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UNRAVELING TRAIT ASSOCIATIONS AND CLUSTERING PATTERNS IN ADVANCED MUNGBEAN BREEDING LINES

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ABSTRACT

This study conducted during *kharif* 2021 at MARS, Dharwad, Karnataka, 130 advanced mungbean breeding lines were examined to understand their relationship with yield and related traits. Through association analysis, significant positive correlations between seed yield per plant and traits such as pods per plant, pods per cluster, clusters per plant, pod length, and test weight were found. Notably, pods per plant had the highest positive impact on yield, followed by pods per cluster, clusters per plant, branches per plant, and test weight underscoring the significance of devising a selection strategy based on these traits. Additionally, this study emphasizes the importance of inter-cluster heterogeneity in guiding parent selection for recombination breeding programs, with an emphasis on leveraging the observed genetic diversity among clusters to produce superior recombinants.

Key words : Advanced breeding lines, Mungbean, Variability, Yield.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is a warm-season pulse crop cultivated predominantly in South and Southeast Asia under various cropping systems due to its short life cycle, water stress tolerance, and nitrogen-fixing ability through rhizobium symbiosis. With vernacular names like greengram and golden gram, it holds significance as a high-protein legume with elevated folate and iron levels compared to other legumes (Arumuganathan and Earle, 1991).

In India, mungbean ranks as the third most important pulse crop, covering approximately 4.5 million hectares and yielding 2.5 million tonnes of grain, with an average productivity of 548 kilograms per hectare (Anonymous, 2021). In Karnataka alone, it spans 859 thousand hectares, yielding 1.80 lakh tonnes with an average productivity of 399 kg ha^{-1} (Anonymous, 2021). The key mungbean growing states include Rajasthan, Maharashtra, Karnataka, and Madhya Pradesh, with prominent districts in Karnataka being Gadag, Kalaburgi, Vijayapura, Bagalkot, Belagavi, Bidar, Raichur, Dharwad and Mysuru.

Correlation coefficient analysis in field trials serves as a valuable tool for assessing associations among essential plant traits and establishing selection criteria based on yield and its components. However, due to the interrelationships among component traits, linear correlations might provide a misleading interpretation. Therefore, partitioning correlation into direct and indirect effects via path coefficient analysis offers a holistic perspective, aiding in the ranking of yield-contributing traits and prioritizing specific traits influencing given correlations (Rao *et al.*, 2006).

Considering the aforementioned points, this study aimed to analyze the correlation and path coefficients for various yield and yield-related traits among advanced mungbean breeding lines. Additionally, clustering based on k-means was employed to identify genetic diversity and facilitate strategic parental selection, thereby enhancing breeding program efficiency.

Materials and Methods

The current study, was conducted at E-block, Main Agricultural Research Station (MARS), College of

Agriculture, Dharwad, during the *kharif* 2021. One hundred and thirty advanced breeding lines of mungbean utilized in this investigation were obtained from AICRP on MULLaRP, UAS, Dharwad. The material contained the stabilized lines derived from different crosses, mutation *per se* and mutation breeding followed by recombination for some desirable traits.

During *kharif* 2021, the test genotypes and the checks were grown using augmented design with all the recommended cultivation practices to study the association between yield and yield related traits. This experiment was laid out with five blocks and each block consisting of 29 rows with 26 entries along with three checks. The spacing of 45 cm between the rows was followed. Three locally popular varieties DGGV-2, TARM1 and IPM-2-14 were used as checks. The phenotypic correlation co-efficients were worked out by adopting the method described by Singh and Chaudhary (1977) and path coefficient analysis was done according to the method suggested by Deway and Lu (1959). The data recorded on each of five random plants for different quantitative traits was averaged and analysed using R software version 4.2.1. The statistical parameters namely, phenotypic correlation co-efficient (r_p) and path co-efficient were computed for all the traits. Furthermore, clustering of the genotypes was done based on k-means. The cluster means and inter cluster distance between three different clusters based on the mean values of ten traits were worked out.

Results and Discussion

The significant and positive association between yield per plant and various traits such as number of branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod length, and test weight underscores their importance in mungbean breeding (Manivelan *et al.*, 2019; Divya *et al.*, 2018; Azam *et al.*, 2018; Bhutia *et al.*, 2016). These findings align with prior studies, indicating the consistency of these relationships across different research contexts. However, traits like plant height and number of seeds per pod showed positive but non-significant correlations with yield, while days to fifty per cent flowering exhibited a negative and non-significant correlation. This suggests that while these traits may influence yield to some extent, their impact may not be statistically significant or consistent across different environments (Table 1).

Path coefficient analysis revealed the direct and indirect effects of these traits on yield per plant. Days to fifty per cent flowering exhibited a negative direct effect on seed yield per plant (Divya *et al.*, 2018; Marawar *et al.*, 2020), indicating that earlier flowering may lead to higher yields. Conversely, traits like number of branches per plant, number of pods per plant, number of clusters per plant, and number of pods per cluster showed high direct effects (Ahmad and Belwal, 2020; Dhunde *et al.*, 2021; Parihar *et al.*, 2018), indicating their strong influence on yield. These traits also displayed positive correlations with seed yield per plant, suggesting their potential as selection criteria for yield improvement in mungbean breeding programs.

Interestingly, traits like number of seeds per pod and test weight showed less negative direct effects but more positive indirect effects on seed yield per plant, indicating their importance in influencing yield through other traits (Mahanta and Sao, 2019; Kumar *et al.*, 2020). Pod length

Table 1 : Phenotypic correlation coefficients of yield and its component traits in mungbean during *kharif* 2021.

	DFF	PH	BPP	CPP	PPP	PPC	SPP	PL	TW	YPP
DFF	1	0.178*	-0.170*	0.067	-0.038	0.045	-0.229**	-0.131	-0.061	-0.017
PH		1	0.004	0.249**	0.129	0.142	-0.043	0.101	-0.042	0.109
BPP			1	0.257**	0.329**	0.268**	0.306**	0.150	-0.082	0.326**
CPP				1	0.496**	0.420**	0.122	0.060	0.021	0.425**
PPP					1	0.634**	0.225**	0.271**	0.203*	0.655**
PPC						1	0.173*	0.251**	0.106	0.589**
SPP							1	0.236**	0.124	0.163
PL								1	0.102	0.254**
TW									1	0.213*
YPP										1

*- Significant at 5 % level of probability

** - Significant at 1 % level of probability

DFF - Days to fifty per cent flowering

PH - Plant height

BPP - Number of branches per plant

CPP - Number of clusters per plant

PPP - Number of pods per plant

SPP- Number of seeds per pod

PL - Pod length

TW – Test weight

YPP - Yield per plant

Table 2 : Direct and indirect effects of yield attributing characters on seed yield in mungbean during *kharif* 2021.

	DFF	PH	BPP	CPP	PPP	PPC	SPP	PL	TW	r
DFF	**-0.019**	-0.001	-0.009	-0.005	-0.039	0.001	0.017	0.294	-0.002	-0.017
PH	0.003	**-0.003**	0.002	-0.019	0.128	-0.001	0.003	-0.303	-0.001	0.109
BPP	-0.003	0.012	**0.054**	-0.020	0.325	-0.001	-0.022	-0.055	-0.002	0.326^{**}
CPP	0.001	-0.001	0.014	**0.078**	0.493	-0.002	-0.009	-0.020	0.001	0.425^{**}
PPP	-0.007	0.011	0.018	-0.039	**0.486**	-0.003	-0.017	-0.519	0.006	0.655^{**}
PPC	0.001	0.003	0.015	-0.033	0.321	**0.124**	-0.012	-0.058	0.003	0.589^{**}
SPP	-0.005	0.021	0.017	-0.009	0.227	-0.001	**-0.072**	-0.128	0.001	0.163
PL	-0.003	0.010	0.008	-0.005	0.266	-0.001	-0.017	**-0.103**	0.012	0.254^{**}
TW	-0.001	0.002	-0.004	-0.002	0.197	0.001	-0.008	-0.013	**0.029**	0.213^{*}

Residual effect= 0.187

DFF - Days to fifty per cent flowering
PH - Plant height
BPP - Number of branches per plant
CPP - Number of clusters per plant
r – Correlation of yield with other traits
PPP - Number of pods per plant
SPP- Number of seeds per pod
PL - Pod length
TW – Test weight
YPP - Yield per plant

Table 3 : Clustering pattern among mungbean genotypes.

Cluster No	Members
I (25)	DGG-1, DGG-19, DGG-20, DGG-21, DGG-64, DGG-73, DGG-80, DGG-125, DGG-176, DGG-177, DGG-180, DGG-185, DGG-186, DGG-187, DGG-190, DGG-193, DGG-197, DGG 254, DGG-313, 5 BRD-11, Virat, Shikha, IPM-2-03, IPM-19-9, GG-K-21-3.
II (38)	DGGV-2, DGG-12, DGG-62, DGG-71, DGG-96, DGG-99, DGG-100, DGG-114-1, DGG-116, DGG-122, DGG-127, DGG-162, DGG-179, DGG-182-3, DGG-188, DGG-191, DGG-225, DGG-227, DGG-231, DGG-232, DGG-250, DGG-252, Karihesaru, NUL7, Samrat, Vaibhav, Rpt 8655460T_1, 3 MBRD -58, 30 GPM-7, 3 BRD – 20 , 8 BRD-9, 5 BRD-10, 7 BRD-12, IPM-3-2, GBRD-9, GG-K-21-2, GG-K-21-4, 6 MBRD-118.
III (70)	DGG-7, DGG-10, DGG-59, DGG-63, DGG-75, DGG-84, DGG-91, DGG-95, DGG-107, DGG-109, DGG-110, DGG-113, DGG-119, DGG-123, DGG-124, DGG-126, DGG-128, DGG-173, DGG-175, DGG-178, DGG-182-1, DGG-182-2, DGG-184, DGG-199, DGG-203, DGG-205, DGG-214, DGG-213-1, DGG-216, DGG-215-1, DGG-215-2, DGG-218, DGG-215-3, DGG-219, DGG-215-5, DGG-215-6, DGG-222, DGG-223, DGG-224, DGG-228, DGG-229, DGG-251, DGG-253, V-02-709, IPM-2-17, GG-K-21-1, GG-K-21-5, 3 MBRD-36, TMB-37, 5 BRD 11, 5 BRD-3, 4BRB-1, 7 BRD-12, MBRD-98, 4 MBRD -76, MBRD-56, TARM1, *V.trilobata*, IPB 3-02-0 2, IPM 99 – 125, AKM 8802, COGG 912, GPM-19, IPM - 2-14, IPM-14-10.

Table 4 : Inter cluster distance between different clusters based on the cluster means of the yield and yield related traits in advanced breeding lines of mungbean.

Cluster numbers	Inter cluster distance
I - II	21.109
I - III	22.559
II-III	19.096

showed a high negative direct effect but a positive correlation with yield, suggesting a balanced impact on yield (Asari *et al.*, 2019). This finding is consistent with previous research, indicating the importance of considering both correlation values and direct effects when interpreting trait contributions to yield (Table 2).

Table 5 : Cluster means for yield and yield related traits in mungbean genotypes.

Character	Cluster means		
	1	2	3
Plant height	28.95	41.298	22.925
Days to fifty per cent flowering	40.24	42.553	45.542
Branches per plant	3.648	3.055	2.841
Clusters per plant	11.245	7.644	5.835
Pods per plant	36.062	19.525	15.164
Pods per cluster	3.506	2.995	2.86
Seeds per pod	9.144	9.303	8.498
Pod length	7.214	7.09	6.949
Yield per plant	5.206	3.187	3.112
Test weight	3.937	4.393	4.342

Finally, clustering analysis revealed inter-cluster heterogeneity among genotypes, providing valuable insights for selecting parents in recombination breeding programs. The classification into three clusters, with the highest inter-cluster distance observed between the first and third clusters, suggests potential opportunities for generating superior recombinants through crosses among genotypes from these clusters. Overall, these findings contribute to our understanding of trait associations and breeding strategies for improving yield in mungbean.

Conclusion

The present study concludes that, the yield attributing traits such as number of pods per plant, number of clusters per plant and number of pods per cluster which showed a high positive direct effect, as well as positive correlation with the seed yield if considered in selection process will steadily support and increase the seed yield in mungbean. Hence, the above mentioned characters should be given topmost priority, while formulating a selection strategy for improvement of yield in mungbean.

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