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Heritability and Correlation Among Physiological and Yield Traits in Chickpea (*Cicer arietinum* L.)

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ABSTRACT

The present research assessed 18 Desi chickpea genotypes at the University of Agriculture Peshawar from November 2020 to May 2021. The plant material was grown using randomized complete block design with three replications to determine genetic variability, heritability, and correlation. Twelve parameters were studied encompassing two phenological and physiological; and eight morpho-yield traits. Significant differences (P<0.05) were estimated for all traits except excise leaf water retention. Genotypes IG2 exhibited early (99-days) flowering. EG1 showed the optimal height (52.45 cm). Furthermore, IG2 displayed maximum (17.11) productive branches per plant. FG1 recorded maximum (52) pod per plant. Meanwhile, IG2 also expressed maximum relative water content, seeds per pod (1.72), biological yield (3765.43 kg/ha), hundred-seed weight (32.43 g), and seed yield (1061.73 kg/ha). However, the maximum harvest index was recorded for genotype GG1. High heritability was registered for seeds per pod (0.74) and flowering days (0.75). Percent genetic advance was the highest for harvest index (62.08%), followed by seeds per pod (33.56%). Seed yield observed a significant positive correlation with seeds per pod (r=0.99**), hundred-seed weight (r=0.99**), biological yield (r=0.81**), plant height (r=0.54**), and productive branches per plant (r=0.49*). Therefore, these traits might indirectly select greater-yielding chickpea genotypes. Genotypes IG2, and BG2, are recommended for future breeding programs developing high-yielding chickpea cultivars.

INTRODUCTION

The global production of chickpeas for 2021 was 15.89 million tonnes with an average yield of 1057.8 kg/ha (Food and Agriculture Organization of the United Nations, 2021). The leading producer was India which accounted for 75% of net produce, followed by Australia, Ethiopia, Türkiye, Myanmar, Russia, and Pakistan. However, despite being in the top-7 producers, Pakistan has plenty of potential for improvement as the chickpea yield of Pakistan is only nearing a quarter of the mean global yield.

Chickpea yield in Pakistan, as of 2020, was 265 kg/ha (Federal Bureau of Statistics, 2021). Kindly incorporate the following sentence in the appropriate location. Even though the total area cultivated under chickpeas was 0.94 million ha, a production of 0.32 million tonnes of chickpeas had Pakistan heavily relying on its imports to compensate for the demand-supply gap. Since

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chickpea is mostly sown in marginal areas, their yield is frequently hampered by unfavorable conditions (Federal Bureau of Statistics, 2021). Moreover, these frequent undesirable fluctuations in weather might be attributed to the changing climate (Haris & Chhabra, 2014).

Climate change is inevitably going to have an impact on all organisms. The increase in global warming would adversely affect temperature-sensitive plants. Chickpea's flowering stage is prone to heat stress, which might affect the yield (Haris & Chhabra, 2014). Therefore, adequate genetic variability must be secured for developing varieties that can grow under warmer climates. However, the development of high-yielding chickpea varieties does not only require the availability of adequate variability. Still, it will also require the knowledge of the heritability of a trait and the correlation between seed yield and other factors influencing it (Khan et al., 2011).

Heritability is vital for developing high-yielding chickpea genotypes since breeding programs rely on selection for improvement, which in turn is dependent upon the influence of genes on the particular trait under selection (Karthikeyan et al., 2022; Ningwal et al., 2023). Heritability is an index for the transmissibility of a character from parents to its progeny, indicating the proportion of existing variation that manifests in genes. Greater heritability marks the effectiveness of selection in improving a trait in the population (Acquaah, 2012). Mathematically, it is the ratio between genetic and phenotypic variance, which is generally categorized as high (above 60%), medium (30-60%), and low (below 30%) (Kumar et al., 2020).

Certain traits are complex, *i.e.,* under the influence of many genes, and selection for such traits can become problematic as the inheritance pattern is abstruse. Selection for such traits is then based on indirect selection, whereby other traits are selected, which tend to have a high association with these traits (Acquaah, 2012). Various studies have used correlation analysis to determine the association between yield and their contributing traits (Girma et al., 2019; Karthikeyan et al., 2022; Kumar et al., 2019; Ningwal et al., 2023).

Although many studies have assessed the heritability and correlation of yield and its related traits in different parts of the globe; however, owing to genotype-by-environment interaction, those researches lack viability for Pakistan (Naz, 2021). In Pakistan, research on genetic variability and heritability among chickpea germplasm is limited, while those assessing the correlation between physiological traits and yield are relatively non-existent (Ashfaq et al., 2017; Gul et al., 2011; Maqbool et al., 2017; Naz, 2021; Rashid et al., 2021; Shah et al., 2020; Sohail, 2018).

Based on the above discussion, the present study has the following objectives: 1) to examine genetic variability, heritability, and genetic advance among chickpea genotypes for morphological, physiological, and yield-related traits; 2) to determine the correlation between physiological and morpho-yield traits of chickpeas; 3) to identify high-yield chickpea genotypes.

MATERIALS AND METHODS

Experimental Site

The research was conducted in the Research Farm of the University of Agriculture Peshawar (UAP) from November 2020 to May 2021. With the following site coordinates, Latitude: 34.019902° and Longitude: 71.467133°.

Climatic Data

The climatic mean annual temperature and precipitation in the Peshawar region from 1980-2018 is 22.25°C and 817 mm, respectively (Ahmad et al., 2023; Burhan et al., 2021). During the research period, the minimum temperature experienced was 3°C (January 2021), while the maximum was 37.2°C (May 2021). There were 36 rainy days, with the maximum rain in March (Climate Data Processing Center - Pakistan Meteorological Department, 2021).

Plant Materials

The experimental material consisted of 18 chickpea genotypes (Table 1), of which 16 were provided by the Plant and Breeding and Genetics Department from the University of Agriculture, Peshawar. At the same time, the other two were procured from the Nuclear Institute of Food and Agriculture (NIFA) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT).

Experimental Design and Treatment Details

The genotypes were evaluated in Randomized Complete Block Design (RCBD) with three replications. Each genotype was sown in plots, which consisted of three rows, with a 3 m row length and a rows-to-row distance of 30 cm. Furthermore, the distance between adjacent plants was 10 cm.

Table 1. List of 18 genotypes studied

Serial no.	Genotypes	Origin
1	AG1	PBG, AUP
2	BG2	PBG, AUP
3	BG4	PBG, AUP
4	BG5	PBG, AUP
5	CG1	PBG, AUP
6	DG3	PBG, AUP
7	DG4	PBG, AUP
8	EG1	PBG, AUP
9	FG1	PBG, AUP
10	GG1	PBG, UAP
11	IG1	PBG, UAP
12	IG2	PBG, UAP
13	IG3	PBG, UAP
14	KG1	PBG, UAP
15	MG1	PBG, UAP
16	MG2	PBG, UAP
17	NIFA-2005	NIFA/Pakistan
18	ICC-19181	ICRISAT/India

Remarks: PBG, UAP= Department of Plant Breeding and Genetics, the University of Agriculture Peshawar; NIFA = National Institute of Food and Agriculture; ICRISAT = International Crop Research Institute for Semi-Arid Tropics

Cultural Practices

Hand weeding was practiced near maturation when excessive weeds would develop after rainfall. Emamectin benzoate was sprayed twice on the field following pod initiation to avoid a pod borer attack. The field was rain-fed, with no irrigation provided at any growth stage.

Data Taken

Days to 50% flowering (DF)

Days to 50% flowering were counted as the days from the sowing date in which 50% of the plots produced their first flower.

Plant height (cm) (PH)

The heights of randomly selected plants were recorded, from the base of the plant near the ground to the tip of the topmost leaf, using a meter rod.

Number of productive branches per plant (PB)

Primary and secondary branches were counted and summed to get productive branches per plant.

Number of pods per plant (PP)

The pods of the randomly selected plant were counted separately after harvesting, and the data was averaged for each genotype.

Number of seeds per pod (SPP)

The number of seeds per pod was determined as the average number per 10 pods.

Days to maturation (DM)

Days to maturity were recorded as the total number of days from the sowing date that a genotype took for 50% of the plot to mature.

100-seed weight (g) (HSW)

A set of 100 random seeds were weighed for each genotype.

Seed-yield (kg/ha) (SY)

The following formula determined seed yield in kg/ha.

$$\text{Seed-yield (kg/ha)} = \frac{seed\ yield\ per\ plant \times 10000}{plot\ area \times 1000} \quad \ldots\ (1)$$

Biological yield (kg/ha) (BY)

The plants were left to sun dry for four days in the field after harvest. Afterward, the whole plot with pods and seed intact was weighed in grams. The calculated weight is the biological weight of the plant. The collected data was then subjected to the following formula to convert to kg/ha.

$$\text{BY (kg/ha)} = \frac{Biological\ yield\ per\ plant \times 10000}{plot\ area \times 1000} \quad \ldots\ (2)$$

Harvest Index (%) (HI)

The Harvest index was estimated using the following formula.

$$\text{HI (\%)} = \frac{Grain\ yield\left(\frac{kg}{ha}\right) \times 100}{Biological\ yield\left(\frac{kg}{ha}\right)} \quad \ldots\ (3)$$

Relative Water Content (%) (RWC)

RWC was estimated following the protocol and estimation method (Blum & Ebercon, 1981)000 (PEG. RWC was determined using the following equation:

$$\text{RWC (\%)} = \frac{(Fresh\ weight - Dry\ weight) \times 100}{Turgid\ weight - Dry\ weight} \quad \ldots\ (4)$$

Excise Leaf Water Retention (%) (ELWR)

To calculate the Excise Leaf Water Retention (ELWR), the following protocol and formula were used following (Clarke & McCaig, 1982). ELWR was determined from the following formula:

$$ELWR\ (\%) = \frac{(Fresh\ Weight - Wilt\ Weight) \times 100}{Fresh\ Weight - Dry\ Weight} \quad \ldots (5)$$

Statistical Analysis

Analysis of variance (ANOVA) and Pearson's correlation analysis was conducted using "LibreOffice-Calc" version '7.1.1.2' (Foundation The Document., 2020). The mean difference among chickpea genotypes for various traits was determined using the Least Significant Difference (LSD) test at a 0.05% significance level (Steel et al., 1997). Heritability, genotypic coefficient variance (GCV), and phenotypic coefficient variance (PCV) were calculated following Sharma (1988). Expected Genetic Advance (G.A.%) for traits was predicted at 10% selection intensity using Allard (1999). The correlation was determined using the following formula from Sharma (1988).

$$r = \frac{\sum XY - \frac{\sum X . \sum Y}{N}}{\sqrt{\left[\sum X^2 - \left(\sum X^2 | N\right)\right]\left[\sum Y^2 - \left(\sum Y^2 | N\right)\right]}} \quad \ldots\ldots\ldots\ldots\ldots\ldots (6)$$

RESULTS AND DISCUSSION

Genetic Variability

The studied genotypes observed sufficient variation in significant differences for all traits except excise leaf water retention (Table 2). Similar results were also observed by Banik et al. (2018), Hotti & Sadhukhan (2018), Kumar et al. (2019), Majhi et al. (2020), and Srivastava et al. (2017) for the mentioned traits. However, the non-significant difference among excise leaf water retention genotypes contradicted Rashid et al. (2021) and Shah et al. (2020), which could be attributed to different environments and genotypes tested.

The mean performance of studied genotypes is given in Table 3 and Table 4. The mean for days to flowering was 106.76 days, which ranged from 99.00–111.67 days. These results indicated that selection might lead to the formation of early maturating varieties. The mean value for days to maturity was 156.02 days, ranging from 150.67-161.67 days. Seed yield ranged from 324.69 to 1061.73 kg/ha with an average of 817.9 kg/ha, indicating that improvement is possible for seed yield.

Phenotypic and Genotypic Coefficient of Variability

CGCV and PCV of different traits are given in Table 5. Slight differences between GCV and PCV mean that greater variability was due to the genetic makeup of genotypes (Kumar et al., 2019). The highest GCV and PCV values were found for harvest index (38.92% and 42.96%) and biological yield (25.39% and 36.14%). (Table 3).

A greater GCV indicates the existence of high genetic variability among the studied genotypes. Hence, higher GCV would mean more options to select from effectively and vice versa (Mallu et al., 2014). Thus, harvest index, biological yield, and seeds per pod in the present study have a better chance of improvement than any other trait owing to their greater GCV.

Heritability and Genetic Advance

The highest broad sense heritability was manifested for harvest index (0.82) followed by seeds per pod (Table 3), similar to Swetha et al. (2019) for seed yield. Moderate heritability was manifested for relative water content (0.30), plant height (0.38), productive branches per plant (0.41), and pods per plant (0.46), similar to the finding of Kumar et al. (2019) and Majhi et al. (2020).

High heritability and moderate G.A.% observed for days to flowering (0.75 and 3.95%) and days to maturity (0.67 and 2.69%) in this study follow those of Kumar et al. (2020). Moreover, moderate heritability (0.49) but high G.A.% (31.39%) was recorded for biological yield, which is backed by Srivastava et al. (2017) and Swetha et al. (2019), who recorded heritability similar to this study. These results indicate that selection would be better if conducted in later generations. Moreover, low heritability (0.3) and G.A.% (4.97%) were observed for relative water content in this study which conflicts with Attri et al. (2018), who observed high heritability as well as G.A.%. These contradictions might be influenced by the difference of genotypes and the experimental environment.

Trait Associations

Days to flowering were found to have a highly significant ($p<0.01$) positive correlation ($r=0.86^{**}$) with days to maturity (Table 6). On the other hand, a significant negative correlation existed with seeds per pod ($r= -0.67^{**}$), biological yield ($r= -0.46$), relative water content ($r= -0.2^{*}$), and excise leaf water retention ($r= -0.11$).

Table 2. Mean Square for various traits of chickpea genotypes

SOV	df	DTF	PH	PB	PP	DTM	SPP	SY	HSW	BY	HI	RWC	ELWR
Replication	2	2.80	1.35	0.32	15.89	2.57	0.00	6,235.57	1.51	289,334.22	9.68	4.80	670.71
Genotypes	17	25.29	63.71	5.17	162.97	29.59	0.27	95,790.78	90.55	1,610,983.04	660.83	85.87	41.30
Error	34	2.48	22.42	1.69	45.62	4.14	0.03	38,045.47	41.90	410,643.02	44.75	37.82	73.04
C.V. (%)	-	1.48	10.30	8.55	18.49	1.30	13.01	23.85	26.16	25.72	18.17	7.96	31.45
LSD (0.05)	-	2.61	7.86	2.16	11.21	3.38	0.28	323.62	10.74	1,063.19	11.10	10.20	14.18

Remarks: SOV = source of variation, C.V. = coefficient of variation, df = degree of freedom, DTF = days to 50% flowering, PH = plant height, PB = productive branches per plant, PP = pods per plant, DTM = days to maturity, SPP = seeds per pod, SY = seed-yield, HSW = hundred-seed weight, BY = biological-yield, HI = harvest index, RWC = relative water content, ELWR = excise leaf water retention

Table 3. Mean ± standard deviation for various traits of studied chickpea genotypes

Genotypes	DTF	PH	PB	PP	DTM	SPP
AG1	105.33 ±0.58	45.62±1.91	14.56±2.27	36.56±7.68	154.33±1.53	1.51±0.16
BG2	103±1	42.72±4.57	15.78±1.58	30.33±1.84	150.67±1.15	1.62±0.07
BG4	105±2	46.40±4.15	15.9±2.18	33.89±7.56	155±1	1.61±0.05
BG5	105±0.58	45.29±2.91	13.56±1.02	26.56±9.03	153.67±1.53	1.21±0.18
CG1	107.33±2.08	43±2.62	14.56±1.35	29±2	157±3.61	1.34±0.13
DG3	109.67±2.52	42.64±2.33	15.36±1.02	37.33±1.53	158.67±3.06	1.25±0.11
DG4	108.33±2.52	47.78±6.52	16±1.45	48.56±2.22	155.67±1.53	1.41±0.36
EG1	104.67±2.52	52.45±3.85	14.75±1.39	31±1.0	154.67±2.31	1.13±0.25
FG1	111.67±0.58	35.69±1.50	15.45±1.22	52±1.0	161.67±1.53	0.53±0.11
GG1	107.33±1.15	37.08±3.55	12±0.33	31±3.48	160.33±2.31	0.82±0.20
ICC-19181	106.33±1.53	49.69±5.63	16.78±1.84	45±1.0	153.67±2.89	1.23±0.14
IG1	106.33±2.08	45.83±6.29	14.9±0.53	28.22±7.6	156.33±2.08	1.35±0.02
IG2	99±1	51.72±6.88	17.11±1.38	44±1.0	151±2	1.72±0.19
IG3	108.67±0.58	52.43±4.56	16.67±0.58	44±1.0	159.67±1.53	1.22±0.23
KG1	108.67±2.08	48.3±4.56	15.33±0.5	36±1.0	157.67±1.15	1.15±0.05
MG1	109.33±0.58	48.19±5.18	14.52±0.36	34.45±10.19	158.67±1.15	1.48±0.10
MG2	108.33±0.58	46.86±5.38	13.65±0.84	32.22±9.89	157.33±2.08	0.99±0.12
NIFA-2005	105.33±1.15	45.78±3.37	16.78±0.3	37.33±12.84	152.33±1.53	1.58±0.07
P-value	7.97765E-09	4.66E-03	2.67E-03	7.71E-04	6.60E-07	1.55E-08
LSD (0.05)	2.61	7.86	2.16	11.21	3.38	0.28
C.V (%)	1.48	10.3	8.55	18.49	1.3	13.01

Remarks: DTF = Days to 50% flowering, PH = plant height, PB = productive branches per plant, PP = pods per plant, DTM = days to maturity, SPP = seeds per pod

Table 4. Mean ± standard deviation for various traits of studied chickpea genotypes (continued)

Genotypes	SY	HSW	BY	HI	RWC	ELWR
AG1	930.86 ±206.62	28.43 ±6.31	3,209.88 ±950.30	31.77 ±15.32	71.11 ± 3.35	25.10 ± 9.73
BG2	993.83 ±298.93	30.35 ±9.13	2,098.77 ±595.30	42.33 ±5.41	78.31 ± 7.57	26.00 ± 6.15
BG4	998.77 ±240.21	30.51 ±7.34	2,902.00 ±2.65	34.41 ±8.26	75.35 ± 2.31	24.73 ± 7.25
BG5	804.94 ±23.52	23.24 ±1.75	2,345.68 ±770.10	37.25 ±1	79.25 ± 12.90	28.50 ± 10.66
CG1	835.80 ±260.43	25.53 ±7.95	2,592.59 ±848.63	32.67 ±5.45	74.75 ± 7.70	23.62 ± 10.11
DG3	830.86 ±102.53	22.08 ±2.02	3,245.11 ±5.03	25.61 ±3.18	78.25 ± 10.29	24.72 ± 12.68
DG4	916.05 ±142.93	27.98 ±4.37	2,592.59 ±848.63	39.70 ±1	74.67 ± 4.58	29.05 ± 8.63
EG1	727.16 ±3.0	22.21 ±10.43	2,592.59 ±667.69	29.22 ±6.88	78.23 ± 4.79	36.47 ± 21.22
FG1	324.69 ±66.70	9.92 ±2.04	925.93 ±320.75	36.67 ±6.96	67.33 ± 0.58	29.36 ± 4.60
GG1	559.26 ±90.80	17.08 ±2.77	740.74 ±370.37	93.83 ±1	75.84 ± 3.52	33.25 ± 24.43
ICC-19181	809.88 ±177.83	24.40 ±5.34	2,283.95 ±748.42	36.60 ±8.25	79.33 ± 4.59	22.81 ± 2.61
IG1	829.63 ±13.35	25.34 ±0.41	2,530.86 ±466.04	33.61 ±6.84	76.42 ± 1.70	22.53 ± 0.39
IG2	1,061.73 ±336.70	32.43 ±10.28	3,765.43 ±213.83	28.03 ±7.9	82.84 ± 7.01	28.83 ± 5.24
IG3	813.58 ±295.28	24.85 ±9.02	2,530.86 ±565.75	31.57 ±4.41	93.67 ± 6.03	23.98 ± 6.07
KG1	787.65 ±158.93	24.06 ±4.86	2,407.41 ±667.69	33.90 ±8.25	75.78 ± 6.45	30.20 ± 7.74
MG1	911.11 ±233.89	27.83 ±7.14	2,839.51 ±913.50	34.88 ±1	77.58 ± 2.07	26.78 ± 7.44
MG2	609.88 ±192.32	18.63 ±5.88	2,222.22 ±848.63	27.89 ±1.78	73.25 ± 4.99	24.74 ± 4.11
NIFA-2005	976.54 ±43.87	29.83 ±1.34	3,024.69 ±385.49	32.75 ±5.53	78.18 ± 2.34	28.41 ± 2.13
P-value	1.07E-02	2.74E-02	3.41E-04	5.06E-11	2.05E-02	8.94E-01
LSD (0.05)	323.62	10.74	1,063.19	11.10	10.20	14.18
C.V (%)	23.85	26.16	25.72	18.17	7.96	31.45

Remarks: SY = seed-yield, HSW = hundred-seed weight, BY = biological-yield, HI = harvest index, RWC = relative water content, ELWR = excise leaf water retention

Table 5. Variance components, heritability, genotypic and phenotypic coefficient of variance and genetic advance of studied traits

Characters	Ve	Vg	Vp	GCV (%)	PCV (%)	H^2	GA	GAM
Days to flowering	2.48	7.6	10.08	2.58	2.97	0.75	4.21	3.95
Plant height	22.42	13.76	36.19	8.07	13.09	0.38	4.03	8.76
Productive branches per plant	1.69	1.16	2.85	7.09	11.1	0.41	1.21	7.96
Pods per plant	45.62	39.12	84.73	17.12	25.2	0.46	7.48	20.48
Day to maturity	4.14	8.48	12.62	1.87	2.28	0.67	4.20	2.69
Seeds per pod	0.03	0.08	0.11	22.12	25.66	0.74	0.43	33.56
Seed-yield	38,045.47	19248.44	57293.91	16.96	29.27	0.34	141.53	17.30
Hundred-seed weight	41.90	16.22	58.11	16.27	30.81	0.28	3.74	15.13
Biological-yield	410,643.02	400113.34	810756.36	25.39	36.14	0.49	782.08	31.39
Harvest Index	44.75	205.36	250.11	38.92	42.96	0.82	22.85	62.08
Relative Water Content	37.82	16.02	53.84	5.18	9.5	0.3	3.84	4.97
Excise Leaf Water Retention	73.04	-	-	-	-	-	-	-

Remarks: Ve = environmental variance, Vg = genetic variance, Vp = phenotypic variance, GCV = genetic coefficient of variance, PCV = phenotype coefficient of variance, H^2 = broad sense heritability, GA = genetic advance, GAM = genetic advance as percentage of mean

Table 6. Correlation among all the studied traits

	DTF	PH	PB	PP	DTM	SPP	BY	SY	HSW	RWC	ELWR	HI
DTF	-											
PH	-0.36	-										
PB	-0.27	0.48*	-									
PP	0.23	0.06	0.61**	-								
DTM	0.86**	-0.41	-0.41	0.19	-							
SPP	-0.67**	0.50*	0.48*	-0.17	-0.74**	-						
BY	-0.47	0.66**	0.51*	-0.03	-0.54*	0.81**	-					
SY	-0.63**	0.54**	0.49*	-0.16	-0.73**	0.99**	0.81**	-				
HSW	-0.65**	0.56**	0.49*	-0.15	-0.73**	0.99**	0.78**	0.99**	-			
RWC	-0.20	0.61**	0.39	0.03	-0.15	0.32	0.32	0.39	0.37	-		
ELWR	-0.11	-0.05	-0.28	-0.01	0.05	-0.32	-0.30	-0.30	-0.28	-0.13	-	
HI	0.06	-0.53*	-0.57**	-0.16	0.28	-0.35	-0.69**	-0.33	-0.31	-0.11	0.39	-

Remarks: * = significant at 0.05 significance level, ** = significant at 0.01 significance level, DTF = days to 50% flowering, PH = plant height, PB = productive branches per plant, PP = pods per plant, DTM = days to maturity, SPP = seeds per pod, BY = biological-yield, SY = seed-yield, HSW = hundred-seed weight, RWC = relative water content, ELWR = excise leaf water retention, HI = harvest index

The current study shows days to flowering are highly significant, positively correlated with days to maturity, and negatively correlated with seed yield, hundred-seed weight, and seeds per pod. This suggests that days to maturity could be predicted by days to flowering and that late flowering and maturation ultimately result in lower yield. This could be probable because late maturation/flowering plants have to bear higher monsoon heat stress, which could devastate their yield. These results correspond with Karthikeyan et al. (2022) and Kumar et al. (2020). The current study found that days to maturity were negatively correlated with seed yield, hundred-seed weight, seeds per pod, and biological yield; these associations are advocated by Kumar et al. (2020). This study's results associated between biological yield and seed yield are supported by Attri et al. (2018), Karthikeyan et al. (2022), Kumar et al., (2020), and Srivastava et al. (2017), who obtained results similar to this research.

CONCLUSION

Sufficient genetic variability was observed among the tested 18 genotypes of chickpeas. Heritability was high for traits, namely, seeds per pod, days to flowering, and days to maturity; thus, further improvement is possible. Seed yield had a significantly positive correlation with seeds per pod, hundred-seed weight, biological yield, plant height, and productive branches per plant. Therefore, these traits indirectly select higher-yielding genotypes of chickpeas. Genotypes BG2 and IG2 showed early maturity and could be used to develop early-maturing varieties. Genotype IG3 exhibited maximum. Genotypes IG2, BG4, and BG2 yielded higher than the checks, and they could produce high-yielding varieties in future breeding programs. Correlation analysis suggests that Indirect selection for seed yield could be conducted by selecting genotypes with higher magnitudes of plant height, productive branches, seeds per pod, biological yield, and hundred-seed weight, or early flowering and maturing features.

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