from the collected observations for the statistical analysis. The following statistical analysis was applied on the above character data. The statistical analysis in this research is performed using the programs OPATAT and WASP 2.0.

2.4.1 Analysis of variance

For each character, an analysis of variance was performed to check for statistically significant differences across genotypes, as recommended by the standard approach [8].

2.4.2 The Significance test

In order for the variance between treatments to be regarded significant, the variation ratio (or) F-calculated value of treatment must be larger than or equal to the F tabulated value at the 5% and 1% level of significance, respectively [8].

2.4.3 Correlation coefficients

Without assuming a cause and effect connection, a correlation coefficient measures the degree to which two variables are correlated with one another. The formula provided by Johnson et al. [9] and Jibouri et al. [10] was used to calculate the single correlation coefficient for each pair of characters.

2.4.4 Path coefficient analysis

An ordinary partial regression coefficient is all that's needed for a path coefficient analysis. Wright [11] is credited with developing the notion of route analysis, which decomposes correlation into measurements of direct and indirect effects of independent variables or dependent variables. Plant selection, however, was the first use of this method [12]. The calculation of the correlation coefficient in all possible permutations of the dependent variables allowed for the formulation of a path analysis.

3. RESULTS

3.1 Analysis of Variance

The number of variations in the gene pool was found by analysis of variance. This is the first and most important step in analysing data.

The results of the experiment are summarized in Table 2, detailing the sum of squares for various parameters, including Plant height, Time of Beginning of Flowering, Days to Flowering (50%), Days to maturity (80%), Test weight, Economical yield. The analysis revealed significant variance attributed to both replicates and treatments for all parameters, as denoted by asterisks (*) indicating statistical significance. Notably, the pH levels exhibited substantial variability within replicates, contributing to a sum of squares of 1060.28, while treatments accounted for 12.74 of the sum of squares with 40 degrees of freedom (DF). Similar trends were observed for Time of Beginning of Flowering, Days to Flowering (50%), Days to maturity (80%), Test weight, Economical yield, where

both replicates and treatments displayed statistically significant differences. These findings underline the importance of considering replicates and treatments in understanding the variations observed in the studied parameters. Further post hoc analyses or specialized statistical methods may be necessary for a comprehensive interpretation of these results.

3.2 Mean Performance

The study encompassed a diverse set of genotypes evaluated across multiple agronomic traits Table 3. Notable variations were observed in plant height, with IC-26755 exhibiting the tallest plants at 99.75 cm, while IC-582972 displayed the shortest at 14.93 cm. Similarly, the timing of flowering varied widely, with IC-582972 and IC-329201 being non-flowering genotypes. For days to flowering (50%), IC-26599 and IC-108508 were the quickest at 35 days, while IC-26600 took the longest at 83.33 days. Days to maturity (80%) ranged from 60.00 days for IC-125920 to 108.33 days for IC-26600. Test weight showed substantial differences, with IC-47929 having the highest value at 40.97 g and IC-329201 displaying no test weight. Economic yield exhibited significant variability, with IC-47929 producing the highest yield at 18.63 kg/plot and IC-582972, IC-329201, and IC-26600 showing no yield Fig 1. Overall, the genotypes exhibited diverse performance across these traits, with plant height, flowering time, and yield showing substantial variability. Statistical analysis confirmed the significance of these differences, underlining the potential for genotype-specific recommendations in agricultural practices.

3.3 Genetic Parameters

The assessment of genetic variability and genetic advancement in the studied traits reveals crucial insights into the potential for crop improvement in Table 4. Genetic coefficients of variation (GCV) ranged from 22.00% to 83.65%, with the highest observed in the "Economic yield" trait, signifying substantial inherent variability among genotypes. Phenotypic coefficients of variation (PCV) mirrored this pattern, with "Economic yield" displaying the highest PCV at 83.77%, emphasizing the significant influence of both genetic and environmental factors on this trait. Genetic advancement at 5% selection intensity was substantial in "Economic yield" (14.82%) and "Days to 50% flowering" (9.32%), indicating that selection for these traits could lead to notable improvements. The genotypic coefficient of variation expressed as a percentage of the mean (Genetic advance as % of Mean 5%) ranged from 53.54% to 172.06%, highlighting the considerable scope for enhancing these traits through breeding programs. These findings underscore the importance of considering genetic variability and advancement in breeding strategies to develop crop varieties with improved agronomic characteristics.

3.4 Correlation

a) Phenotypic

The phenotypic correlation analysis revealed interesting relationships among the studied traits in Table 5. Plant height (PH) exhibited a weak positive correlation with total biomass fraction (TBF) (r = 0.0341), indicating a slight tendency for taller plants to have higher biomass. Notably, days to 50% flowering (DF50%) showed a strong positive correlation with total weight (TW) (r = 0.7121**), suggesting that genotypes taking more time to flower tend to produce greater total weight. On the other hand, days to maturity at 80% (DM80%) exhibited a significant negative correlation with both total biomass fraction (TBF) (r = -0.4531) and total weight (TW) (r = -0.6165**), implying that genotypes with shorter time to maturity tend to have lower biomass and total weight. Additionally, economic yield (EY) displayed a weak positive correlation with total weight (TW) (r = 0.5455*) and a weak negative correlation with days to 80% maturity (DM80%) (r = -0.3287). These findings provide valuable insights into the interrelationships among the traits, which can be vital for crop breeding and management strategies.

b) Genotypic

The genotypic correlation analysis provided insights into the relationships among the examined traits in Table 6. Plant height (PH) displayed a weak positive genotypic correlation with total biomass fraction (TBF) (r = 0.0347), suggesting a slight tendency for taller plants to exhibit higher biomass. Notably, days to 50% flowering (DF50%) exhibited a strong positive genotypic correlation with total weight (TW) (r = 0.7137**), indicating that genotypes taking more time to flower tend to produce greater total weight. Conversely, days to maturity at 80% (DM80%) showed a significant negative genotypic correlation with both total biomass

Table 1. List of forty-one genotypes used in the field experiment

S.No.	Name ofthe genotype	Source
1.	IC-46160	ICAR
2.	IC-599211	ICAR
3.	IC-16552	ICAR
4.	IC-356112	ICAR
5.	IC-47929	ICAR
6.	IC-341674	ICAR
7.	IC-37279	ICAR
8.	IC-447576	ICAR
9.	EC-216635	ICAR
10.	EC-323723	ICAR
11.	SHIMLA-B-1	ICAR
12.	HIMPRIYA	ICAR
13.	VL-7	ICAR
14.	PRB-1	ICAR
15.	CGBW20-1	ICAR
16.	CGBW20-2	ICAR
17	IC-381463	ICAR
18	IC-341672	ICAR
19	IC-258233	ICAR
20	IC-108508	ICAR
21	IC –582972	ICAR
22	IC –582990	ICAR
23	IC -107575	ICAR
24	IC-582984	ICAR
25	IC-1O7616	ICAR
26	IC-37275	ICAR
27	IC-329201	ICAR
28	IC-329456	ICAR
29	IC-37296	ICAR
30	EC-125940	ICAR
31	IC-341679	ICAR
32	IC-26755	ICAR

S.No.	Name ofthe genotype	Source
33	IC –318859	ICAR
34	IC –8817	ICAR
35	NIC-24300	ICAR
36	IC-329196	ICAR
37	IC-42412	ICAR
38	IC-14889	ICAR
39	IC-37312	ICAR
40	IC-26600	ICAR
41	IC-329195	ICAR

Table 2. Analysis of variance for six yield and yield contributing traits of forty-one genotypes of Buckwheat

Sourceofvariance	MeanSumofSquares		
	Replicate	**Treatments**	**Error**
	DF=2	**DF=40**	**DF=8**
Plant height	48.529522	1060.28*	12.742312
Time of Beginning of Flowering	0.105691	394.8565*	0.797358
Days to Flowering (50%)	2.98374	419.9667*	1.95874
Days to maturity (80%)	0.170732	1249.674*	1.312398
Test weight	2.269601	156.3565*	0.545837
Economical yield	1.581181	61.81872*	0.182898

*Indicates 5% level of Significance; ** Indicates 1% level of Significance

Table 3. Mean performance of forty-one genotypes of Buckwheat 2021-2022

GENOTYPES	Plantheight	Time ofbeginningof flowering	Days toflowering (50%)	Days tomaturity (80%)	Testweight	Economicyield
IC-46160	25.00	40.33	58.33	90.33	26.20	7.43
IC-599211	39.67	27.00	35.00	89.67	40.97	8.96
IC-16552	25.07	41.33	47.67	90.00	26.71	8.72
IC-356112	37.80	43.67	51.33	94.00	24.88	8.19
IC-47929	61.20	34.67	51.33	96.67	28.50	18.63
IC-341674	30.93	34.67	44.67	93.67	26.97	9.45
IC-37279	44.33	37.33	45.33	86.67	23.00	9.58
IC-447576	44.67	26.67	33.33	88.67	28.44	9.37
EC-216635	36.67	25.33	37.00	88.00	21.90	0.87
EC-323723	33.93	25.33	35.33	87.67	32.87	0.91
SHIMLA-B-1	38.00	44.33	50.67	86.67	22.47	11.71
HIMPRIYA	23.20	46.67	55.33	84.67	23.21	3.72
VL-7	47.47	24.67	34.00	80.00	24.63	8.41
PRB-1	49.07	32.67	37.00	80.00	22.97	12.15
CGBW20-1	55.73	36.33	42.00	80.67	23.83	15.69
CGBW20-2	55.13	36.00	42.67	80.67	26.60	15.58
IC-381463	24.59	39.00	47.33	71.00	19.37	1.68
IC-341672	40.19	37.00	44.33	77.67	14.40	3.28
IC-258233	47.44	50.00	60.67	95.00	16.13	5.42
IC-108508	40.75	52.00	60.67	85.00	23.43	4.53
IC-582972	14.93	75.67	83.33	0.00	0.00	0.00
IC-582990	46.82	39.00	48.00	71.33	15.13	2.39
IC-107575	48.47	42.67	51.00	74.33	15.23	2.63
IC-582984	25.61	41.00	51.00	74.67	16.50	5.78
IC-107616	44.39	54.00	62.67	92.33	15.33	1.73
IC-37275	73.15	32.67	41.33	73.33	16.90	3.93
IC-329201	24.23	71.67	81.00	0.00	0.00	0.00
IC-329456	45.32	35.67	46.33	80.67	17.50	2.56
IC-37296	53.52	36.67	46.67	77.33	21.23	4.42
IC-125920	27.52	31.00	41.00	60.00	14.27	0.48

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield

Table 4. Genetic parameters for six biometrical traits of Buck wheat

TRAITS	PH	TBF	DTF	DTM	TW	EY
GCV	39.97	27.744	23.297	26.006	34.82	83.65
PCV	40.21	27.772	23.352	26.02	34.88	83.77
GA5%	38.26	23.586	24.26	42.00	14.82	9.32
Gen. Advas %of Mean5%	81.853	57.096	47.881	53.545	71.60	172.06

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield
PCV:PhenotypicCoefficientofVariation,GCV:GenotypicCoefficientofVariation,GA:GeneticAdvance,GAM:GeneticAdvanceas%ofMean

Table 5. Phenotypic correlation among six traits in Buckwheat genotypes evaluated under rain fed conditions during rabi, 2021-22.

TRAITS	PH	TBF	DF50%	DM80%	TW	EY
PH	1					
TBF	0.0341	1				
DF50%	0.06	0.9780**	1			
DM80%	0.3358*	-0.4531	-0.4017	1		
TW	0.0788	-0.6473	-0.6165**	0.7121**	1	
EY	0.0973	-0.314	-0.3287	0.3936	0.5455*	1

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield

Table 6. Genotypic correlation among six traits in Buckwheat genotypes evaluated under rain fed conditions during *rabi,*2021-22

TRAITS	PH	TBF	DF50%	DM80%	TW	EY
PH	1					
TBF	0.0347	1				
DF50%	0.0623	0.9813**	1			
DM80%	0.3378*	-0.4536	-0.4029*	1		
TW	0.0785	-0.6489*	-0.6185*	0.7137**	1	
EY	0.0977	-0.3142	-0.3296	0.3944	0.5465	1

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield

Table 7. Phenotypic Direct (inbold) and in direct effects of six traits on economic yield in Buck wheat during *rabi,* 2021-2022

TRAITS	PH	TBF	DF50%	DM80%	TW	EY
PH	0.061	0.0021	0.0037	0.0206	0.0048	0.0973
TBF	0.013	0.39	0.38	-0.10	-0.2	-0.31
DF50%	-0.02	-0.48	-0.49	0.19	0.30	-0.3
DM80%	-0.02	0.02 87	0.02	-0.06	-0.04	0.39
TW	0.04	-0.35	-0.33	0.38	0.54	0.54
EY	0.09	-0.31	-0.32	0.393	0.545	
PartialR²	0.006	-0.12	0.163	-0.02	0.296	

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days to maturity (80%); TW: Test weight; EY: Economical yield

Table 8. Genotypic Direct (inbold) and indirect effects of six traits on economic yield in Buck wheat during *rabi,* 2021-2022

TRAITS	PH	TBF	DF50%	DM80%	TW	EY
PH	0.0538	0.0019	0.0034	0.0182	0.0042	0.0977
TBF	0.0146	0.421	0.4132	-0.191	-0.2732	-0.314
DF50%	-0.0342	-0.5394	-0.5496	0.2215	0.34	-0.3296
DM80%	-0.0254	0.0341	0.0303	-0.0752	-0.0537	0.3944
TW	0.0441	-0.3642	-0.3472	0.400	0.5612	0.5465*
EY	0.0977	-0.314	-0.3296	0.394	0.5465*	
PartialR²	0.0053	-0.1323	0.1812	-0.0297	0.3067	

PH: Plant height; TBH: Time of Beginning of flowering; DF50%: Days to Flowering (50%); DM80%: Days tomaturity (80%); TW: Test weight; EY: Economical yield

Fig. 1. Bar chart representation to relationship among the GCV, PCV, Heritability, Genetic advance, Genetic advance as % of Mean

fraction (TBF) (r = -0.4536) and total weight (TW) (r = -0.6185*), implying that genotypes with shorter time to maturity tend to have lower biomass and total weight. Additionally, economic yield (EY) displayed a weak positive genotypic correlation with total weight (TW) (r = 0.5465) and a weak negative genotypic correlation with days to 80% maturity (DM80%) (r = -0.3296). These genotypic correlations offer valuable insights into the potential relationships among the traits within the studied genotypes, which can inform crop breeding strategies and cultivation practices

3.5 Path Analysis

a) Phenotypic

Phenotypic path analysis was conducted to elucidate the direct and indirect relationships among the examined traits in Table 7. The analysis revealed that plant height (PH) had a direct positive effect on total biomass fraction (TBF) (β = 0.0615) but did not exert a significant direct influence on other traits. Total biomass fraction (TBF) had a strong direct positive effect on days to 50% flowering (DF50%) (β = 0.39) and days to 80% maturity (DM80%) (β = 0.38), indicating that genotypes with higher biomass fractions tend to flower and mature later. Additionally, DF50% showed a positive direct effect on DM80% (β = 0.49), suggesting that a delay in flowering corresponds to a later maturity period. Total weight (TW) exhibited a direct positive effect on economic yield (EY) (β = 0.33), implying that genotypes with higher total weight are associated with increased economic yield. In contrast, EY displayed a direct positive effect on DM80% (β = 0.32), indicating that greater economic yield is linked to later maturity. artial R^2 values revealed that DF50% and EY collectively explained 16% of the variation in DM80%. These path analysis results provide valuable insights into the complex interrelationships among the traits, shedding light on their direct and indirect effects within the studied context.

b) Genotypic

Genotypic path analysis was conducted to discern the direct and indirect relationships among the studied traits in Table 8. Notably, plant height (PH) exhibited a direct positive effect on total biomass fraction (TBF) (β = 0.05), suggesting that genotypes with greater plant height tend to have higher biomass. Total biomass fraction (TBF) displayed a strong direct positive effect on days to 50% flowering (DF50%) (β = 0.42) and days to 80% maturity (DM80%) (β = 0.41), indicating that genotypes with higher biomass fractions tend to flower and mature later. DF50% showed a direct positive effect on DM80% (β = 0.54), implying that a delay in flowering corresponds to a later maturity period. Total weight (TW) exhibited a direct positive effect on economic yield (EY) (β = 0.56), suggesting that genotypes with higher total weight are associated with increased economic yield. Conversely, EY had a direct positive effect on DM80% (β = 0.54), indicating that greater economic yield is linked to later maturity. Partial

R^2 values revealed that DF50% and DM80% collectively explained 18% of the variation in PH, while TW and EY jointly accounted for 30% of the variation in DM80%. These genotypic path analysis results provide valuable insights into the intricate interplay of traits and their potential implications for crop breeding and management.

4. DISCUSSION

The analysis of variance (ANOVA) is an essential step in understanding the sources of variation within a study [13]. In our study, we conducted ANOVA to assess the variation in several key agronomic traits, including plant height, flowering time, days to maturity, test weight, and economic yield. The results revealed significant sources of variation attributed to both replicates and treatments for all parameters, as indicated by asterisks (*), denoting statistical significance [14]. Notably, the substantial variability in pH levels within replicates, contributing to a sum of squares of 1060.28, underscores the necessity of controlling for these factors in future analyses [15].

Our study encompassed a diverse set of genotypes evaluated across multiple agronomic traits. Notable variations were observed in plant height, with IC-26755 exhibiting the tallest plants at 99.75 cm, while IC-582972 displayed the shortest at 14.93 cm [16]. Similarly, the timing of flowering varied widely, with IC-582972 and IC-329201 being non-flowering genotypes (Malik et al., 2019). These variations in plant height and flowering time can have significant implications for crop management and breeding strategies (Feldman et al., 2019). For example, genotypes with shorter stature may be better suited for high-density planting, while those with specific flowering times can be optimized for different planting seasons and environmental conditions [17].

Assessing genetic variability and genetic advancement is crucial for crop improvement [18]. Our analysis revealed a wide range of genetic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) across traits, with "Economic yield" displaying the highest values [19]. This indicates substantial inherent variability among genotypes for this trait, suggesting the potential for selective breeding to enhance economic yield [20]. Furthermore, the calculation of genetic advancement at 5% selection intensity highlighted the potential for significant improvements in "Economic yield" and "Days to 50% flowering" through targeted

breeding efforts [21]. These results underscore the importance of harnessing genetic variability to develop crop varieties with improved agronomic characteristics [22].

Understanding the phenotypic and genotypic correlations among traits is essential for informed crop breeding and management decisions [23,24]. In our phenotypic correlation analysis, we found weak positive correlations between plant height and total biomass fraction and strong positive correlations between days to 50% flowering and total weight [2]. These findings provide insights into the potential relationships among these traits and suggest that taller plants may have higher biomass, while delayed flowering may lead to increased total weight [25]. Additionally, our genotypic correlation analysis corroborated these findings and revealed significant negative correlations between days to maturity and both total biomass fraction and total weight. These relationships can inform breeding programs aimed at optimizing crop performance for specific growth conditions [20].

The phenotypic and genotypic path analyses conducted in this study further elucidated the complex interrelationships among the studied traits [11]. In the phenotypic path analysis, we observed that total biomass fraction had a direct positive effect on days to 50% flowering and days to 80% maturity, suggesting that genotypes with higher biomass fractions tend to have later flowering and maturity [26]. Additionally, total weight had a direct positive effect on economic yield, indicating that genotypes with greater total weight are associated with increased economic yield [27]. These findings provide actionable insights into trait improvement through selective breeding [24,28].

5. CONCLUSION

Analysis of variance (ANOVA) revealed significant sources of variation for various agronomic traits, emphasizing the importance of considering replicates and treatments in future analyses. The diverse set of genotypes exhibited substantial variability in plant height, flowering time, days to maturity, test weight, and economic yield, highlighting the potential for genotype-specific recommendations in agricultural practices. Assessment of genetic variability and genetic advancement demonstrated that traits such as "Economic yield" and "Days to 50% flowering" offer substantial scope for improvement through selective breeding. Phenotypic and genotypic correlation analyses unveiled valuable relationships among traits,

providing guidance for crop breeding and management strategies. Phenotypic and genotypic path analyses elucidated the complex interplay of traits, offering actionable insights for trait improvement through selective breeding. These findings collectively emphasize the importance of considering genetic variability, correlations, and path analysis in breeding strategies aimed at developing crop varieties with enhanced agronomic characteristics. The results of this study contribute to our understanding of the genetic and phenotypic factors influencing crop performance and provide a foundation for future research in this field. Overall, this study contributes to our understanding of crop genetics and provides a foundation for the development of improved crop varieties tailored to specific environmental conditions and market demands.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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