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Genetic analysis for seed yield and yield component traits in recombinant inbred lines (RIL) population of blackgram (*Vigna mungo* (L.) Hepper)

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Abstract

An inter sub specific mapping population (RIL) was developed by crossing VBN(Bg)5 x *Vigna mungo* var. *silvestris* 22/10 by single seed decent method. The genetic variability parameters for ten yield and yield contributing traits were studied in a RIL population consisted of 193 lines. The high PCV and GCV was found for the traits viz., single plant yield, clusters per plant, pods per plant and branches per plant. High heritability was observed for all traits and ranged from 75.46 (pods per cluster) to 96.57 per cent (clusters per plant). High genetic advance as per cent of mean was observed for plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, hundred seed weight and single plant yield. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, hundred seed weight and single plant yield. Transgressive segregants were observed for all the traits. Five RILs viz., RIL 11, RIL12, RIL67, RIL73 and RIL168 showed superiority over cultivated variety viz., VBN (Bg) 5 for all traits except branches per plant. The trait based classification of RILs for yield contributing traits and for biotic stress resistance could be used as a pre breeding material for the improvement of blackgram.

Keywords: Blackgram, RIL, genetic variability, heritability, transgressive recombinants

Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an annual leguminous crop belongs to family Fabaceae and sub-family Papilionaceae with a chromosome number of $2n=22$. It is popularly known as “urdbean, urd or mash”, and an excellent source of easily digestible good quality proteins, carbohydrates, calcium and phosphoric acid, also popular for its fermenting action. In addition, being an important source of human food and animal feed, it also plays an important role in sustaining soil fertility by improving soil physical properties and fixing atmospheric nitrogen. Being a drought resistant crop, it is suitable for dry land farming and predominantly used as an inter crop with other crops. Blackgram is the fourth important pulse crop in India which holds 13 per cent of the total pulse area and contributing about 10 percent to the total pulse production. In India, blackgram is grown on 54.39 lakh hectares’ area with a production of 35.26 lakh tones and 655 kg/ha productivity (Annual Report, 2017-18) [1]. It is mostly grown in Andhra Pradesh, Uttar Pradesh, Maharashtra, Madhya Pradesh, Tamil Nadu, Rajasthan, Orissa, and Bihar.

India is the largest producer and consumer of blackgram in the world and its total production is not able to fulfill its domestic consumption demand. The domestic demand for this pulse makes India the largest importer as well. Therefore, it is necessary to undertake an indepth analysis of the genetic architecture of the plant that gives an idea on the current status of variability parameters that contribute towards yield and its attributing traits. Hence, the present study was undertaken to study the variability parameters in an inter-sub specific Recombinant Inbred Lines (RILs) mapping population of blackgram.

Material and Methods

The experimental material consisted of a Recombinant Inbred Lines (RIL) derived from a cross viz., VBN(Bg) 5 x *Vigna mungo* var. *silvestris* 22/10, a wild progenitor of blackgram. The RIL population which consisted of 193 individuals was developed through a single seed descent method. The experiment was laid out in homogeneous block following randomized block design replicated twice with 193 RILs during Rabi, 2018-2019 at the Department of Pulses, Tamil Nadu Agricultural University, Coimbatore.

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The RILs were planted in a row of 4 m in length with a spacing of 30×10 cm. The recommended package of practices was followed to raise a healthy crop. Observations on 10 biometrical traits *viz.*, days to 50% flowering, plant height, branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, hundred seed weight and single plant yield were recorded in three randomly selected plants in the 193 lines of mapping population.

The mean data were subjected to statistical analysis for the study of phenotypic and genotypic variances by (Burton, 1952) [6], heritability by (Lush, 1940) [13], genetic advance by Johnson *et al.* (1955) [10]. Statistical analysis was calculated using statistical software, INDOSTAT.

Results and Discussion

Analysis of variance (ANOVA) for the 193 lines of the RIL population had highly significant differences for all the 10 traits (Table 1). The existence of wide variability was observed with respect to different traits in the RIL population. The general mean value for each trait and its range among the RIL population are given in Table 2.

Per se performance

The mean performance of RIL's exhibited a wide range of variation for all the traits studied (Table 2). The traits showed more variation *viz.*, plant height (14.50-45.90 cm), clusters per plant (3.25-30.88), pods per plant (9.33-86.56) and single plant yield (1.10-16.87 g). Wide variations were observed for several traits by Konda *et al.* (2009) [11], Baisakh *et al.* (2014) [4], Gill *et al.* (2017) [8], Bishnoi *et al.* (2017) [2], Rolaniya *et al.* (2017) [7], Tank *et al.* (2018) [9], and Kuralarasan *et al.* (2018) [12] in blackgram. This indicates sufficient variation among the lines for the traits studied. This reflected that there is greater opportunity to improve the yield and its related traits in blackgram.

Genetic variability

The PCV and GCV were high for single plant yield (45.00, 42.23%), pods per plant (37.47, 35.65%) and clusters per plant (32.97, 32.40%), respectively. Moderate and high estimates of PCV and GCV were observed for branches per plant (22.47, 20.28%). Moderate PCV and GCV along with narrow difference among them were observed for plant height (18.68, 18.15%), pods per cluster (14.89, 12.94%), hundred seed weight (12.41, 11.88%) and pod length (11.95, 11.26%), respectively. Malik *et al.* (2008) [14], Konda *et al.* (2009) [11], Bhareti *et al.* (2011) [5], Baisakh *et al.* (2014) [4], Vinoth and Jayamani, (2014) [15], Asif *et al.* (2015) [3], Gill *et al.* (2017) [8], Bishnoi *et al.* (2017) [2], Rolaniya *et al.* (2017) [7], Tank *et al.* (2018) [9] and Kuralarasan *et al.* (2018) [12] have found the similar result in blackgram. Selection for these traits will be effective only on lesser environmental impact over the traits. Low estimates of PCV and GCV were observed for days fifty per cent flowering (7.11, 6.60%) which is highly influenced by the environment and selection would be ineffective (Table 2).

Heritability and genetic advance as a percentage of mean

High heritability coupled with high genetic advance as percentage of mean was found for plant height (94.42, 36.33%), branches per plant (81.44, 37.70%), clusters per plant (96.57, 65.60%), pods per cluster (75.46, 23.15%), pods

per plant (90.54, 69.89%), pod length (88.50, 21.85%), hundred seed weight (91.65, 23.44%) and single plant yield (88.10, 81.66%), respectively in which selection may be effective due to the additive gene effects. It is in accordance with the findings of Malik *et al.* (2008) [14], Konda *et al.* (2009) [11], Bhareti *et al.* (2011) [5], Baisakh *et al.* (2014) [4], Vinoth and Jayamani, (2014) [15], Asif *et al.* (2015) [3], Gill *et al.* (2017) [8], Bishnoi *et al.* (2017) [2], Rolaniya *et al.* (2017) [7], Tank *et al.* (2018) [9] and Kuralarasan *et al.* (2018) [12] in blackgram. High heritability coupled with moderate genetic advances as percentage of mean was recorded for days to fifty percent flowering (86.27, 12.63%) and seeds per pod (88.19, 19.51%) which revealed the additive gene effects coupled with high environmental impact (Table 2).

Skewness and Kurtosis

Skewness and Kurtosis were studied for all the traits. The skewness revealed that all the traits are in normal population distribution. Positive skewness was observed for all traits except seeds per pod. Clusters per plant (0.663), pods per cluster (0.742), pods per plant (0.803) and single plant yield (0.759) had moderate and positive value (Fig 1).

In case of kurtosis all traits showed positive except days to fifty percent flowering and seeds per pod. All the traits were mesokurtic in nature (Fig 1).

Transgressive recombinants

The prime objective of any crop improvement program is to improve the yield potential of the respective crop. From the inter-sub specific cross of the present investigation, 36 RILs were isolated for single plant yield which was above VBN (Bg) 5. A total of 54 RILs were identified as bold seeded with hundred seed weight exceeding the VBN (Bg) 5 (Table 2). Thus, these RILs could be further tested for yield and exploited.

Early flowering lines with short stature are the preferable traits for the intercropping situation. A total of 174 lines were found to be earlier and 49 lines with shorter plant height than VBN (Bg)5. Those RILs, with short duration coupled with less plant height, could be tested in various inter cropping situations to identify best performing lines. Genotypes with more branches and bearing more clusters per plant have direct contribution towards yield. Thus, six and 45 RILs with more branches and clusters, respectively could be selected for the improvement of blackgram (Table 2).

Pods per plant is the primary yield contributing trait in blackgram, 30 RILs recorded more pods per plant. These RILs could be tested further for commercial cultivation. Pods per cluster contribute indirectly for yield improvement, 71 RILs with more pods per cluster could be used as donors in the crossing program. Lengthy pods having more number of seeds, which will increase the yield correspondingly. Thus, the 98 RILs with more seeds per pod and 71 RILs with increased pod length could be selected as pre-breeding material for the improvement of blackgram (Table 2).

Based on the present study, the RILs with better mean values for yield attributing traits will be helpful to develop high yielding varieties. The RILs, which are superior over cultivated variety VBN (Bg) 5 could be used as pre-breeding material for further improvement of the blackgram. The mapping population could be further utilized for mapping of genes/QTLs for biotic stress and yield traits.

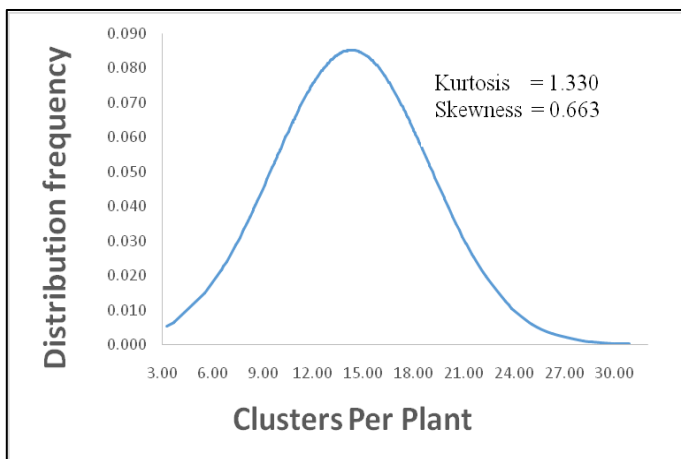
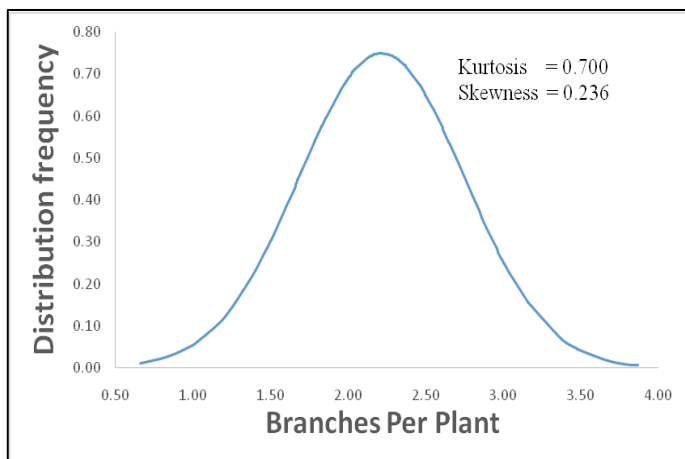
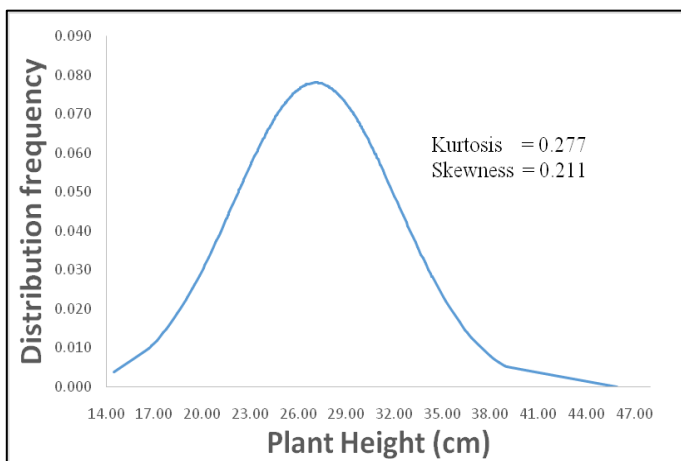
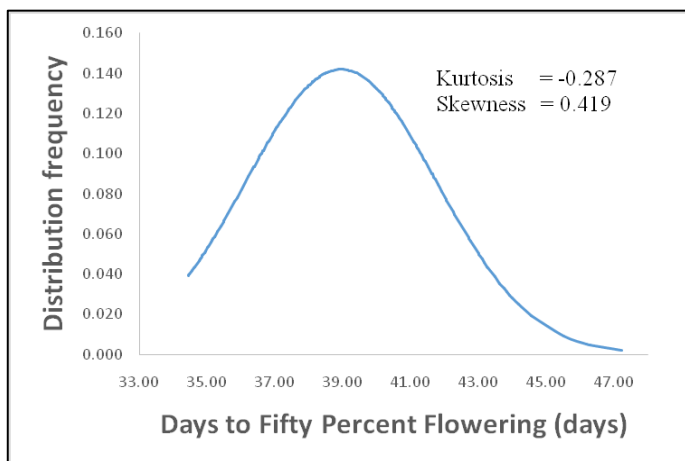
Table 1: Analysis of variance for yield and yield component traits in RIL population

Source of variation	df	Days to 50% flowering	Plant height	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	100 seed weight	Single plant yield
Replication	1	0.041	5.818	0.002	0.365	0.206	106.601	0.90	0.284	0.042	8.115
Treatment	192	15.252**	50.926**	0.476**	44.234**	0.786**	349.104**	0.541**	0.774**	0.601**	19.065**
Error	192	2.093	2.840	0.0884	1.515	0.193	33.017	0.060	0.091	0.50	2.269

**significant at 1% level

Table 2: Coefficient of variation, Heritability (broad sense), Genetic advance and Genetic advance as per cent of mean of yield and yield component traits in RIL population.

S. No	Traits	Female parent (VBN (Bg) 5)	Male parent (<i>V. mungo</i> var. <i>silvestris</i> 22/10)	General mean	Range	PCV %	GCV %	Heritability (h ²) %	Genetic advance (GA)	GA as per cent of mean	Number of transgressive recombinants higher than VBN (Bg) 5
1	Days to 50% flowering	43	44	38.86± 1.02	35.00 - 47.00	7.11	6.60	86.27	4.90	12.63	174
2	Plant height (cm)	23.83	39.02	27.01± 1.19	14.50 - 45.90	18.68	18.15	94.42	9.82	36.33	49
3	Branches per plant	3.17	2.17	2.17± 0.21	0.66 - 3.83	22.47	20.28	81.44	0.82	37.70	6
4	Clusters per plant	17.33	14.50	14.26± 0.87	3.25 - 30.88	32.97	32.40	96.57	9.36	65.60	45
5	Pods per cluster	4.33	3.17	4.21± 0.31	2.84 - 6.75	14.89	12.94	75.46	0.97	23.15	71
6	Pods per plant	46.33	31.67	35.26± 4.05	9.33 - 86.56	37.47	35.65	90.54	24.64	69.89	30
7	Pod length (cm)	4.50	3.57	4.36 ± 0.17	3.00 - 6.40	11.95	11.26	88.50	0.95	21.85	71
8	Seeds per pod	5.75	6.33	5.80 ± 0.21	4.00 - 7.17	10.74	10.09	88.19	1.13	19.51	98
9	100 seed weight (g)	4.70	2.50	4.42 ± 0.16	2.95 - 6.10	12.41	11.88	91.65	1.04	23.44	54
10	Single plant yield (g)	9.17	6.00	6.86± 1.06	1.10 - 16.87	45.00	42.23	88.10	5.60	81.66	36



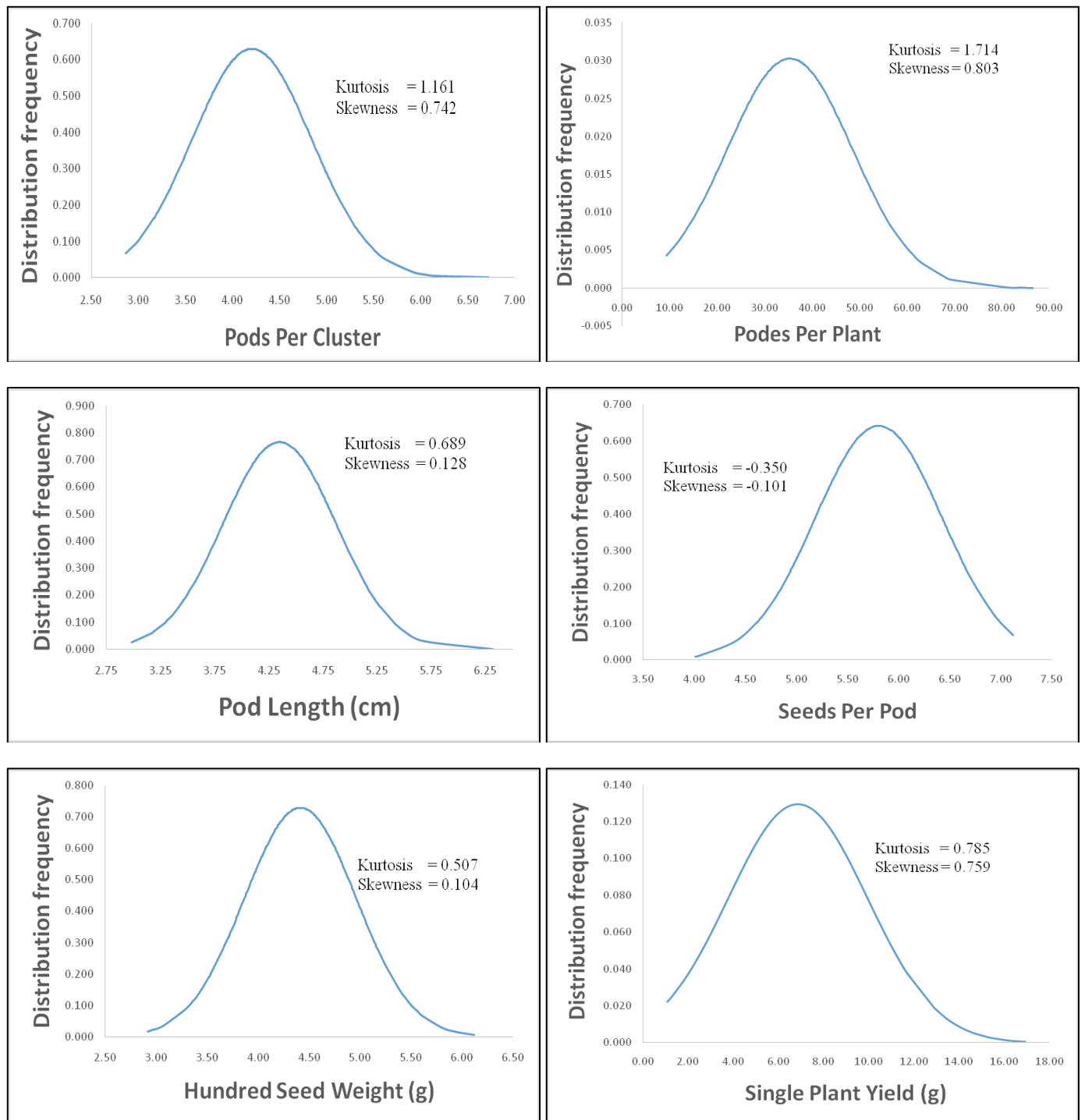


Fig 1: Frequency distribution for different traits

References

1. Annual report 2017-2018, Directorate of pulses development, vidhyachal bhavan 2018, 43.
2. Anu Bishnoi, Priyanka Gupta, Meghawal DR, Lal GM. Evaluation of genetic variability and heritability in blackgram (*Vigna mungo* (L.) Hepper) genotypes. Journal of Pharmacognosy and Phytochemistry. 2017;6(4):493-496.
3. Asif Hadimani, Konda CR, Rajendragouda Patil, Guru PN, Veena Krishna Hegde, Vijakumar L. Assessment of Genetic Variability, Heritability and Genetic Advance for Yield and yield attributing traits in blackgram (*Vigna mungo* (L.) hepper) Genotypes. National academy of agricultural science 2015;33(4):2473-2476.
4. Baisakh B, Das TR, Panigrahi KK. Genetic variability and correlation analysis for yield and yield contributing traits in advanced mutant lines of blackgram. Journal of Food Legumes 2014;27(3):202-205.
5. Bhareti P, Singh DP, Khulbe RK. Genetic variability and association analysis of advanced lines and cultivars following inter varietal and interspecific crosses in blackgram. Crop Improvement 2011;38(1):67-70.
6. Burton GW. Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress. 1952;1:227-283.
7. Dharmendra Kumar Rolaniya, Mahendra Kumar Jinjwadiya, Deva Ram Meghawal, Lal GM. Studies on genetic variability in Blackgram (*Vigna mungo* L. Hepper) germplasm. Journal of Pharmacognosy and Phytochemistry 2017;6(4):1506-1508.
8. Gill RK, Ashok Kumar, Inderjit Singh, Vikrant Tyagi. Assessment of induced genetic variability in blackgram

- (*Vigna mungo* (L.) Hepper). Journal of Food Legumes 2017;30(2):31-34.
9. Harish Kumar Tank, Sharma PP, Nagar KK, Bairwa LL, Meghawal DR. Genetic variability and heritability studies in blackgram (*Vigna mungo* (L.) Hepper). International Journal of Chemical Studies 2018;6(6): 642-646.
 10. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic variability and environmental variability in soybean. Agronomy Journal 1955;47:314-318.
 11. Konda CR, Salimath PM, Mishra MN. Genetic diversity in blackgram (*Vigna mungo* (L.) Hepper). Legume Research 2009;30(3):212-214.
 12. Kuralarasan V, Vanniarajan C, Kanchana S, Veni K, Anandhi Lavanya S. Genetic divergence, heritability and genetic advance in mutant lines of urdbean (*Vigna mungo* (L.) Hepper). Legume Research 2018;41(6):833-836.
 13. Lush JL. Intra sire correlation and regression of offspring on dams as a method of estimating heritability of characters. Journal of animal science 1940;33:293-301.
 14. Malik MFA, Awan SI, Niaz S. Comparative study of quantitative traits and association of yield and its components in blackgram (*Vigna mungo*) genotypes. Asian Journal of Plant Sciences 2008;7(1):26-29.
 15. Vinoth R, Jayamani P. Genetic variability studies for yield and its component traits in inter sub specific RIL population of blackgram (*Vigna mungo* (L.) Hepper). Trends in bioscience 2014;7(2):243-245.