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Correlation studies for yield and its related traits in relation to yellow mosaic virus reaction in mungbean (*Vigna radiata* L. Wilczek)

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Abstract
The present investigation was carried out to determine the nature of association between seed yield and its contributing traits under yellow mosaic virus (YMV) stress using correlation analysis. A total of 30 genotypes, including six generations derived from five mungbean crosses, were evaluated in a randomized block design with three replications. Phenotypic and genotypic correlation coefficients were computed for twelve quantitative and disease-related characters. The results revealed that seed yield per plant exhibited strong and significant positive correlations with pods per plant, plant height, pod length, seeds per pod, and 100-seed weight at both phenotypic and genotypic levels. Conversely, disease incidence, percent disease index (PDI), and area under disease progress curve (AUDPC) showed significant negative associations with yield and its components. These findings highlight the importance of selecting positively correlated traits while minimizing disease effects for enhancing yield potential in MYMV-affected environments.

Keywords: Mungbean, correlation, yellow mosaic virus, PDI, AUDPC, seed yield, 100-seed weight

Introduction
Mungbean (*Vigna radiata* (L.) Wilczek), commonly known as green gram, is a diploid (2n = 2x = 22), self-pollinated pulse crop of the Fabaceae family and subgenus *Ceratotrophis*. It is believed to have originated in the Indo-Burma region and is widely cultivated across Asia, Africa, and Latin America. In India, it is grown under various names such as moong, golden gram, and mash bean. Its short duration (60-65 days), nitrogen-fixing ability, photo-insensitivity, and adaptability to diverse agro-climatic conditions make it ideal for multiple cropping systems, including *kharif*, *rabi*, and summer seasons. It thrives well under low-input conditions and is important for sustainable agriculture.

Despite its agronomic and nutritional value, mungbean productivity is often limited by biotic stresses, particularly Mungbean Yellow Mosaic Virus (MYMV), a serious disease transmitted by whitefly (*Bemisia tabaci*), which leads to severe yield losses. Correlation coefficient analysis is an essential tool for assessing the relationship between yield and its contributing traits, enabling the identification of traits most relevant for selection. This understanding is vital for improving genetic gain and formulating breeding strategies. Hence, the present study aimed to investigate such associations in mungbean for developing high-yielding and MYMV-resistant lines.

Materials and Methods
Six generations, namely P_1, P_2, F_1, F_2, BC_1 and BC_2 from five crosses viz., Kopergaon x PUSA 9531, Kopergaon x PDM 139, TAKM 140 x PANT M-5, TAKM 140 x PDM 139, SML 668 x BM 2003-2, were developed during summer and kharif 2024 and along with three checks were evaluated during summer 2025 at the experimental field of Seed Technology Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experiment was laid out in a Randomized Block Design (RBD) with three replications. All 30 genotypes were planted in 3 m long rows keeping 45cm distance between rows and 15cm between plants.

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Six generations, namely P_1, P_2, F_1, F_2, BC_1 and BC_2 from five crosses viz., Kopergaon x PUSA 9531, Kopergaon x PDM 139, TAKM 140 x PANT M-5, TAKM 140 x PDM 139, SML 668 x BM 2003-2, were developed during summer and kharif 2024 and along with three checks were evaluated during summer 2025 at the experimental field of Seed Technology Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experiment was laid out in a Randomized Block Design (RBD) with three replications. All 30 genotypes were planted in 3 m long rows keeping 45cm distance between rows and 15cm between plants. All recommended agronomic practices were adopted for proper crop growth. Observations were recorded on randomly selected five plants from each generation for recording the observations viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, seed yield per plant, disease incidence, percent disease index, area under disease progression curve values.

Results and Discussion

Crop improvement programmes depend to a large extent on the availability of sufficient variability among different characters, which are the pre-requisite for executing an effective selection programme. Seed yield, being a complex quantitative trait, is dependent on a number of component characters. Twelve characters under study are presented in Table 1 and Table 2.

The seed yield per plant exhibited highly significant and positive phenotypic correlation with pods per plant (0.827), plant height (0.532), pod length (0.527), seeds per pod (0.427), and 100-seed weight (0.483), whereas it showed significant negative correlation with incidence (-0.464), percent disease index (PDI) (-0.524), and area under disease progress curve (AUDPC) (-0.447). At the genotypic level, seed yield per plant showed very high order positive correlation with plant height (0.985), pods per plant (0.909), pod length (0.710), seeds per pod (0.463), and 100-seed weight (0.769), whereas it had strong negative correlation with disease incidence (-0.676), PDI (-0.740), and AUDPC (-0.658).

The 100-seed weight showed highly significant and positive phenotypic correlation with pod length (0.622). At genotypic level, 100-seed weight showed highly significant positive association with pod length (0.991) and plant height (0.453), while it had negative association with disease traits.

Pods per plant recorded significant positive phenotypic correlation with plant height (0.380), days to maturity (0.363) and branches per plant (0.327). At genotypic level, it showed strong and positive correlation with plant height (0.995), branches per plant (0.706), days to maturity (0.711) and seeds per pod (0.578).

Plant height recorded significant positive phenotypic correlation with days to maturity (0.419), pods per plant (0.380), pod length (0.340) and yield per plant (0.532). Genotypically, it showed very strong association with days to maturity (0.895) and yield (0.985). Pod length was positively and significantly correlated both phenotypically and genotypically with seeds per pod (0.429 and 0.449), and also had strong positive association with 100-seed weight and yield per plant, suggesting its indirect contribution to seed yield.

Branches per plant showed positive phenotypic correlations with pods per plant (0.327) and plant height (0.221). Genotypically, it recorded strong and positive associations with pods per plant (0.706) and plant height (0.499). Days to maturity exhibited moderate positive associations with several yield traits but showed negative phenotypic correlation with incidence (-0.540), PDI (-0.520) and AUDPC (-0.496), and strong negative genotypic association with incidence (-0.685), PDI (-0.629) and AUDPC (-0.638), indicating early maturing genotypes are more susceptible to YMV.

Among disease parameters, incidence, PDI, and AUDPC were positively correlated among themselves, but showed strong and significant negative associations with seed yield and its components, reiterating the adverse impact of YMV on productivity.

Phenotypic (Table 1) and genotypic (Table 2) correlation coefficients were computed among 12 characters. Seed yield per plant showed highly significant and positive phenotypic correlation and very high order genotypic correlation with pods per plant, plant height, pod length, seeds per pod, 100-seed weight, and had negative correlations with disease incidence, PDI, and AUDPC. These traits emerged as the most important associates of seed yield per plant under YMV stress.

The positive associations between the above-mentioned characters have also been reported by Rao *et al.* (2006) [14], Azam *et al.* (2018) [3], Srivastava *et al.* (2024) [19], Patel *et al.* (2022) [13], and Khanpara *et al.* (2012) [6]. Negative correlation of disease-related traits with yield is supported by Jayappa *et al.* (2017) [5] and Mahanta *et al.* (2019) [8], who confirmed the yield-suppressing effect of YMV infection. Furthermore, similar findings for 100-seed weight, pods per plant, and plant height as reliable contributors to seed yield were also observed by Hemavathy *et al.* (2015) [4], Parsaniya *et al.* (2022) [13], Alqama Khan *et al.* (2024) [1], Sharma *et al.* (2024) [20] and Shakeer *et al.* (2022) [15].

Table 1: Estimates of phenotypic correlation coefficients

Traits	D50%f	DM	PH	PB/P	P/P	PL	S/P	100-SW	DI	PDI	AUDPC	SY/P
D50%F	1											
DM	-0.128	1										
PH	0.037	0.419**	1									
PB/P	-0.041	0.173	0.221*	1								
P/P	-0.017	0.363**	0.380**	0.327**	1							
PL	0.086	0.319**	0.340**	-0.025	0.180	1						
S/P	0.001	0.374**	0.197	0.052	0.320**	0.429**	1					
100-SW	0.048	0.159	0.183	-0.092	0.181	0.622**	0.081	1				
DI	-0.039	-0.540**	-0.513**	-0.104	-0.312**	-0.513**	-0.186	-0.453**	1			
PDI	-0.053	-0.520**	-0.554**	-0.122	-0.357**	-0.583**	-0.239*	-0.487**	0.939**	1		
AUDPC	-0.135	-0.496**	-0.515**	-0.151	-0.333**	-0.532**	-0.179	-0.425**	0.869**	0.858**	1	
SY/P	0.066	0.409**	0.532**	0.200	0.827**	0.527**	0.427**	0.483**	-0.464**	-0.524**	-0.447**	1

Traits: D 50% f = Days to 50% flowering, DM = Days to maturity, PH = Plant height(cm), PB/P = Primary branches plant^{-1}, P/P = Pods plant^{-1}, PL = Pod length(cm), S/P = Seeds pod^{-1}, 100-SW = 100-Seed weight(g), DI = Disease incidence(%), PDI = Percent Disease Index, AUDPC = Area under disease progression curve, SY/ P = Seed Yield Plant^{-1}(g)

Table 2: Estimates of Genotypic correlation coefficients

Traits	D50%f	DM	PH	PB/P	P/P	PL	S/P	100-SW	DI	PDI	AUDPC	SY/P
D50%F	1											
DM	-0.350**	1										
PH	0.105	0.895**	1									
PB/P	-0.185	0.568**	0.499**	1								
P/P	0.125	0.711**	0.995**	0.706**	1							
PL	0.172	0.459**	0.352**	-0.299**	0.384**	1						
S/P	-0.211*	0.611**	0.277**	0.342**	0.578**	0.449**	1					
100-SW	0.176	0.249*	0.453**	-0.065	0.381**	0.991**	0.284**	1				
DI	-0.075	-0.685**	-0.850**	-0.288**	-0.483**	-0.770**	-0.352**	-0.531**	1			
PDI	-0.165	-0.629**	-0.842**	-0.293**	-0.539**	-0.762**	-0.361**	-0.594**	0.983**	1		
AUDPC	-0.238*	-0.638**	-0.760**	-0.439**	-0.531**	-0.702**	-0.299**	-0.542**	0.932**	0.888**	1	
SY/P	0.206	0.406**	0.985**	0.462**	0.909**	0.710**	0.463**	0.769**	-0.676**	-0.740**	-0.658**	1

Conclusions

The present study's correlation analysis under YMV stress revealed that seed yield per plant is strongly and positively associated with key yield components such as pods per plant, plant height, pod length, seeds per pod, and 100-seed weight both at phenotypic and genotypic levels. In contrast, disease-related traits like incidence, PDI, and AUDPC exhibited significant negative correlations with seed yield and its components. These findings emphasize the importance of selection for positively associated traits while minimizing disease impact to enhance yield potential in yellow mosaic virus-affected environments.

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