Original Research Article

Effects of yield contributing characters on seed yield in black gram [*Vigna mungo* L. Hepper]

ABSTRACT

The present study was designed in order to evaluate the genetic variability parameters, correlation coefficients and path analysis in black gram genotypes for eastern zone of Uttar Pradesh, India.Twenty-one genotypes of black gram were evaluated for the study. The experiment was conducted in a Randomized Block Design with three replications during the *Kharif* season 2023 at the Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agriculture Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Naini, Prayagraj, U.P. the plant to plant distance was 10 cm and row to row distance was 30 cm. the data were recorded from randomly selected five plants for each genotype for each replication for thirteen characters *viz*. days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index and seed yield per plant (g).From the present investigation it is concluded that analysis of variance showed significant variation among different genotypes for all characters studied. The number of pods per plant, number of clusters per pod, number of primary branches per plant, seed yield per plant, biological yield, harvest index and plant height exhibited high estimates of GCV and PCV. Genetic parameters also revealed that high heritability (broad sense) was observed for harvest index, biological yield, seed yield per plant, seed index, number of pods per plant, days to maturity, days to 50% flowering, number of primary branches per plant, number of clusters per plant, plant height, days to 50% pod setting, number of seeds per pod. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with days to 50% flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, seed index and biological yield at phenotypic level. Path coefficient analysis revealed that characters like biological yield, harvest index, seed index, number of seeds per pod, pod length, number of clusters per plant, days to 50% pod setting and days to 50% flowering showed the maximum positive direct effects on seed yield at the phenotypic level.This indicated that seed yield was mainly a product of direct and indirect impact of the above attributing characters and priority should be given to these characters during selection for improvement in black gram.

Keywords: *Vigna mungo*,GCV, PCV, Variability, Heritability, Path coefficient.

Introduction

"Pulse crops are the most important food crops after cereals, referred to as "grains legumes." They are rich sources of proteins containing about 20-30% of protein content. In India, pulse are an integral part of the diet as also a source of protein and also rich in Calcium and Phosphorous. It is the second major source of dietary protein (27%) after cereals (55%). The share of animal protein is as low as 18%" (**Saran *et al.*, 2021**). "Food legumes are commonly known as "poor man's meat" because of their high protein content, low price and widespread access to the poor. Pulses can fix atmospheric nitrogen and their deep penetrating root system enables the plants to utilize limited available moisture more efficiently. It improves the physical condition of the soil like soil aeration, water holding capacity, improving microbial population, breaking of hard pans and moisture retention. Pulses can be use as catch crop, cover crop, intercrop, and crop rotation.Black gram botanically known as *Vigna mungo* [(L.) Hepper], popularly known as urdbean or mash, is a grain legume domesticated from *Vigna mungo var. silvestris*. It is also a good source of phosphoric acid and calcium. It contains a wide variety of nutrients and is popular for its fermenting action and thus it is largely used in making fermented foods. Black gram, cultivated as a sole crop and intercrop. Black gram is an important short duration crop widely cultivated in India which gives us an excellent source of easily digestiblequality protein and the ability to restore the fertility of soil through symbiotic nitrogen fixation. Black gram is a perfect combination of all nutrients which include 20 to 25% of proteins which is almost three times that of cereals, 40 to 47% of starch along with ash, fats, carbohydrates, and essential vitamins. Black gram is reported to be originated in India. India is the largest producer and consumer of Black gram in the world. Black gram is an annual, short duration, self-pollinated, leguminous crop that belongs to family Leguminosae sub-family Papillionaceae with a chromosome number of 2n=2x=22, it is commonly known as urd bean" (**Khan *et al.*, 2020**). "Yield is considered as an end product of a set of plant processes which are related to each other. It is very complex trait which controlled by poly genes and interlinked with other yield components; hence it is very difficult often to improve yield directly. It can be achieved by improving closely related traits. The systematic collection of black grams has displayed inadequate variability for biotic and abiotic genes. It is possible that genes for high productivity could have been lost due to overriding role of natural selection" (**Roopalakshmi*et al.*, 2003**) and the genetic base of the present-day collection remains poor due to lack of variability owing to its autogamous nature. "The creation of variability is difficult through hybridization due to its high self-pollination and flower droop" (**Deepalakshmi and Anandakumar, 2004**). "Besides the major constrains in achieving higher yield of black gram is absence of suitable ideotypes for different cropping system, poor harvest index and susceptibility to disease" (**Souframanien and Gopalakrishnan, 2004**). "Plant breeders can begin their breeding programmes with germplasm, which is the basic material at their disposal. Genetic variability for both qualitative and quantitative traits is included. Plant breeders can benefit greatly from a thorough understanding of how mungbean germplasm is categorised based on these traits, as it can help with crop selection and improvement. For any endeavour to improve crops, genetic variability and its quantification for both qualitative and quantitative traits of economic significance are essential. With the help of this information, breeders can start successful breeding programmes by identifying superior parents who possess desired traits. Therefore, it is essential to have superior parents who demonstrate high heritability and genetic advancement across a variety of traits for any yield enhancement initiative.The significance of genetic variability was initially recognized by Russian scientist" (**Vavilov, 1935**), who advised that a wide range of variability offers better opportunities for selecting desirable genotypes. Assessments of correlation coefficients offer a chance to determine the strength and direction of the relationship between yield and its component traits as well as among various traits (**Panigrahi and Baisakh, 2014**). "An effective statistical method known as path coefficient analysis was created specifically to measure the relationships between various components and their direct and indirect impacts on grain yield" (**Pushpa et al., 2013**). Therefore, the present research was designed in order to evaluate the genetic variability parameters, correlation coefficients and path analysis in black gram genotypes for eastern zone of Uttar Pradesh.

MATERIALS AND METHODS

The present study aimed to explore the genetic diversity, heritability, and trait associations among different black gram varieties. It was carried out at the Experimental Research Centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj, during the Kharif season of 2023. SHUATS is situated approximately 5 kilometres from Prayagraj City, on the left side of the Prayagraj–Rewa National Highway.At the Naini Agricultural Institute of Sam Higginbottom University of Agriculture, Technology, and Sciences in Prayagraj, Uttar Pradesh, the Department of Genetics and Plant Breeding supplied labour, inputs, irrigation facilities, field preparation, and other resources needed for a crop's successful cultivation. Prayagraj is situated in Agroclimatic Zone V's central plain sub-zone.

Naini is situated between longitudes 73° 27' 58" and 73° 56' 36" E and latitudes 20° 33' 40" to 21".50' N. This area experiences moderately hot summers, mildly cold winters, and warm, humid monsoons. Heavy rains usually fall in this area between June and September. The south-west advancing monsoon, which is most noticeable in July and August, is when most of the precipitation falls.The land used for the experiment is levelled, and the soil is a uniformly fertile sandy loam with a high sand content and low clay content. Soil samples were taken at a depth of 0 to 30 cm, chosen at random. The soil was then tested for available potassium (206.11 kg/ha), available phosphorus (4.56 kg/ha), available nitrogen (142.33 kg/ha), organic carbon (0.52%), and pH (7.1). Ten centimetres separated plants and thirty centimetres separated rows.“The data were recorded from randomly selected five plants for each genotypes for each replications for thirteen characters *viz.* thirteen characters *viz.* days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed index (g), biological yield (g), harvest index and seed yield per plant (g). The experiment was set up using a Randomized Block Design (RBD). The Fisher and Yates, 1963 method was used to statistically analyse the data”(**Johnson*et al.*, 1955)**; formulae was used to calculate GCV and PCV. Heritability (in the broad sense) was eliminated by the formula **Burton and Devane (1953)**. Correlation was calculated using methods suggested by **Al-Jibouri*et al.*, (1958)** while path coefficient analysis was worked out my method suggested by **Dewey and Lu (1959)**. The details of genotypes used in experiment has been enlisted below in table 1.

RESULTS AND DISCUSSION

Analysis of Variance

Mean sum squares data for 13 characters were subjected to analysis of variance for experimental design. The analysis of variance for different characters calculated is presented in Table 2. The analysis of variance showed highly significant differences (α=0.05) among 20 genotypes for all characters studied indicating the presence of considerable amount of genetic variability among black gram germplasms. It also indicated the scope of selection for genetic improvement of black gram. Based on data on character values and analysis of variance, significant genotype differences were found for all 13 characters, indicating that the material has enough genetic variability to support a breeding programme aimed at increasing the yield of black gram seeds. The results are in line with studies conducted by **Patel and Bala (2020); Yergude*et al.*, (2021)** and **Deekshith *et al.*, (2007)**.

Genetic parameters

From table 3, Wide range of differences observed for genotypic coefficient of variation (GCV) varied from 5.51% (days to 50% pod setting) to 43.83% (number of pods per plant)suggesting a significant degree of genotype variability. Phenotypic coefficient of variation (PCV) varied from 5.97% (days to 50% flowering) to 45.98% (number of pods per plant).Characters like number of pods per plant, seed index, harvest index, biological yield and seed yield per plant observed to have comparably less difference between its GCV and PCV value predicting lesser influence of environment in expression of character by genotypes. Rest characters observed to have comparably significant and more difference between GCV and PCV value depicting greater influence of environment on expression of character. **Baral *et al.*, (2022), Rana *et al.*, (2022), Gnanasekaran *et al.*, (2023)**have previously reached similar conclusions. The characters that showed lesser influence of environment on expression should be selected for breeding programme.

Black gram germplasm exhibited the highest GCV and PCV for number of pods per plant, number of clusters per pod, number of primary branches per plant, seed yield per plant, biological yield, harvest index and plant height. In black gram germplasm, however, the number of seeds per plant and seed index revealed the moderate GCV and PCV. These characters displayed a high degree of genetic variability in comparison to other characters, indicating that hybridization and selection-induced variability can be used to improve crops. The low GCV and PCV values of variances were noted for the remaining characters studied.

High PCV and GCV was recorded for number of pods per plant, number of clusters per plant in black gram was earlier reported by **Arulbalachandran*et al.*, (2010), Chaithanya *et al.*, (2019)**, and for biological yield, harvest index and plant height by **Khan *et al.*, (2020)**. Moderate PCV and GCV were recorded for seed index was earlier concluded by **Mishra and Lavanya (2021)**. The results obtained for PCV and GCV showed that there is considerable possibility of further improvement through hybridization followed by appropriate selection for these characters.

Genetic variability

Given that environmental factors can modify a genotype's phenotypic expression at different stages of development, the heritability estimate of a quantitative character is crucial. The degree to which genotypes can be effectively selected based on phenotypic variation is indicated by their heritability. However, because the environment can mask the genotypic effect, selection might not be effective for a character with low heritability. The amount of heritable variation determines how selection responds. Therefore, it is desirable to partition the observed variability into heritable and non-heritable components. Burton (1952) suggested that GCV along with heritability would give a better idea about the efficiency of selection. Thus, a character with high GCV and high heritability will be more valuable in selection programme. As demonstrated by Johnson *et al.* (1955), heritability can be categorized as low (0-30%), moderate (30-60%) and high (60% and above). In present study, the estimates of heritability (%) in broad sense for 13 characters studied, ranged from 52.80 % to 99.40% for pod length and harvest index respectively. High heritability (broad sense) (>60%) was recorded for harvest index, biological yield, seed yield per plant, seed index, number of pods per plant, days to maturity, days to 50% flowering, number of primary branches per plant, number of clusters per plant, plant height, days to 50% pod setting, number of seeds per pod. Moderate heritability (broad sense) (30-60%) was observed for pod length. Such characters, according to **Panse and Sukhatme (1957),** are primarily controlled by additive gene action and, because of their high heritability values, could be enhanced by individual plant selection. Similar results for high heritability for number of pods per plant, biological yield was reported earlier by **Patel and Bala(2020), Bharathi *et al.*, (2022)**. High heritability was found earlier by **Saran *et al.*, (2021), Yergude*et al.*, (2021), and Aman and Singh (2022)** for the number of seeds per pod, harvest index, seed index, plant height. High heritability was also observed in number of clusters per plant per plant **Bharathi *et al.*, (2022), Deekshith *et al.*, (2022), and Gnanasekaran *et al.*, (2023)** came to similar conclusions in their research.

In the current study, For the number of pods per plant, number of clusters per pod, number of primary branches per plant, seed yield per plant, biological yield, harvest index and plant height, in the current study found high GCV coupled with high estimate of heritability, and high genetic advance as a percentage of mean. In addition to High heritability with moderate GCV coupled with high to genetic advance as percent of mean was observed for number of seeds per pod and seed index. Since these characteristics are determined by additive gene effects, direct selection may be used to enhance them. **Chaithanya *et al.*, (2019), Saran *et al.*, (2021), and Mishra and Lavanya (2021)** all reported similar results for the harvest index.

Correlation and path analysis

The potential productivity of a crop is fundamentally determined by its seed yield per unit area. Improving this trait through direct selection is challenging due to its polygenic nature, which depends on various contributing characteristics and environmental factors. Therefore, it is crucial to estimate the relationship between seed yield and these contributing traits, as well as the interrelationships among the traits themselves. Selection efficiency can be enhanced by selecting for multiple traits that are associated with yield simultaneously.

For quantitative traits, the genotype, which is influenced by the environment, affects their phenotypic expression, association, and the direction of their association. By examining the strength and direction of correlations, one can determine how changes in one trait will affect others. A high positive correlation coefficient between contributing traits and seed yield is important for indirect selection for seed yield. The "t-test" is commonly used to test the phenotypic correlation coefficient, as there is no suitable significance test for the genotypic correlation coefficient.

Positive and significant correlation was observed for days to 50% flowering (0.366**), plant height (0.585*), number of primary branches per plant (0.722**), number of clusters per plant (0.694**), number of pods per plant (0.517*), seed index (0.645**) and biological yield (0.872**) were all positively correlated with the seed yield per plant. While days to 50% pod setting (-0.288*) and days to maturity (-0.851**) showed negative significant correlation with seed yield in black gram at phenotypic level (Table 4).For phenotypic correlation coefficient, **Sagar *et al.*, (2021), and Mishra and Lavanya (2021)** reported significant and positive correlation with seed yield per plant for plant height, number of primary branches. **Aman and Singh (2021), Saran *et al.*, (2022) and Vikas *et al.*, (2023)** concluded seed yield per plant to be significantly and positively correlated with number of pods per plant, pod length and seed index. Seed yield per plant had negative and significant correlation with days to maturity, similar results were also reported by **Yadav *et al.*, (2023)**.

Path coefficient analysis was conducted using seed yield per plant as the dependent variable to break down the correlation coefficient into direct and indirect effects, aiming to identify the contribution of various traits to seed yield. This analysis revealed a consensus on the direction and magnitude of the direct effects of different traits and their correlation with seed yield. Therefore, selecting traits that have a high positive direct effect should lead to a significant increase in seed yield.

In the present investigation, at phenotypic level (Table 5 and Figure 1) the highest positive direct effects on seed yield at phenotypic level was depicted by biological yield, harvest index, seed index, number of seeds per pod, pod length, number of clusters per plant, days to 50% pod setting and days to 50% flowering while the days to maturity, plant height, number of primary branches per plant and number of pods per plant showed the maximum negative direct effects.The residual component of phenotypic path analysis indicated that 78.30% of variability of seed yield was accounted for by these thirteen characters. Similar results have been reported from earlier researchers. **Sagar *et al.*, (2021), Saran *et al.*, (2022)** reported that seed index had maximum positive direct effect on seed yield per plant. Senthilkumar *et al.*, (2018) reported number of primary branches per plant had positive direct effect on seed yield. Seed index and biological yield, harvest index, number of seeds per pod, pod length, number of clusters per plant having positive direct effect on seed yield for black gram, similar conclusion was also drawn by **Sohel *et al.*, (2016), Suryawanshi*et al.*, (2018) and Charitha and Lal (2021)**. Hence selection based on these characters would bring an improvement in seed yield in black gram.

CONCLUSION

From the present investigation it is concluded that analysis of variance showed significant variation among different genotypes for all characters studied. Number of pods per plant, number of clusters per pod, number of primary branches per plant, seed yield per plant, biological yield, harvest index and plant height exhibited high estimates of GCV and PCV. Genetic parameters also revealed that high heritability (broad sense) was observed for harvest index, biological yield, seed yield per plant, seed index, number of pods per plant, days to maturity, days to 50% flowering, number of primary branches per plant, number of clusters per plant, plant height, days to 50% pod setting, number of seeds per pod. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive association with days to 50% flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, seed index and biological yield at phenotypic level. Path coefficient analysis revealed that characters like biological yield, harvest index, seed index, number of seeds per pod, pod length, number of clusters per plant, days to 50% pod setting and days to 50% flowering showed the maximum positive direct effects on seed yield at the phenotypic level.This indicated that seed yield was mainly a product of direct and indirect effects of above attributing characters and priority should be given to these characters during selection for improvement in black gram.

Table 1 Genotypes Details

S. No	Genotypes	S. No	Genotypes	S. No	Genotypes	S. No	Genotypes
1	PLU-1016	6	PLU-86-C	11	AKU-13-15	16	TBG-104
2	IPU 99-18	7	DH-85-2	12	PLU-302	17	KV – 96-14
3	KC-153	8	BGP-21-28	13	PLU-547	18	PU-31
4	TLC-328	9	VBN-08	14	LBG-648	19	PLU-856
5	ADT-3	10	VBN-11-16	15	PL-416	20	SHEKAR-2 (**check**)

Table 2 Analysis of Variance (ANOVA) for 13 characters in black gram.

Characters		**Mean sum of Squares**		
		Replication (*df*=2)	**Genotypes (*df*=19)**	**Error (*df*=38)**
01	Days to 50% flowering	1.32	18.40**	0.74
02	Days to 50% pod setting	0.95	28.60**	4.06
03	Days to Maturity	19.32	137.00**	4.72
04	Plant height	183.75	553.87**	46.33
05	Number of primary branches	1.72	29.79*	1.96
06	Number of clusters per plant	0.95	43.20**	2.86
07	Number of pods per plant	15.82	224.52**	7.29
08	Pod length	0.11	0.30*	0.07
09	Number of seeds per pod	1.95	1.88**	0.32
10	Seed Index	0.03	0.73**	0.01
11	Harvest index	0.35	144.96*	0.29
12	Biological yield	1.69	91.28**	1.06
13	Seed yield per plant	0.15	7.71**	0.02

Table 3. Genetic Parameters for 13 characters of 20 Black gram genotype.

Sl. No.	Characters	Range	GCV (%)	PCV (%)	h2 (Broad Sense) (%)	Genetic Advance	Genetic Adv. as percent of Mean
1	**Days to 50% flowering**	39.33-47.00 days	5.63	5.97	88.90	4.71	10.93
2	**Days to 50% pod setting**	48.00-55.67 days	5.51	6.74	66.90	4.82	9.28
3	**Days to Maturity**	59.67-80.00 days	9.91	10.43	90.30	13.00	19.40
4	**Plant height**	31.33-83.00 cm	22.50	25.40	78.50	23.74	41.07
5	**Number of primary branches**	4.67-13.67 branches/plant	32.51	35.79	82.50	5.70	60.85
6	**Number of clusters per plant**	4.00-16.00 clusters/plant	41.20	45.37	82.40	6.86	77.06
7	**Number of pods per plant**	10.00-39.67 pods/plant	43.83	45.98	90.90	16.71	86.05
8	**Pod length**	3.23-4.53 cm	6.96	9.57	52.80	0.41	10.42
9	**Number of seeds per pod**	3.67-6.33 seeds/pod	13.99	17.77	62.00	1.17	22.70
10	**Seed Index**	3.87-5.40 g	11.16	11.49	94.40	0.98	22.34
11	**Harvest index**	17.98-54.51%	24.25	24.32	99.40	14.26	49.81
12	**Biological yield**	8.37-26.66 g	25.90	26.35	96.60	11.10	52.44
13	**Seed yield per plant**	3.22-7.37 g	27.49	27.57	95.23	3.29	56.46

Table 4. Correlation coefficient between yield and its attributing traits in 20 black gram genotypes at phenotypic level

Phenotypical Correlation Matrix													
Characters	**DF50**	**DPS50**	**DM**	**PH**	**NPB**	**NCPP**	**NPPP**	**PL**	**NSPP**	**SI**	**HI**	**BY**	**SYPP**
DF50	**1.000**	-0.133	-0.295*	0.197	0.229	0.092	0.182	-0.180	-0.218	0.207	0.277*	0.215	0.366**
DPS50		**1.000**	0.258*	-0.036	0.089	-0.212	-0.155	-0.256*	-0.151	0.078	0.124	-0.325*	-0.288*
DM			**1.000**	-0.606**	-0.732**	-0.596**	-0.353**	-0.056	-0.072	-0.691**	-0.061	-0.757**	-0.851*
PH				**1.000**	0.504**	0.500**	0.241	-0.167	0.054	0.467**	-0.241	0.689**	0.585**
NPB					**1.000**	0.568**	0.505**	0.157	0.048	0.595**	0.088	0.650**	0.722**
NCPP						**1.000**	0.510**	0.189	0.505**	0.430**	0.026	0.643**	0.694**
NPPP							**1.000**	0.320*	0.295*	0.326*	0.049	0.481**	0.517**
PL								**1.000**	0.234	-0.020	-0.071	0.242	0.243
NSPP									**1.000**	0.124	-0.011	0.177	0.223
SI										**1.000**	-0.004	0.592**	0.645**
HI											**1.000**	-0.346**	0.092
BY												**1.000**	0.872**

Abbreviations: - DF50:-Days to 50% flowering**, DPS50:-**Days to 50% pod setting**, DM:-**Days to maturity**, PH:-**Plant height (cm)**, NPB:-**Number of primary branches per plant**, NCPP:-**Number of clusters per plant**, NPPP:-**Number of pods per plant**, NSPP:-**Number of seeds per pod**, PL:-**Pod length (cm)**, SI:-**Seed index (g)**, BY:-** Biological Yield (g)**, HI:-**Harvest index (%)**, SYPP:-**Seed yield per plant (g)**.**

*,** **at 5% and 1% Level of Significance**

Table 5. Direct and Indirect effects of yield attributing traits on seed yield at phenotypic level in black gram genotypes

Phenotypic Path matrix												
Characters	**DF50**	**DPS50**	**DM**	**PH**	**NPB**	**NCPP**	**NPPP**	**PL**	**NSPP**	**SI**	**HI**	**BY**	**SYPP**
DF50	**0.0713**	-0.0095	-0.0211	0.0141	0.0163	0.0066	0.013	-0.0128	-0.0156	0.0147	0.0197	0.0153	0.366**
DPS50	-0.0031	**0.0236**	0.0061	-0.0008	0.0021	-0.005	-0.0037	-0.006	-0.0036	0.0018	0.0029	-0.0077	-0.288*
DM	0.0566	-0.0493	**-0.1916**	0.1162	0.1403	0.1141	0.0676	0.0107	0.0138	0.1324	0.0117	0.145	-0.851*
PH	-0.0067	0.0012	0.0207	**-0.0341**	-0.0172	-0.0171	-0.0082	0.0057	-0.0018	-0.0159	0.0082	-0.0235	0.585**
NPB	-0.0039	-0.0015	0.0124	-0.0085	**-0.017**	-0.0096	-0.0086	-0.0027	-0.0008	-0.0101	-0.0015	-0.011	0.722**
NCPP	0.0013	-0.0029	-0.0081	0.0068	0.0078	**0.0137**	0.007	0.0026	0.0069	0.0059	0.0004	0.0088	0.694**
NPPP	-0.0021	0.0018	0.0041	-0.0028	-0.0059	-0.0059	**-0.0116**	-0.0037	-0.0034	-0.0038	-0.0006	-0.0056	0.517**
PL	-0.0103	-0.0146	-0.0032	-0.0095	0.0089	0.0108	0.0182	**0.057**	0.0134	-0.0012	-0.004	0.0138	0.243
NSPP	-0.0148	-0.0102	-0.0049	0.0036	0.0032	0.0342	0.02	0.0159	**0.0678**	0.0084	-0.0007	0.012	0.223
SI	0.0046	0.0017	-0.0153	0.0104	0.0132	0.0096	0.0072	-0.0004	0.0027	**0.0222**	-0.0001	0.0131	0.645**
HI	0.095	0.0424	-0.0209	-0.0827	0.0303	0.0089	0.0169	-0.0243	-0.0036	-0.0014	**0.3434**	-0.1189	0.092
BY	0.1783	-0.2701	-0.6289	0.5721	0.5401	0.5338	0.3992	0.2007	0.1469	0.4915	-0.2877	**0.8308**	0.872**

Residual: 0.217

Abbreviations: - DF50:-Days to 50% flowering**, DPS50:-**Days to 50% pod setting**, DM:-**Days to maturity**, PH:-**Plant height (cm)**, NPB:-**Number of primary branches per plant**, NCPP:-**Number of clusters per plant**, NPPP:-**Number of pods per plant**, NSPP:-**Number of seeds per pod**, PL:-**Pod length (cm)**, SI:-**Seed index (g)**, BY:-**Biological Yield (g)**, HI:-**Harvest index (%)**, SYPP:-**Seed yield per plant (g)**.**

***,** at 5% and 1% Level of Significance**

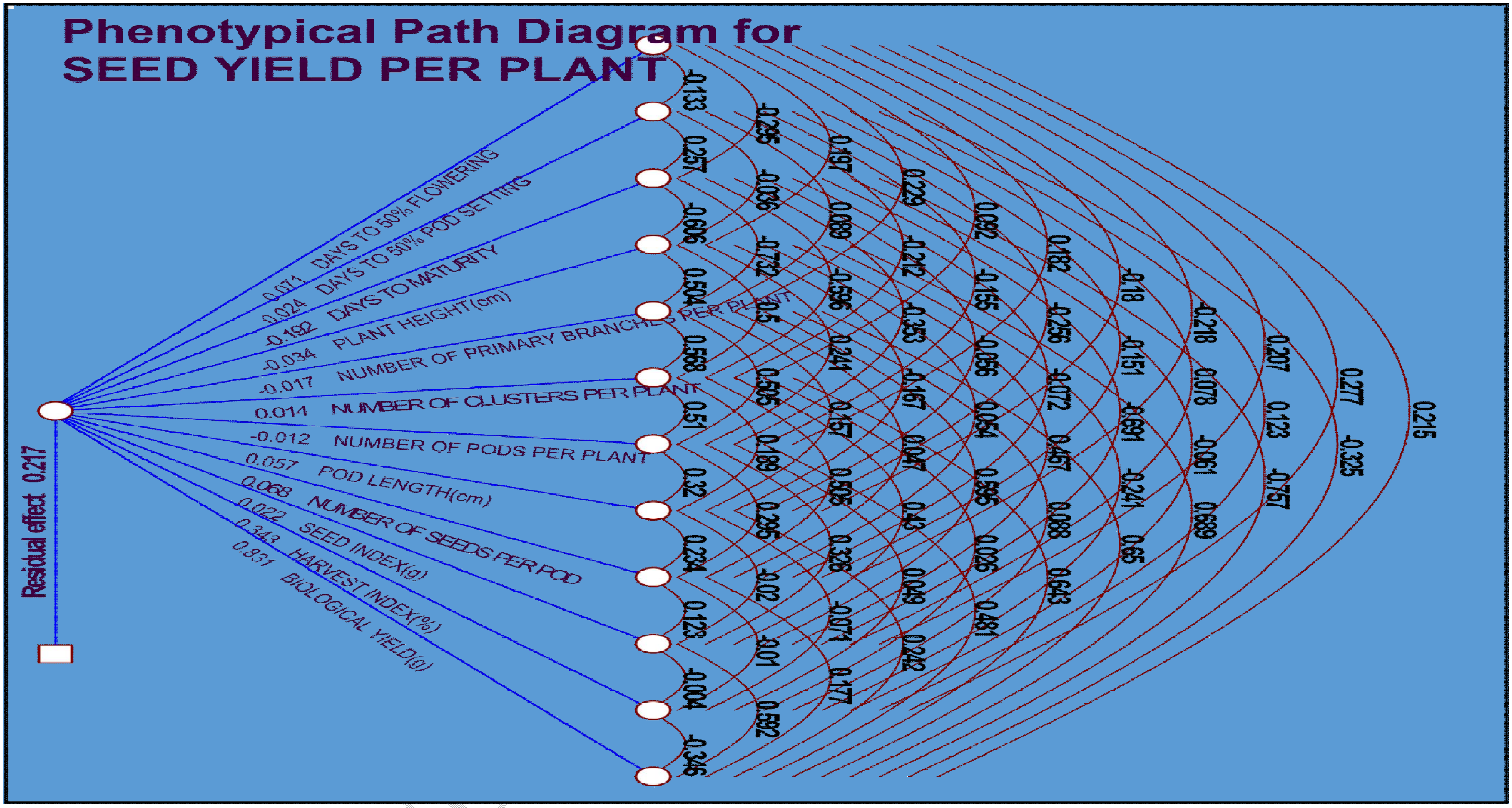

Fig 1 Phenotypic path diagram for seed yield per plant

Disclaimer (Artificial intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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