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Research Note

Genetic relatedness and distribution pattern of yield attributing traits in horsegram mutants

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Abstract
A total of 110 mutants derived from two horsegram varieties PAIYUR 2 and CRIDA 1-18 R through 32 mutagenic combinations were evaluated during *rabi,*2020 to ascertain the breeding value. The analyses like trait dependence, character interrelationship, and nature of gene action were done by utilizing data on 11 yield attributing quantitative traits. Yield per plant recorded a highly significant positive association with the number of primary branches per plant (0.895), plant height (0.705), the number of pods per plant (0.703), days to maturity (0.568), the number of pods per cluster (0.444), the number of clusters per plant (0.332), the number of seeds per pod (0.299), and days to 50% flowering (0.207). The character number of pods per plant (0.699), days to 50% flowering (0.550), plant height (0.425), the number of seeds per pod (0.377), the number of primary branches per plant (0.286), 100-seed weight (0.271) and days to maturity (0.175) recorded the highest positive direct effect on yield per plant. Based on the estimates of coefficients of skewness and kurtosis, it is ascertained that the traits number of clusters per plant (0.81), the number of primary branches per plant (0.96), and the number of pods per plant (0.55) are governed by complementary gene action. This gene action suggests further intense selection for genetic gain.

Key words: Horsegram mutants, correlation, path analysis, skewness and kurtosis

Horsegram (*Macrotyloma uniflorum* (Lam) Verdc.) is a diploid (2n=2x=20), self pollinated, and nutritious rainfed *rabi* legume whose genome size is approximately 400 Mbps (Hirakawa *et al*., 2017). It is mostly cultivated in the Central and Southern region of India (Dikshit *et al*.,2014). Its stress tolerance is well proven (Kiranmai *et al*., 2018). Horsegram is enriched with protein, iron and molybdenum (Viswanatha *et al*., 2016 and Longvah *et al*., 2017). It is one of the ingredients of many traditional medicines used for curing kidney stones, urinary diseases, cardiac problems, asthma, common cold, fever and reduces obesity (Dhali *et al*., 2021). The productivity of horsegram is dwindled by a few undesirable botanical traits and limited variation for economic characters. Mutation breeding can be successfully employed to induce variability in horsegram (Priyanka *et al*., 2021). Estimation of genetic relatedness and inter-dependency of traits would help in improving yield directly and indirectly. Correlation and path studies helped in such estimation in horsegram (Singh *et al.,*2020 and Pawar *et al.,*2020). The coefficients of skewness and kurtosis are useful in understanding the inheritance pattern of quantitative traits as they estimate the nature of gene action and the number of genes governing the traits (Savitha and Usha kumari, 2015).

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Estimation of the nature of gene interaction is undeniably required to increase the effectiveness of selection in the breeding program. The usefulness of skewness and kurtosis in horsegram improvement was reported by Priyanka *et al*. (2019). Therefore, the present experiment was undertaken to estimate the dependability among quantitative traits, the correlation between traits and distribution pattern in a mutant population so as to frame breeding strategies for further exploitation of promising mutants.

Two well-known horsegram varieties PAIYUR 2 and CRIDA 1-18 R were irradiated with 32 mutagenic treatments involving gamma rays (G), electron beam (EB), G+EB and a combination of Gamma rays and ethyl methane sulfonate (EMS) to generate variability. The M_1, M_2 and M_3 generations were grown during *rabi,* 2017, 2018 and 2019, respectively at the Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The current experiment comprising of 110 homozygous M_4 mutant families was conducted at Sugarcane Research Station, Melalathur in a randomized block design with three replications during *rabi*, 2020 to ascertain the economic value of mutants. The breeding procedures pertaining to generation advancement during M_1, M_2, M_3 and M_4 were followed scrupulously. All the agronomic practices were adopted to raise a healthy crop. Observations for 11 quantitative traits were recorded *viz*., days to first flowering, days to 50% flowering, days to maturity, plant height (cm), the number of primary branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, the number of seeds per pod, 100-seed weight (g) and yield per plant (g). The data were documented as per Mahajan *et al*. (2000). The flowering traits were observed at appropriate growth stages and all other traits were recorded at maturity. Correlation coefficients were worked out as per Miller *et al*. (1958) and path analysis was estimated as suggested by Dewey and Lu (1959). The coefficients of skewness and kurtosis were estimated as per the formula of Snedecor and Cochran, 1967 using SPSS software (version 11) so as to establish the extent and frequency pattern of variability. The significance was estimated by comparing the calculated 't' value with table 't' value at (n-1) degrees of freedom at 0.05% probability.

Horsegram is a promising legume grown in marginal arid land in India. Improvement in horsegram is slowed down by the narrower genetic variability. It can be created through a dedicated plant breeding program *via* either classical hybridization or induced mutagenesis or a combination of both. The potential of induced mutagenesis is proven in evolving variability in horsegram (Priyanka *et al*., 2021). However, estimation of variability, dependency of traits and association between yield attributing traits in a mutant population at advanced stages of evaluation is vital so as to ascertain the economic value of mutants. The trait association was utilized to evaluate the relationship among the yield and its component traits to intensify the usefulness of selection (**Table 1**). Yield per plant recorded a highly significant positive association with the number of primary branches per plant (0.895), plant height (0.705), the number of pods per plant (0.703), days to maturity (0.568), the number of pods per cluster (0.444), the number of clusters per plant (0.332), the number of seeds per pod (0.299) and days to 50% flowering (0.207). The yield is a complex trait which can be improved through selection for associated traits indirectly. Therefore, it is established that yield improvement in horsegram can be brought through selecting the aforesaid traits. Earlier, the

Table 1. Correlation estimates of eleven quantitative characters in horsegram mutants

Character	DFfF	DM	PH	NPB	NCR	NPC	NPP	NSP	TW	SPY
DFsF	0.974**	0.724**	0.532**	0.200*	0.090	0.167	0.390**	0.039	-0.369**	0.157
DFfF		0.709**	0.536**	0.215*	0.137	0.120	0.389**	0.047	-0.312**	0.207*
DM			0.676**	0.448**	0.176	0.463**	0.673**	0.155	-0.326**	0.568**
PH				0.657**	0.697**	0.155	0.851**	-0.056	-0.220*	0.705**
NPB					0.165	0.551**	0.663**	0.013	0.263**	0.895**
NCR						-0.425**	0.576**	0.003	-0.373**	0.332**
NPC							0.476**	-0.064	-0.016	0.444**
NPP								-0.052	-0.429**	0.703**
NSP									-0.208*	0.299**
TW										0.149
SPY										

***, ** indicates significance at 5% and 1%, respectively**

DFsF – Days to first flowering; DFfF- Days to 50% flowering; DM - Days to maturity; PH - Plant height; NPB - Number of primary branches per plant; NCR- Number of clusters per plant; NPC- Number of pods per cluster; NPP- Number of pods per plant; NSP - Number of seeds per pod; TW - 100-seed weight; SPY - Yield per plant.

following similar findings were reported in horsegram. Khulbe *et al*. (2013) observed similar results between pods per plant and yield. The association of yield with plant height, the number of pods per plant was documented by Prabha *et al*. (2010). Neelam *et al*. (2014) reported a significant correlation between yield and the number of clusters per plant, the number of pods per plant. Alle *et al*. (2016) revealed a positive relationship for seed yield with the number of pods per plant, the number of clusters per plant, the number of primary branches, the number of seeds per pod and plant height. Contrarily, Singh *et al*. (2020) reported a negative and significant correlation of yield with days to maturity.

The correlation analysis established a positive and significant correlation among the flowering traits (days to first flowering, days to 50% flowering, and maturity) and their association with other quantitative traits *viz*., plant height, the number of pods per plant and the number of primary branches per plant. The number of pods per plant exhibited a significant and positive correlation with all the studied traits. Yield is positively correlated with all traits except days to first flowering and 100-seed weight. The pod traits are positively associated with plant height, the number of primary branches, and the number of clusters per plant. The character 100-seed weight showed a negative correlation with all other traits except the number of primary branches per plant. Similar results were recorded in horsegram by Vijayakumar *et al*. (2016) and Prakash and Khanure, (2000) and Srivastava and Singh (2012) in mungbean.

Path coefficient analysis is used to partition the correlation coefficients into direct and indirect effects. The seed yield was treated as a dependent variable and its component characters as an independent variable (**Table 2**). The component of residual effect of path analysis was 0.0437. The result of a path analysis revealed that the number of pods per plant recorded the highest positive direct effect (0.699) on yield per plant followed by days to 50% flowering (0.550), plant height (0.425), the number of seed per pod (0.377), the number of primary branches per plant (0.286), 100-seed weight (0.271), and days to maturity (0.175). The characters days to first flowering (-0.889), the number of clusters per plant (-0.459), the number of pods per cluster (-0.277) recorded a negative direct effect. These findings are in agreement with the earlier findings in horsegram by Paliwal *et al*. (2005), Bhave *et al*. (2007) and Khulbe *et al*. (2013).

The number of primary branches is the only trait that showed a positive indirect effect through all the other test traits on yield. Days to first flowering exhibited a positive indirect effect only through 100-seed weight. While days to 50% flowering and maturity displayed a positive indirect effect *via* all quantitative traits except 100-seed weight. The traits number of clusters per plant, the number of pods per cluster and 100-seed weight exerted a negative indirect effect through most of the quantitative traits on yield. The results were also confirmed by Singh *et al*. (2020), Lakshmi Narayanan (2018) in redgram and Sidramappa (2020) in blackgram. Therefore, yield in horsegram can directly be improved by the trait number of pods per plant and indirectly through the number of primary branches per plant.

The nature of gene action can be ascertained through the estimates of coefficients of skewness. It refers to asymmetry of the distribution curve (Fisher *et al*., 1932). Positive skewed distribution (skewed towards right)

Table 2. Path estimates of eleven quantitative characters in horsegram mutants

Character	DFsF	DFfF	DM	PH	NPB	NCR	NPC	NPP	NSP	TW	SPY
DFsF	**-0.889**	-0.866	-0.644	-0.473	-0.177	-0.080	-0.149	-0.347	-0.035	0.328	0.157
DFfF	0.536	**0.550**	0.390	0.295	0.119	0.075	0.066	0.214	0.026	-0.172	0.207*
DM	0.127	0.124	**0.175**	0.118	0.078	0.031	0.081	0.118	0.027	-0.057	0.568**
PH	0.226	0.228	0.287	**0.425**	0.279	0.296	0.066	0.362	-0.024	-0.094	0.705**
NPB	0.057	0.062	0.128	0.188	**0.286**	0.047	0.157	0.189	0.004	0.075	0.895**
NCR	-0.041	-0.063	-0.081	-0.320	-0.076	**-0.459**	0.195	-0.264	-0.001	0.171	0.332**
NPC	-0.046	-0.033	-0.129	-0.043	-0.153	0.118	**-0.277**	-0.132	0.018	0.004	0.444**
NPP	0.273	0.272	0.470	0.595	0.463	0.402	0.332	**0.699**	-0.036	-0.300	0.703**
NSP	0.015	0.018	0.058	-0.021	0.005	0.001	-0.024	-0.019	**0.377**	-0.078	0.299**
TW	-0.100	-0.084	-0.088	-0.060	0.071	-0.101	-0.004	-0.116	-0.056	**0.271**	0.149

Diagonal and bold indicates the direct effects, Residual effect = 0.0437

*, ** indicates significance at 5% and 1%, respectively

DFsF – Days to first flowering; DFfF- Days to 50% flowering; DM - Days to maturity; PH - Plant height; NPB - Number of primary branches per plant; NCR- Number of clusters per plant; NPC- Number of pods per cluster; NPP- Number of pods per plant; NSP - Number of seeds per pod; TW - 100-seed weight; SPY – Yield per plant .

Table 3. Estimtes of coefficients of skewness and kurtosis for 11 quantitative characters in horsegram mutants

Character	Skewness	Kurtosis
Days to first flowering	-2.39*	11.79*
Days to 50% flowering	-3.82*	19.94*
Days to maturity	-2.03*	4.62*
Plant height	-0.27	-0.43
Number of primary branches per plant	0.96*	0.09
Number of clusters per plant	0.81*	1.11*
Number of pods per cluster	0.32	-0.19
Number of pods per plant	0.55*	0.41
Number of seeds per pod	0.11	-0.16
100-seed weight	-0.44	-0.20
Yield per plant	0.3	-0.31

* Significance at 5% probability

is linked to complementary gene interaction whereas negatively skewed distribution (skewed towards left) is correlated with the duplicate type of gene interactions. Kurtosis is the measure of peakeness of the distribution curve which denotes information on the number of genes involved (Robson, 1956). The traits are classified as leptokurtic (kurtosis > 3) and platykurtic (kurtosis < 3) distribution and the number of genes governing is fewer and larger, respectively. The estimates of coefficients of skewness and kurtosis are presented in **Table 3.** The traits days to first flowering, days to 50% flowering, and days to maturity showed a significant and negative coefficient of skewness with leptokurtic curve. It indicated that these traits are controlled by a few genes with duplicate gene interaction in the inheritance. Therefore, it is suggested to adopt mild selection to achieve faster gain for these traits (Roy, 2000). Priyanka *et al*. (2019) reported a genotypic dependant gene interaction for days to 50% flowering in horsegram. Contrarily, Mariyammal *et al*. (2019) recorded positively skewed with platykurtic kurtosis for days to first flowering in greengram. The traits plant height, the number of pods per cluster, the number of seeds per pod, 100-seed weight, and yield per plant displayed non-significant skewness and kurtosis indicating the absence of gene interaction and a normal distribution. Earlier Priyanka *et al*. (2019) reported a similar result for the number of seeds per pod. The trait number of clusters per plant showed significant and positive coefficients of skewness and kurtosis with platykurtic curve. It implies the preponderance of dominance based complementary gene interaction involving larger genes. Hence, it is suggested to practice intense selection to achieve genetic gain (Roy, 2000). In contrast, governance of complementary gene interaction in the inheritance with leptokurtic kurtosis was reported for the number of clusters per plant (Priyanka *et al*., 2019). Similarly, Vadivel *et al*. (2019) reported that the number of clusters per plant had leptokurtic nature in blackgram. Significant positive skewness was observed for the number of primary branches per plant and the number of pods per plant which indicates the presence of complementary gene action. This trait can be improved faster with intensive selection (Roy, 2000). It can be concluded that the performance of this mutant population could be improved further through intense selection for traits *viz*., the number of clusters, the number of branches per plant, and the number of pods per plant. These traits exhibited a significant effect on yield and were also governed by complementary gene action (Choo and Reinbergs, 1982).

REFERENCES

Alle, R., Hemalatha, V., Eshwari, K.B. and Swarnalatha, V. 2016. Genetic variability, correlation and path analysis for yield and its components in horsegram (*Macrotyloma uniflorum* [Lam.] Verdc.). *Green Farming*., **7**: 1-4.

Bhave, S.G., Joshi, S.N., Sawant, S.S., Bendale, V.W and Desai, S.S. 2007. Analysis of genetic parameter for yield and certain yield contributing traits in horsegram. *J Maha. Agric. Uni*., **32**: 239-241.

Choo, T. M. and Reinbergs, E. 1982. Analysis of skewness and kurtosis for detecting gene interaction in a double haploid population. *Crop Sci*., **22**: 231-235. [Cross Ref]

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron J*., **51**: 575-581. [Cross Ref]

Dhali, S., Pradhan, M., Sahoo, R.K., Mohanty, S. and Pradhan, C.2021. Alleviating Cr (VI) stress in horsegram (*Macrotyloma uniflorum* Var. Madhu) by native Cr-tolerant nodule endophytes isolated from contaminated site of Sukinda. *Environ Sci Pollut Res*., **28**:31717–31730. [Cross Ref]

Dikshit, N., Katna G., Mohanty C.S., Das A.B. and Sivaraj, N. 2014. Horsegram. In: Singh M., Bisht I., Dutta M. (eds) Broadening the genetic base of grain legumes. *Springer*. [Cross Ref]

Fisher, R.A., Immer, F.R. and Tedin, O. 1932. The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics.*, **17**:107-124. [Cross Ref]

Hirakawa, H., Chahota, R.K., Shirasawa, K., Sharma, T.R. and Isobe, S.2017. Draft genome sequencing of horsegram (*Macrotyloma uniflorum*); PAG Asia, South Korea.

Khulbe, R. K., Pant, D. P. and Singh, D. V. 2013. Genetic studies in horsegram from NW himalayan regions of Uttarakhand, India. *Crop Res*., **43**: 194-196.

Kiranmai, K., Rao, G.L., Pandurangaiah, M., Nareshkumar, A., Vennapusa, V.A., Lokesh, U., Venkatesh, B., Johnson, M.A. and Sudhakar, C. 2018. A novel WRKY transcription factor, MuWRKY3 (*Macrotyloma uniflorum* Lam. verdc.) enhances drought stress tolerance in transgenic groundnut (*Arachis hypogaea* L.) Plants. *Front. Plant Sci*., **9**: 346. [Cross Ref]

Narayanan, S. L., Manivannan, N. and Mahalingam, A. Correlation and path analysis of yield and its component traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. 2018. *Int.J.Curr. Microbiol. App. Sci*., **7**:614-618. [Cross Ref]

Longvah, T., Ananthan, R., Bhaskarachar, K. and Venkaiah, K. 2017. Indian food composition tables. Hyderabad: National Institute of Nutrition. http://www.indiaenvironmentportal.org.in/files/file/IFCT%202017%20Book.pdf.

Mahajan, R. K., Sapra, R. L., Umesh, S., Singh, M. and Sharma, G.D. 2000. Minimal descriptor (for characterization and evaluation) of agri-Horticultural crops: National Bureau of Plant Genetic Resources, New Delhi.

Mariyammal, Pandiyan, M., Vanniarajan, C., Kennedy, J.S. and Senthil, N. 2019. Studies in three F_2 populations of greengram (*Vigna radiata* L. Wilzeck). *Genetics.*, **11**:564-568.

Miller, P.A., Williams, J.E., Robinson, H.F. and Comstock, R.E. 1958.Estimataes of variance and co- variance in upland cotton and implication in selection. *Agron J*., **50**: 126-131. [Cross Ref]

Neelam,S., Kumar,V., Natarajan,S., Kamala Venkateshwaran and Pandravada, S.R.2014. Evaluation and diversity observed in horsegram (*Macrotyloma uniflorum* (Lam) Verdc.) Germplasm from Andhra Pradesh, India. *Int. J. Plant Res*., **4**: 17-22.

Paliwal, R. V., Sodani S. N. and Jain, L. K. 2005. Correlation and path analysis in horsegram (*Macrotyloma uniflorum* (L.) Verdc.). *J. Arid Leg*., **2**: 309-310.

Pawar,A.B., Najan,B.R. and Lad,D.B.2020. Association of characters and path coefficient analysis for yield and its components in horsegram (*Macrotyloma uniflorum* L. Verdc.). *Ind. J. Pure App. Biosci.,* **8**:177-182. [Cross Ref]

Prabha, S.S., Rajendra Prasad and Sambhoo Prasad. 2010. Study on genetic and seed quality parameter in horsegram genotype under mid hills of north western himalaya. *Trends in Biosci*., **3**:187-189.

Prakash, B.C. and Khanure, S.K. 2000. Genetic parameters, correlation and path coefficient analysis in horsegram. *Karnataka J. Agric. Sci*., **13**:313-315.

Priyanka, S., Sudhagar, R.,Vanniarajan, C., Ganesamurthy, K. and Souframanien, J. 2019. Combined mutagenic ability of gamma ray and EMS in horsegram (*Macrotyloma uniflorum* (Lam) Verdc.). *Electronic Journal of Plant Breeding*, **10**: 1086 – 1094. [Cross Ref]

Priyanka,S., Sudhagar,R., Vanniarajan,C., Ganesamurthy,K. and Souframanien,J. 2021. Induction of genetic variability for quantitative traits in horsegram (*Macrotyloma uniflorum*) through irradiation mutagenesis. *J. Environ. Biol*., **42**: 597-608.

Robson, D.S. 1956. Application of K_4 statistics to genetic variance component analysis. *Biometrics*, **12**:433-444. [Cross Ref]

Roy, D. 2000. Plant Breeding - The analysis and exploitation of variability. Narosa publishing house, New Delhi, India, p. 300-304.

Savitha,P. and Usha Kumari, R. 2015. Studies on skewness, kurtosis and parent progeny regression for yield and its related traits in segregating generations of rice. *Oryza.*, **52**: 80-86.

Sidramappa, Kuchanur,P. H., Shobharani, M., Arunkumar, B., Kulkarni, S.A., Sowmya, H.C., Sheela, D., Laxuman and Bharati,S..2020. Correlation and path coefficient analysis in Blackgram [*Vigna mungo* (L.) Hepper] across seasons. *Int.J.Curr.Microbiol.App. Sci*., **9**: 873-878. [Cross Ref]

Singh,M.K., Ekka,R.E., Sinha, S.K., Sandilya, V.K., Sahu, V.P. and Birjhu. 2020. Correlation and path coefficient analysis in horsegram [*Macrotyloma uniflorum* (Lam) Verdc.]. *Int.J.Curr.Microbiol.App. Sci*., **9**: 604-610. [Cross Ref]

Snedecor, G.W. and Cochran, W.G. 1967. Statistical methods. 6th Edn, Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, India, p. 593.

Srivastava, R.L. and Singh, G. 2012. Genetic variability, correlation and path analysis in mung bean (*Vigna radiata* (L.). *IJLS.*, **2**: 61 – 65.

Vadivel, K., Manivannan, N., Mahalingam, A., Satya, V.K., Vanniarajan, C., and Saminathan, V.R. 2019. Assessment of variability for seed yield, component characters and MYMV disease resistance in segregating populations of blackgram [*Vigna mungo* (L.) Hepper]. *Electronic Journal of Plant Breeding*, **10**: 732-735. [Cross Ref]

Vijayakumar, A. G., Shruti Koraddi, Ishwar, H., Boodi and Kallesh, D.T. 2016. Genetic variability studies in horsegram (*Macrotyloma uniflorum* (Lam.) Verdc.) *The Biscan.*, **11**: pp. 1255-1259.

Viswanatha, K.P., Yogeesh, L.N. and Amitha, K. 2016. Morphological diversity study in horsegram (*Macrotyloma uniflorum* (Lam.)Verdc) based on Principal Component Analysis (PCA). *Electronic Journal of Plant Breeding*, **7**: 767-770. [Cross Ref]