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ASSESSMENT OF YIELD COMPONENTS AND MUNGBEAN YELLOW MOSAIC VIRUS RESISTANCE IN BLACKGRAM (*Vigna mungo* L. Hepper) UNDER RICE FALLOW CONDITIONS

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ABSTRACT

Blackgram (*Vigna mungo* (L.) Hepper) is an important pulse crop valued for its high protein content, but its productivity is severely constrained by biotic stresses such as Mungbean Yellow Mosaic Virus (MYMV). The present study was conducted during rabi 2017–18 at Agricultural Research Station, Gantasala, Andhra Pradesh, to evaluate 45 genetically diverse blackgram genotypes under rice fallow conditions for yield, yield component traits, and MYMV resistance. The experiment was laid out in a randomized complete block design with three replications, and observations were recorded on 13 quantitative traits along with MYMV disease score. Correlation analysis revealed that seed yield per plant exhibited significant positive associations with number of pods per plant, pod length, number of seeds per pod, biological yield, and number of clusters per plant, indicating their importance in yield improvement. Path coefficient analysis showed that biological yield per plant, number of pods per plant, pod length, and number of branches per plant had high positive direct effects on seed yield, suggesting their utility as reliable selection criteria. Screening for MYMV resistance indicated considerable variability among genotypes, with 13 classified as resistant and 14 as moderately resistant. Genotypes such as LBG-20, LBG-787, GBG-1, GP-11, GP-13, PU-31, TBG-104, Uttara, TU 94-2, DPU 8831×VBG 4-008, KUG 216×PU-40, and KUG 216×SPS 5 exhibited stable resistance under field conditions. Notably, LBG-20 and LBG-787 combined high yield with resistance, while LBG-752, GBG-12, and GP-15 showed moderate resistance along with good yield potential. The study suggests that simultaneous selection for key yield-contributing traits and MYMV resistance would be effective for developing high-yielding and stable blackgram cultivars under rice fallow conditions

Keywords : Blackgram, Seed yield, Correlation, Path analysis, MYMV resistance.

Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an important pulse crop cultivated in India, valued for its high protein content. In India it is cultivated in 58.96 lakh ha producing 26 lakh tons with an average productivity of 558 kg/ha (Source: Directorate of Economics and Statistics, 2024-25 and directorate of pulses development annual report, 2023-24). Blackgram is a nutritionally significant pulse crop widely grown in tropical and subtropical regions.

Despite its importance, productivity is often constrained by biotic stresses, particularly Mungbean Yellow Mosaic Virus (MYMV), which can severely reduce yield. The disease, transmitted by whitefly vectors, causes chlorosis, stunted growth, and in severe cases, complete crop failure.

Seed yield is a complex character resulting from the interaction of various component characters. Therefore, knowledge of inter-relationships existing among yield components is essential to make selection

to be effective. Correlation coefficients reveal the magnitude and direction of association of yield components. It gives a measure of the mutual relationship between various plant characters and determines component characters on which selection is practiced for the improvement of economic important character (Hemalatha *et al.*, 2017). Path analysis identifies components which directly and indirectly influences the yield. Both character association and path analysis helps in formulating an effective breeding strategy to develop productive genotypes. In addition, identifying MYMV-resistant genotypes is critical for developing stable and high-yielding cultivars. This study was designed to address these aspects comprehensively.

Therefore, the present study was undertaken to access character association and path analysis for seed yield and its contributing traits in blackgram genotypes under rice fallow conditions with an objective of identifying key traits for effective selection and improvement along with identification of MYMV resistant genotypes.

Materials and Methods

The present experiment was carried out during Rabi, 2017-18 at Agricultural Research Station, Ghantasala, Krishna District, Andhra Pradesh, India which is located at 16.0° North Latitude and 81.0° Eastren Longitude. The soils are Black alluvial in texture and drainage facility is available. The experimental material consisted of 45 genetically diverse blackgram genotypes obtained from ARS, Madhira (4), National Pulse Research Centre, Vamban, (2) and ARS, Ghantasala (39) was evaluated under rice fallow conditions. The experimental material was evaluated in a folded randomized complete block design with three replications. List of blackgram genotypes used in the present study and their source of origin are given in Table 1.

Five plants per genotype were randomly selected from two central rows for recording data on 13 characters namely days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%) and Score on MYMV. All recommended agronomic practices were followed throughout the crop growth period to ensure a healthy and uniform stand.

Correlation coefficients were calculated to assess relationships among traits at both genotypic and phenotypic levels. Phenotypic and genotypic

correlation was worked out by adopting the formulae suggested by Johnson *et al.* (1955). Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits towards seed yield. Mungbean yellow mosaic disease severity was recorded on plot basis at the time of pod filling stage. Modified scale of Alice and Nadarajan (2007) was used for disease scoring (0-9) in Table 2.

Results and Discussion

The phenotypic and genotypic correlation coefficients among seed yield and its component traits (Table 3) revealed that genotypic correlations were generally higher than phenotypic ones, indicating a strong genetic control over trait associations with minimal environmental influence (Johnson *et al.*, 1955). Days to 50% flowering and days to maturity showed significant positive associations with seed yield and related traits such as pod length, number of seeds per pod, and biological yield, suggesting their indirect contribution to yield improvement, although their negative association with harvest index indicates a trade-off in assimilate partitioning. Plant height, number of branches, and clusters per plant were also positively correlated with yield, highlighting their role in enhancing reproductive capacity.

Among yield components, number of pods per plant exhibited the strongest positive association with seed yield, confirming its importance as a key selection criterion, in agreement with Dewey and Lu (1959). Pod length, number of seeds per pod, test weight, and biological yield also showed significant positive correlations with seed yield, indicating that both sink size and biomass production contribute to productivity. However, biological yield was negatively associated with harvest index, suggesting that increased biomass does not always ensure efficient partitioning. Overall, traits such as number of pods per plant, clusters per plant, pod length, and biological yield may be effectively utilized for indirect selection to improve seed yield.

The path coefficient analysis was carried out to partition the correlation coefficients into direct and indirect effects of yield component traits on seed yield (Table 4). The results indicated that biological yield per plant exerted the highest positive direct effect on seed yield at both genotypic and phenotypic levels, followed by number of pods per plant, pod length, and number of branches per plant, highlighting their primary importance in yield determination. These traits also exhibited strong positive correlations with seed yield, confirming their reliability as effective selection

criteria. Similar findings have been reported by Rajasekhar *et al.* (2017). In contrast, traits such as number of clusters per plant, number of seeds per pod, and 100 seed weight showed negative direct effects despite having significant positive correlations with seed yield, indicating that their influence is mainly through indirect effects.

The indirect effects revealed that traits such as days to 50% flowering, days to maturity, plant height, and number of clusters per plant contributed positively to seed yield primarily through biological yield per plant and number of pods per plant. Pod length also played a crucial role by contributing indirectly via seed number and biomass. Although harvest index showed positive direct effects at the phenotypic level, its inconsistent performance at the genotypic level suggests limited reliability as an independent selection trait. Overall, the results emphasize that biological yield per plant, number of pods per plant, pod length, and number of branches per plant are the most influential traits, and selection based on these characters would be effective for improving seed yield in blackgram. The genotypic and phenotypic path diagrams for seed yield are given in the figures 1 and 2 respectively.

Screening of 45 blackgram genotypes against MYMV under natural field conditions during rabi 2017-18 revealed substantial variation in disease reaction (Table 5). Based on disease scoring, 13 genotypes were categorized as resistant (score 1.0–2.0), 14 as moderately resistant (2.1–4.0), 5 as moderately susceptible (4.1–5.0), 10 as susceptible (5.1–7.0), and 3 as highly susceptible (7.1–9.0). Resistant genotypes such as LBG-20, LBG-787, GBG-1, GP-11, GP-13, PU-31, TBG-104, Uttara, TU 94-2, DPU 8831×VBG 4-008, KUG 216×PU-40 and KUG 216×SPS 5 recorded very low percent disease index (PDI) and MYMV incidence, indicating stable resistance under field conditions. In contrast, susceptible and highly susceptible genotypes exhibited severe yellow mosaic symptoms, including chlorotic patches, leaf yellowing, reduced flowering, malformed pods, and in severe cases, plant death. The disease spread was attributed to the vector whitefly (*Bemisia tabaci*), emphasizing the high disease pressure in the experimental field.

The differential response among genotypes suggests the presence of inherent genetic variability for MYMV resistance, which can be effectively exploited in breeding programmes. Resistant genotypes likely

possess mechanisms that restrict virus multiplication and spread, whereas susceptible genotypes lack such defense responses. Notably, genotypes such as LBG-20 and LBG-787 exhibited both resistance and high yield, while LBG-752, GBG-12, and GP-15 combined moderate resistance with good yield potential, making them valuable candidates for varietal improvement. The identification of resistant sources is a reliable and eco-friendly approach for managing MYMV, a major yield-limiting disease in blackgram. Similar findings on variability and identification of resistant genotypes have been reported by Bashir and Zubair (2002), Ganapathy *et al.* (2003), Kumar *et al.* (2006), Singh *et al.* (2008), Prasanthi *et al.* (2013), Ashutoshkumar *et al.* (2014), Equbal *et al.* (2015), Gopi *et al.* (2016), Parihar *et al.* (2017), and Mahalingam *et al.* (2018), supporting the present results.

Conclusion

The present study revealed significant genetic variability among blackgram genotypes for yield, its component traits, and resistance to Mungbean Yellow Mosaic Virus (MYMV). Correlation analysis indicated that seed yield per plant exhibited strong positive associations with number of pods per plant, pod length, number of seeds per pod, biological yield, and number of clusters per plant, suggesting their importance in yield improvement. Path coefficient analysis further demonstrated that biological yield per plant, number of pods per plant, pod length, and number of branches per plant exerted high positive direct effects on seed yield, indicating that these traits can be effectively utilized as reliable selection criteria in breeding programmes. Screening for MYMV resistance identified several resistant and moderately resistant genotypes, with LBG-20, LBG-787, GBG-1, GP-11, GP-13, PU-31, TBG-104, Uttara, TU 94-2, DPU 8831×VBG 4-008, KUG 216×PU-40, and KUG 216×SPS 5 showing stable resistance under field conditions. Notably, genotypes such as LBG-20 and LBG-787 combined high yield with MYMV resistance, while LBG-752, GBG-12, and GP-15 exhibited moderate resistance along with good yield potential. These genotypes can be effectively utilized as donor parents in breeding programmes aimed at developing high-yielding and MYMV-resistant cultivars. Overall, the study suggests that simultaneous selection for key yield traits along with disease resistance would be a promising strategy for improving productivity and stability in blackgram under rice fallow conditions.

Table 1 : List of 45 blackgram genotypes and their source of collection

S.No.	Genotype	Source of collection
1	LBG 17(Krishnaiah)	ARS, Ghantasala
2	LBG 20(Teja)	ARS, Ghantasala
3	LBG 402(Prabhava)	ARS, Ghantasala
4	LBG 623	ARS, Ghantasala
5	LBG 645(Banda polish)	ARS, Ghantasala
6	LBG 648(Sanna polish)	ARS, Ghantasala
7	LBG 685	ARS, Ghantasala
8	LBG 709	ARS, Ghantasala
9	LBG 752	ARS, Ghantasala
10	LBG 787(Tulasi)	ARS, Ghantasala
11	LBG 788	ARS, Ghantasala
12	GBG-1	ARS, Ghantasala
13	GBG-12	ARS, Ghantasala
14	MBG-1046	ARS, Madhira
15	MBG-1050	ARS, Madhira
16	MBG-1053	ARS, Madhira
17	MBG-1069	ARS, Madhira
18	GP- 6(Local collection)	ARS, Ghantasala
19	GP- 11(Local collection)	ARS, Ghantasala
20	GP-12 (Local collection)	ARS, Ghantasala
21	GP- 13(Local collection)	ARS, Ghantasala
22	GP-14 (Local collection)	ARS, Ghantasala
23	GP-15 (Local collection)	ARS, Ghantasala
24	GP-27 (Local collection)	ARS, Ghantasala
25	GP-31 (Local collection)	ARS, Ghantasala
26	GP-33 (Local collection)	ARS, Ghantasala
27	VBG 4-008	NPRC, Vamban
28	VBG 4-14	NPRC, Vamban
29	PU 31	G.B. Pant university of Agril. Science and Technology, Pantnagar
30	PU 40	G.B. Pant university of Agril. Science and Technology, Pantnagar
31	TBG 104 (Tirupathi Minumu -1)	RARS, Tirupati
32	WBG 108	ARS, Warangal
33	Uttara	ARS, Ghantasala
34	KKB 05011	ARS, Ghantasala
35	TU 18	ARS, Ghantasala
36	TU 94-2	ARS, Ghantasala
37	IPU 2-43	ARS, Ghantasala
38	T 9	ARS, Ghantasala
39	Thootiminumu	ARS, Ghantasala
40	Buttaminumu	ARS, Ghantasala
41	MASH-114	ARS, Ghantasala
42	KUG 216 x BG 018-2	ARS, Ghantasala
43	DPU 88 31 x VBG 4-008	ARS, Ghantasala
44	KUG 216 x PU 40	ARS, Ghantasala
45	KUG 216 x SPS 5	ARS, Ghantasala

Table 2 : Modified disease scale (0-9) for scoring MYMV disease

Scale	Description
0	No visible symptoms on leaves
1	Very minute yellow specks on leaves
2	Small yellow specks with restricted spread covering 0.1-5% leaf area of plant
3	Yellow mottling of leaves covering 5.1-10% leaf area of plant
4	Yellow mottling of leaves covering 10.1-15% leaf area of plant
5	Yellow mottling and discolouration of 15.1-30% leaf area of plant
6	Yellow discolouration of 30.1 to 50% leaf area of plant

7	Pronounced yellow mottling and discolouration of leaves and pods, reduction in leaf size and stunting of plants covering 50.1-75% foliage of plant
8	Severe yellow discolouration of leaves covering 75.1 to 90% of foliage, stunting of plants and reduction in pod size
9	Severe yellow discolouration of leaves covering above 90.1% of foliage of plant, stunting of plants and no pod formation

Table 3 : Genotypic and Phenotypic Correlation Coefficients of yield and yield component characters in Blackgram under rice fallow situation

Character	Correlation	Days to 50% Flowering	Days to Maturity	Plant Height	Number of Branches per Plant	Number of Clusters per Plant	Number of Pods per Plant	Pod Length	Number of Seeds per Pod	100 Seed Weight	Biological Yield per Plant	Harvest Index	Seed Yield per Plant
Days to 50% Flowering	G	1.0000	0.7023**	0.1743*	0.1566	0.1693*	0.2114*	0.3315**	0.3741**	0.0045	0.4096**	-0.4676**	0.2825**
	P	1.0000	0.6445**	0.1597	0.1132	0.0800	0.1590	0.2226**	0.2692**	0.0178	0.3243**	-0.2909**	0.1941*
Days to Maturity	G		1.0000	0.2269**	0.0910	0.1541	0.3412**	0.4070**	0.3237**	0.1488	0.4190**	-0.4048**	0.3172**
	P		1.0000	0.1691*	0.0413	0.1004	0.2772**	0.2733**	0.2327**	0.1428	0.3359**	-0.1951*	0.2518**
Plant Height	G			1.0000	0.4121**	0.5350**	0.3601**	0.4362**	0.4692**	0.2213*	0.5769**	-0.3509**	0.4550**
	P			1.0000	0.2872**	0.3742**	0.2479**	0.3024**	0.3091**	0.1759*	0.4301**	-0.2188*	0.3194**
Number of Branches per Plant	G				1.0000	0.5747**	0.4943**	-0.0380	-0.0379	0.1820*	0.5104**	-0.4349**	0.4236**
	P				1.0000	0.5106**	0.4482**	0.0413	0.0421	0.1514	0.4316**	-0.2286**	0.3519**
Number of Clusters per Plant	G					1.0000	0.8125**	0.3121**	0.2393**	0.1543	0.6831**	-0.0123	0.7050**
	P					1.0000	0.7161**	0.2390**	0.1715*	0.1300	0.6346**	-0.0344	0.6096**
Number of Pods per Plant	G						1.0000	0.4754**	0.2604**	0.3849**	0.8002**	0.0683	0.8702**
	P						1.0000	0.3676**	0.2006*	0.3388**	0.7090**	0.0099	0.7147**
Pod Length	G							1.0000	0.8909**	0.4649**	0.7689**	0.0402	0.6995**
	P							1.0000	0.6193**	0.3565**	0.5042**	-0.0490	0.4540**
Number of Seeds per Pod	G								1.0000	0.0999	0.5412**	-0.2121*	0.4470**
	P								1.0000	0.0491	0.4053**	-0.0871	0.3318**
100 Seed Weight	G									1.0000	0.4237**	0.1020	0.4501**
	P									1.0000	0.3910**	0.0046	0.3674**
Biological Yield per Plant	G										1.0000	-0.2076*	0.9635**
	P										1.0000	-0.1746*	0.8669**
Harvest Index	G											1.0000	0.1027
	P											1.0000	0.2229**

Table 4 : Genotypic and Phenotypic Path Coefficient of yield and yield components in Blackgram under rice fallow situation

Character	Path analysis	Days to 50% Flowering	Days to Maturity	Plant height	Number of Branches per Plant	Number of Clusters per Plant	Number of Pods per Plant	Pod Length	Number of Seeds per Pod	100 Seed Weight	Biological Yield per Plant	Harvest Index
Days to 50% Flowering	G	0.1073	0.0754	0.0187	0.0168	0.0182	0.0227	0.0356	0.0401	0.0005	0.0440	-0.0502
	P	0.0033	0.0022	0.0005	0.0004	0.0003	0.0005	0.0007	0.0009	0.0001	0.0011	-0.0010
Days to Maturity	G	-0.1027	-0.1462	-0.0332	-0.0133	-0.0225	-0.0499	-0.0595	-0.0473	-0.0217	-0.0613	0.0592
	P	0.0074	0.0115	0.0020	0.0005	0.0012	0.0032	0.0032	0.0027	0.0016	0.0039	-0.0023
Plant Height	G	0.0123	0.0160	0.0704	0.0290	0.0376	0.0253	0.0307	0.0330	0.0156	0.0406	-0.0247
	P	0.0007	0.0008	0.0045	0.0013	0.0017	0.0011	0.0013	0.0014	0.0008	0.0019	-0.0010
Number of Branches per Plant	G	0.0204	0.0118	0.0536	0.1300	0.0747	0.0643	-0.0049	-0.0049	0.0237	0.0664	-0.0566
	P	0.0036	0.0013	0.0090	0.0314	0.0160	0.0141	0.0013	0.0013	0.0047	0.0135	-0.0072
Number of Clusters per Plant	G	-0.0125	-0.0114	-0.0396	-0.0425	-0.0740	-0.0601	-0.0231	-0.0177	-0.0114	-0.0505	0.0009
	P	-0.0001	-0.0001	-0.0004	-0.0005	-0.0009	-0.0007	-0.0002	-0.0002	-0.0001	-0.0006	0.0000
Number of Pods per Plant	G	0.0739	0.1193	0.1259	0.1728	0.2841	0.3497	0.1662	0.0910	0.1346	0.2798	0.0239
	P	0.0141	0.0246	0.0220	0.0398	0.0636	0.0889	0.0327	0.0178	0.0301	0.0630	0.0009
Pod Length	G	0.2581	0.3169	0.3396	-0.0296	0.2430	0.3701	0.7785	0.6935	0.3619	0.5985	0.0313
	P	0.0036	0.0044	0.0049	0.0007	0.0038	0.0059	0.0161	0.0100	0.0057	0.0081	-0.0008
Number of Seeds per Pod	G	-0.2010	-0.1739	-0.2521	0.0204	-0.1286	-0.1399	-0.4786	-0.5372	-0.0537	-0.2908	0.1139
	P	-0.0037	-0.0032	-0.0042	-0.0006	-0.0023	-0.0027	-0.0084	-0.0136	-0.0007	-0.0055	0.0012
100 Seed Weight	G	-0.0009	-0.0298	-0.0443	-0.0365	-0.0309	-0.0771	-0.0932	-0.0200	-0.2004	-0.0849	-0.0204
	P	-0.0002	-0.0014	-0.0017	-0.0015	-0.0013	-0.0033	-0.0035	-0.0005	-0.0098	-0.0038	0.0000
Biological Yield Per Plant	G	0.1828	0.1870	0.2574	0.2278	0.3048	0.3571	0.3431	0.2415	0.1891	0.4462	-0.0927
	P	0.2763	0.2862	0.3664	0.3677	0.5407	0.6040	0.4296	0.3453	0.3331	0.8519	-0.1487
Harvest Index	G	-0.0552	-0.0478	-0.0414	-0.0513	-0.0015	0.0081	0.0047	-0.0250	0.0120	-0.0245	0.1180
	P	-0.1110	-0.0745	-0.0835	-0.0872	-0.0131	0.0038	-0.0187	-0.0333	0.0018	-0.0666	0.3817
Seed Yield per Plant	G	0.2825**	0.3172**	0.4550**	0.4236**	0.7050**	0.8702**	0.6995**	0.4470**	0.4501**	0.9635**	0.1027
	P	0.1941*	0.2518**	0.3194**	0.3519**	0.6096**	0.7147**	0.4540**	0.3318**	0.3674**	0.8669**	0.2229**

R SQUARE = 0.9795

RESIDUAL EFFECT = 0.1433

Genotypic

R SQUARE = 0.9017

RESIDUAL EFFECT = 0.3135

Phenotypic

Table 5 : Grouping of genotypes based on scoring for Mungbean yellow mosaic virus in forty-five genotypes of Blackgram [*Vigna mungo* (L.) Hepper] under rice fallow situation

Rating	Reaction	Genotype(s)
1.0 to 2.0	Resistant (R)	LBG-20, LBG-787, GBG-1, GP-11, GP-13, PU-31, TBG-104, Uttara, TU-18, TU 94-2, DPU 8831×VBG 4-008, KUG 216×PU-40, KUG 216×SPS 5
2.1 to 4	Moderately resistant (MR)	LBG-709, LBG-752, GBG-12, GP-6, GP-31, GP-14, GP-27, GP-15, GP-12, VBG 4-008, VBG 4-14, WBG-108, IPU 2-43, MASH-114
4.1 to 5	Moderately susceptible (MS)	MBG-1046, MBG-1050, MBG-1053, PU-40, KUG 216×BG 018-2
5.1 to 7	Susceptible (S)	LBG-17, LBG-645, LBG-648, LBG-788, MBG-1069, GP-33, KKB 05011, T-9, Thootiminumu, Buttaminumu
7.1 to 9	Highly susceptible (HS)	LBG-402, LBG-623, LBG-685

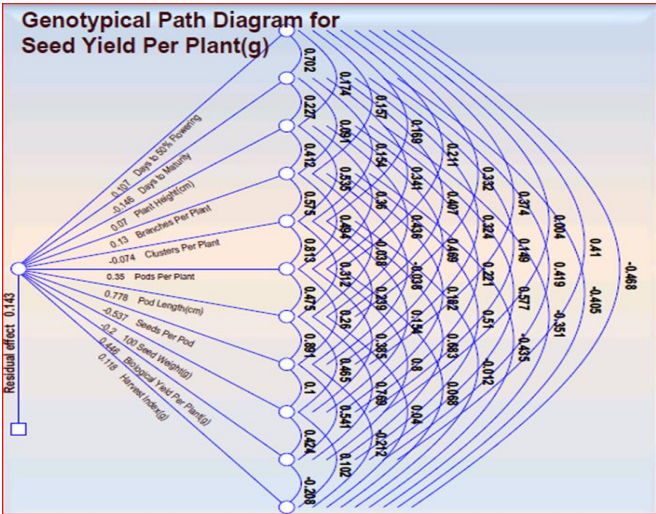


Fig. 1 : Genotypic Path diagram for seed yield per plant

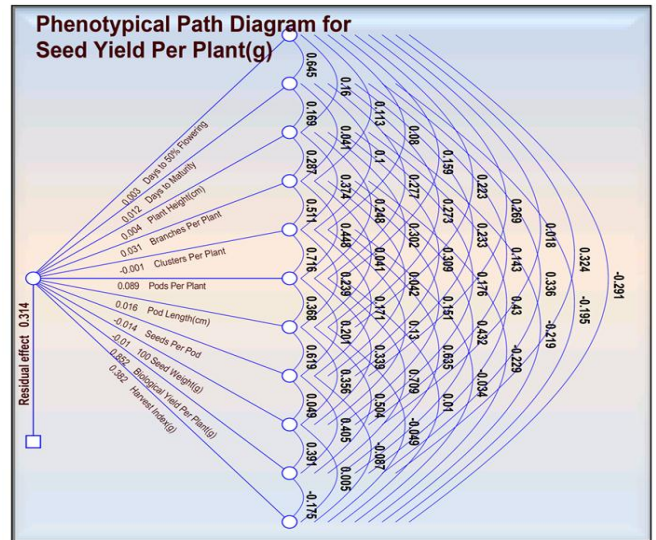


Fig. 2 : Genotypic Path diagram for seed yield per plant

References

Alice, D. and Nadarajan, N. (2007). Pluses: Screening techniques and assessment for disease resistance. All India Co-Ordinated Research Project on MULLaRP, Tamil Nadu Agricultural University, Kasturi Graphics and Printers, Coimbatore, India.

Ashutosh Kumar, Parihar, A.K., Dixit, G.P. and Gupta, S. (2014). Zonal occurrence of mungbean yellow mosaic disease in mungbean cultivars released for different zones in India. *International Quarterly Journal of Environmental Sciences*. **6**(Special): 111–114.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*. **51**(9): 515–518.

Directorate of Pulses Development (2024). Annual Report 2023–2024. Available at: <https://dpd.gov.in/Reports.html>

Equbal, M.J., Sahni, S., Singh, D. and Kumar, B. (2015). Exploitation of urdbean germplasms for mungbean yellow mosaic virus (MYMV) management and improved seed yield. *International Journal of Agriculture Sciences*. **7**(6): 536–539.

Gopi, P., Satyanarayana, A., Rama Krishna, A. and Sambasiva Rao, K.R.S. (2016). Evaluation of blackgram germplasm for resistance against YMV. *Journal of Plant Pathology & Microbiology*. **7**(7): 1–3.

Hemalatha, K., Lal, S.S. and Lal, G.M. (2017). Study on genetic variability and correlation in black gram (*Vigna mungo* L. Hepper). *Journal of Pharmacognosy and Phytochemistry*. **6**(4): 674–676. Available at: <https://www.phytojournal.com/archives/2017/vol6issue4/Part K/6-4-102-123.pdf>

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal*. **47**: 314–318.

Kumar, R., Ali, S. and Rizvi, S.M.A. (2006). Screening of mungbean genotypes for resistance against whitefly (*Bemisia tabaci*) and mungbean yellow mosaic virus. *Indian Journal of Pulses Research*. **19**: 135–136.

Mahalingam, A., Satya, V.K., Manivannan, N., Lakshmi, S., Narayanan and Sathya, P. (2018). Inheritance of mungbean yellow mosaic virus disease resistance in greengram [*Vigna radiata* (L.) Wilczek]. *International Journal of Current Microbiology and Applied Sciences*. **7**(1): 880–885.

Parihar, A.K., Kumar, A., Dixit, G.P. and Gupta, S. (2017). Seasonal effects on outbreak of yellow mosaic disease in released cultivars of mungbean (*Vigna radiata*) and urdbean (*Vigna mungo*). *Indian Journal of Agricultural Sciences*. **87**(6): 734–738.

- Prasanthi, L., Bhaskara Reddy, B.V., Geetha, B., Ramya Jyothi and Abhishek (2013). Molecular marker for screening yellow mosaic disease resistance in blackgram [*Vigna mungo* (L.) Hepper]. *Electronic Journal of Plant Breeding*. **4**(2): 1137–1141.
- Rajasekhar, D., Lal, S.S. and Lal, G.M. (2017). Character association and path analysis for seed yield and its components in blackgram [*Vigna mungo* (L.) Hepper]. *Plant Archives*. **17**(1): 467–471.
- Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*. **20**: 557–585.