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Analysis of Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Chilli (*Capsicum annuum* L.)

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ABSTRACT

Thirty five chilli genotypes were evaluated in a randomized block design at College of Horticulture, Rajendranagar, Sri Konda Laxman Telangana State Horticultural University, Hyderabad, Telangana state, India during *Kharif*, 2019 for seven months and at National Bureau of Plant Genetic Resources, Regional station, Rajendranagar, Hyderabad during *Rabi* 2019-20 for seven months to estimate genetic variability, heritability, genetic advance and genetic advance as % of mean of seventeen yield and yield related traits. For all the traits studied, the magnitude of PCV was higher than corresponding GCV. High Phenotypic coefficient of variation and genotypic coefficient of variation estimates were recorded for plant height, plant spread, fruit length, fruit diameter, number of fruits plant^{-1}, fruit weight, fruit yield plant^{-1}, fruit yield plot^{-1}, ascorbic acid, capsaicin content and capsanthin content indicating the existence of wider genetic variability for these traits in the genotypes studied. High heritability was recorded for the traits Days to first flowering, Fruit length, Fruit diameter, No. of fruits plant^{-1}, Fruit weight, Fruit yield plant^{-1}, Fruit yield plot^{-1}, Ascorbic acid, Chlorophyll content, Capsaicin content and Capsanthin content. High heritability coupled with high genetic advance as % mean indicates existence of additive gene action which was observed in fruit length, fruit diameter, number of fruits plant^{-1}, fruit weight, fruit yield plant^{-1}, fruit yield plot^{-1}, ascorbic acid, chlorophyll content, capsaicin content and capsanthin content. Hence these traits can be improved by direct selection.

KEYWORDS: Chilli, genetic advance, genetic variability, heritability

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1. INTRODUCTION

Chilli (*Capsicum annuum* L.) (2n=24) is one of the most popular vegetables, originated from South and Central America (Bahurupe et al., 2013). It is the second most important solanaceous vegetable after tomato grown worldwide both as a spice or vegetable crop (Hasan et al., 2014). It is probably introduced by Portuguese into Southern parts of India in 16th century and cultivation spread out throughout India by the end of 19th century. Rich variability in morphological traits in chilli occurs throughout India particularly in south peninsular region, North Eastern foot hills of Himalayas and Gangetic plains (Pradheep and Veeraragavathatham, 2006). It is a spice, a fruit vegetable widely cultivated in the world and its importance in human food is capital (Dias et al., 2013). It is mainly used for its pungency and pleasant flavor. Particularly in India, there is no home which does not consume chilli. India is the world's largest producer, consumer and exporter of chilli. Chilli is rich in proteins, lipids, carbohydrates, fibres, mineral salts (Ca, P, Fe) and in vitamins A, D3, E, C, K, B2 and B12 (El-Ghoraba et al., 2013). It is sometimes referred as capsule of vitamin C because of rich vitamin C content in the fruit (Durust et al., 1997). Consumption of small amount of chilli enriches diet and considered as of minerals, vitamins and other food components (Farhad et al., 2010).

Due to long history of cultivation, selection and popularity of crops sufficient genetic variability has been generated. Germplasm characterization is essential to utilize and improve plant genetic resources in various breeding programs (Pidigam et al., 2019). Improvement of any crop depends on magnitude of genetic variability and the extent of heritability of economically important characters, though the part played by environment in the expression of such character also needs to be taken into account. Plant breeding programs focus on increasing crop yield in a wide range of growing conditions (Saidaiah et al., 2021a). Hence new genotypes must be characterized to assess the variability and identify promising genotypes which can be used in further breeding programmes (Munshi et al., 2000; Sarma and Roy, 1995, Sreelathakumary and Rajamony, 2004, Pidigam et al., 2021). Therefore, identification and utilization of diverse genotypes is essential for breeding new cultivars in a desired direction (Aparna et al., 2014). The knowledge of variability provided by principal component analysis is helpful to select genetically and agronomically-important genotypes (Isong et al., 2017). Greater the variability in a population, there will be the greater chance for effective selection for desirable types (Vavilov, 1951). Generally, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are measured to study the variability. Heritability estimates give a measure of transmission of characters from one generation to another (Sabri et al., 2020, Saidaiah et al., 2021a, b, c). After all, the trait improvements that can be made through direct selection are estimated by the availability of heritable variation (Khan et al., 2020). Phenotypic plant expression may not be actual genetic potential of genotypes since environment can affect genotype response, genetic analysis determine the breeding method to achieve maximum genetic advancement with available resources (Manjunathagowda and Anjanappa, 2021). Heritability and genetic advance helps in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection. Genetic advance provides information on expected gain resulting from selection of superior individuals (Lingaiah et al., 2019). Efficiency of selection can be determined by using genetic advance (Ashish et al., 2017). In this regard the present investigation was carried out to study genetic variability, heritability and genetic advance for yield and yield related traits.

2. MATERIALS AND METHODS

The present experiment was laid out in a Randomized Block Design with 35 chilli accessions as treatments at College of Horticulture, Rajendranagar, Sri Konda Laxman Telangana State Horticultural University, Hyderabad, Telangana State, India during seven months of *Kharif*, 2019 for seven months and at NBPGR Regional station, Rajendranagar, Hyderabad during *Rabi*, 2019-20 for seven months. The site of the experiment is situated in semi arid tropical zone at an altitude of 542.6 m above mean sea level. Geographically, it lies at latitude of 17°19' N and a longitude of 79°23' E. Each treatment was randomly replicated thrice. The experimental material used in this experiment were presented in Table 1.

Nursery of 35 chilli genotypes was raised in protrays with 50 cells. Vermicompost, FYM and red earth were taken in the ratio of 2:1:1 and filled in pro trays. Each seed was sown in each cell of the pro tray. Six weeks old healthy seedlings were transplanted in the main field after allotting entries randomly in each replication. Each germplasm line was grown in a plot of 1.8 ×4.2 m^2 (7.56 Sq. meters), 7 plants per row with spacing of 60×60 cm^2 per replication. The plots were kept free of weeds and irrigated as and when required depending on soil moisture content. Need based plant protection measures were taken up to keep the plot free from pests and diseases.

Data was collected for 17 characters related to growth and fruit yield viz., plant height (cm), plant spread (cm^2), number of primary branches $plant^{-1}$, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length(cm), fruit diameter(cm), number of

Table 1: Analysis of Variance for 17 yield and yield attributes in 35 genotypes of chilli

Sl. No.	Character	Mean Sum of Squares		
		Replications (df=2)	Treatments (df=34)	Error (df=68)
1.	Plant height (cm)	11.96	946.55***	118.49
2.	Plant spread (cm^2)	77.69	7555136.93***	1434964.10
3.	No. of primary branches $plant^{-1}$	0.36	1.62***	0.50
4.	Days to first flowering	8.82	161.99***	14.84
5.	Days to 50 % flowering	5.10	148.81***	18.96
6.	Days to first harvest	29.39	357.60***	57.25
7.	Days to last harvest	21.60	400.60***	114.50
8.	Fruit length (cm)	0.02	30.32***	1.52
9.	Fruit diameter (cm)	0.0008	0.47***	0.03
10.	No. of fruits $plant^{-1}$	18.14	6347.56***	74.04
11.	Fruit weight (g)	0.05	29.51***	0.27
12.	Fruit yield $plant^{-1}$ (kg)	0.0005	0.16***	0.003
13.	Fruit yield $plot^{-1}$ (Kg)	0.15	31.62***	0.61
14.	Ascorbic acid (mg/100g)	3.20	11554.87***	2.50
15.	Chlorophyll content (%)	0.01	0.34***	0.01
16.	Capsaicin content (%)	0.0001	0.16***	0.001
17.	Capsanthin content (ASTA units)	0.63	15796.45***	5.36

fruits $plant^{-1}$, fruit weight (g), fruit yield $plant^{-1}$ (kg $plant^{-1}$), fruit yield $plot^{-1}$ (kg), ascorbic acid content (mg 100 g^{-1} of fruit), chlorophyll content of green chilli, capsaicin content (%) and capsanthin content (ASTA units). The data was subjected to biometrical analysis. The simple measures of variability like mean, range and the major components of variability were calculated from the pooled data.

2.1. Genotypic variance and phenotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by Cochran and Cox (1957).

Genotypic variance(σ^2_g)=(MSS due to genotypes-MSS due to error)/r

Phenotypic variance=Genotypic variance (σ^2_g)+Error variance (σ^2_e)

2.2. Co-efficient of variability

Both phenotypic and genotypic co-efficients of variability for all characters were estimated using the formula of Burton and De Vane (1953).

Phenotypic Co-efficient of variability (PCV %) =(√Phenotypic variance/grand mean)×100

Genotypic Co-efficient of variability (GCV %) =(√Genotypic variance/Grand mean)×100

PCV and GCV were classified as per Sivasubramanian and Menon (1973) as shown below:

Low : Less than 10%

Moderate : 11–20%

High: 21% and above

2.3. Heritability in broad sense (h^2)

Broad sense heritability (h^2_{bs}) was estimated and expressed as the ratio of genotypic variance to the phenotypic variance and expressed in % (Lush, 1949 and Hanson et al., 1956).

h^2 =(Genotypic variance/Phenotypic variance)×100

The range of heritability was categorized as follows (Johnson et al., 1955)

Low : Less than 30%

Moderate: 30–60%

High : 60% and above

2.4. Genetic advance (GA)

The expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson et al. (1955).

$GA=h^2_{bs} \times \sigma_p \times K$

Where,

h^2_{bs}=Heritability estimate in broad sense

σ_p=Phenotypic standard deviation of the trait

K=Standard selection differential which is 2.06 at 5% selection intensity.

Further the Genetic advance as per cent of mean was computed by using the following formula

GA as % of mean =(GA/Grand mean)×100

The range of genetic advance as % of mean was classified as suggested by Johnson et al. (1955).

Low : Less than 10%

Moderate: 10–20%

High: 20% and above

3. RESULTS AND DISCUSSION

Analysis of variance (Table 2) revealed that there was significant difference among the 35 genotypes for all the traits studied indicating the presence of significant variability in the genotypes These findings are in line with earlier reports of Singh and Singh, (2011) and Krishnamurthy et al. (2013). The simple measures of variability like mean, range and the major components of variability such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in broad sense (h^2), genetic advance and genetic advance as % of mean are presented in Table 3 and Table 4. All the 17 characters under study exhibited high variability as evident from the estimates of mean, range, coefficients of variation, heritability and genetic advance.

Table 2: List of chilli genotypes used for evaluation along with their sources

Tr. No.	Genotype	Source	Tr. No.	Genotype	Source
T_1	IC-347044	NBPGR Regional Station, Hyderabad	T_{19}	IC-528442	NBPGR Regional Station, Hyderabad
T_2	IC-363918	NBPGR Regional Station, Hyderabad	T_{20}	EC-399535	NBPGR Regional Station, Hyderabad
T_3	IC-363993	NBPGR Regional Station, Hyderabad	T_{21}	EC-378632	NBPGR Regional Station, Hyderabad
T_4	IC-561676	NBPGR Regional Station, Hyderabad	T_{22}	IC-215012	NBPGR Regional Station, Hyderabad
T_5	IC-561622	NBPGR Regional Station, Hyderabad	T_{23}	EC-378688	NBPGR Regional Station, Hyderabad
T_6	IC-610381	NBPGR Regional Station, Hyderabad	T_{24}	IC-214966	NBPGR Regional Station, Hyderabad
T_7	IC-505237	NBPGR Regional Station, Hyderabad	T_{25}	IC-319335	NBPGR Regional Station, Hyderabad
T_8	IC-447018	NBPGR Regional Station, Hyderabad	T_{26}	IC-394819	NBPGR Regional Station, Hyderabad
T_9	IC-572459	NBPGR Regional Station, Hyderabad	T_{27}	IC-572498	NBPGR Regional Station, Hyderabad
T_{10}	IC-610383	NBPGR Regional Station, Hyderabad	T_{28}	EC-399581	NBPGR Regional Station, Hyderabad
T_{11}	IC-214965	NBPGR Regional Station, Hyderabad	T_{29}	IC-526737	NBPGR Regional Station, Hyderabad
T_{12}	EC-402113	NBPGR Regional Station, Hyderabad	T_{30}	IC-570408	NBPGR Regional Station, Hyderabad
T_{13}	IC-410423	NBPGR Regional Station, Hyderabad	T_{31}	IC-561648	NBPGR Regional Station, Hyderabad
T_{14}	IC-526448	NBPGR Regional Station, Hyderabad	T_{32}	IC-334383	NBPGR Regional Station, Hyderabad
T_{15}	EC-399567	NBPGR Regional Station, Hyderabad	T_{33}	SINDHURc	NBPGR Regional Station, Hyderabad
T_{16}	IC-561655	NBPGR Regional Station, Hyderabad	T_{34}	LCA-625c	NBPGR Regional Station, Hyderabad
T_{17}	EC-390030	NBPGR Regional Station, Hyderabad	T_{35}	PUSA JWALAc	NBPGR Regional Station, Hyderabad
T_{18}	IC-528433	NBPGR Regional Station, Hyderabad			

Among different characters studied high PCV and GCV estimates were recorded for plant height (25.52% and 18.72%), plant spread (42.66% and 27.50%), fruit length (33.69% and 29.34%), fruit diameter (25.79% and 21.47%), number of fruits plant^{-1} (49.34% and 47.68%), fruit weight (49.83% and 48.49%), fruit yield plant^{-1} (61.68% and 58.16%), fruit yield plot^{-1} (61.14% and 57.81%), ascorbic acid (47.03% and 47.00%), capsaicin content (38.51 % and 37.47%) and capsanthin content (21.39% and 21.36%) indicating the existence of wider genetic variability for these traits in the genotypes studied. This also indicates the presence of broad genetic base and these traits are under the control of additive gene effects and hence, there is a good scope for further improvement of these characters through simple selection. On the other hand, PCV and GCV estimates were moderate to low for number of primary branches plant^{-1} (19.65% and 10.23%), days to first flowering (12.46% and 9.83%), days to 50% flowering (11.32% and 8.26%), days to first harvest (12.17% and 8.31%), days to last harvest (8.64% and 4.68%) and chlorophyll content (13.82% and 12.19%) suggesting moderate to narrow range of genetic variability.

For all the traits studied, the magnitude of PCV was higher than corresponding GCV indicating that the apparent variation is not only due to genotype but also due to the favourable influence of environment. Hence for these traits selection based on phenotype is not suitable as their

Table 3: Estimates of mean, range, components of variance, heritability and genetic advance in chilli genotypes from pooled data

Sl. No.	Character	Mean Sum of Squares		Mean	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)
		Minimum	Maximum					
1.	Plant height (cm)	47.53	102.48	62.73	256.50	138.01	25.52	18.72
2.	Plant spread (cm^2)	1707.83	5950.50	3672.08	2454993.00	1020029.00	42.66	27.50
3.	No. of primary branches $plant^{-1}$	3.26	5.15	4.22	0.68	0.18	19.65	10.23
4.	Days to first flowering	36.25	59.60	50.35	39.36	24.52	12.46	9.83
5.	Days to 50 % flowering	45.78	66.28	56.27	40.60	21.64	11.32	8.26
6.	Days to first harvest	66.66	98.66	85.09	107.31	50.05	12.17	8.31
7.	Days to last harvest	131.50	163.66	147.26	162.18	47.68	8.64	4.68
8.	Fruit length (cm)	2.88	14.80	7.46	6.32	4.80	33.69	29.34
9.	Fruit diameter (cm)	0.86	2.21	1.26	0.10	0.07	25.79	21.47
10.	No. of fruits $plant^{-1}$	15.16	166.66	67.80	1119.63	1045.58	49.34	47.68
11.	Fruit weight (g)	1.78	11.81	4.55	5.14	4.87	49.83	48.49
12.	Fruit yield $plant^{-1}$ (kg)	0.11	0.82	0.28	0.03	0.02	61.68	58.16
13.	Fruit yield $plot^{-1}$ (Kg)	1.52	11.54	3.93	5.78	5.16	61.14	57.81
14.	Ascorbic acid (mg/100g)	44.71	191.80	93.36	1927.90	1925.39	47.03	47.00
15.	Chlorophyll content (%)	1.13	2.24	1.90	0.07	0.05	13.82	12.19
16.	Capsaicin content (%)	0.21	0.83	0.44	0.02	0.02	38.51	37.47
17.	Capsanthin content (ASTA units)	137.55	373.52	240.08	2637.21	2631.84	21.39	21.36

expression depends more on environmental factors. Similar observations were reported in chilli by Shah et al. (1986).. The difference between PCV and GCV was narrow for the traits plant height, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit diameter, number of fruits plant-1, fruit weight, fruit yield $plant^{-1}$, fruit yield $plot^{-1}$, ascorbic acid, chlorophyll content, capsaicin content and capsanthin content indicating the little influence of environment on the expression of these characters. These results are supported by earlier observations of Krishnamurthy et al. (2013) and Sandeep et al. (2013). The difference between PCV and GCV was high for the traits plant spread and number of primary branches $plant^{-1}$ indicating considerable influence of environment in expression of these traits.

Heritability estimates the proportion of phenotypic variation due to genetic variation, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite genotype in the crop. High heritability was recorded for the traits days to first flowering, fruit length, fruit diameter, number of fruits $plant^{-1}$, fruit weight, fruit yield $plant^{-1}$, fruit yield $plot^{-1}$, ascorbic acid, chlorophyll content, capsaicin content and capsanthin content. Similar results were reported by Sreelathakumary and Rajamony (2004) for the traits fruit length, No. of fruits $plant^{-1}$ and Fruit yield $plant^{-1}$. In broad sense, high heritability of these traits indicated that large proportion of phenotypic variance was due to the genotypic variance and influence of environment is very less. Hence, selection can bring worthwhile improvement in these traits.

Heritability and genetic advance helps in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection. High heritability coupled with high genetic advance as % mean indicates existence of additive gene action which was observed in fruit length, fruit diameter, number of fruits $plant^{-1}$, fruit weight, fruit yield $plant^{-1}$, fruit yield $plot^{-1}$, ascorbic acid, chlorophyll content, capsaicin content and capsanthin content. Hence, direct selection could be effective for desired genetic improvement for these traits. For the traits fruit length, fruit diameter, capsanthin and capsaicin content Similar results were reported by Pandiyaraj et al. (2017). For the traits No. of fruits $plant^{-1}$ and fruit weight, the results are in conformity with Sran and Jindal (2019). High heritability along with high genetic advance reported for these traits provide good scope for further improvement in advance generation if subjected to mass progeny or family selection.

Moderate to high heritability coupled with high genetic advance as % of mean was exhibited by plant height and

Table 4: Estimates of heritability, genetic advance and genetic advance as percent of mean in chilli genotypes from pooled data

Sl. No.	Character	h^2	Genetic advance	Genetic advance as % of mean
1.	Plant height (cm)	53.80	17.75	28.29
2.	Plant spread (cm^2)	41.50	1341.08	36.52
3.	No. of primary branches $plant^{-1}$	27.10	0.46	10.97
4.	Days to first flowering	62.30	8.05	15.99
5.	Days to 50% flowering	53.30	6.99	12.43
6.	Days to first harvest	46.60	9.95	11.69
7.	Days to last harvest	29.40	7.71	5.23
8.	Fruit length (cm)	75.90	3.93	52.64
9.	Fruit diameter (cm)	69.30	0.46	36.83
10.	No. of fruits $plant^{-1}$	93.40	64.37	94.29
11.	Fruit weight (g)	94.70	4.42	97.20
12.	Fruit yield $plant^{-1}$ (kg)	88.90	0.31	112.99
13.	Fruit yield $plot^{-1}$ (kg)	89.40	4.42	112.63
14.	Ascorbic acid (mg $100\ g^{-1}$)	99.90	90.33	96.75
15.	Chlorophyll content (%)	77.90	0.42	22.18
16.	Capsaicin content (%)	94.70	0.33	75.12
17.	Capsanthin content (ASTA units)	99.80	105.57	43.97

plant spread which indicates that these traits are simply inherited in nature and controlled by few major genes or possessed additive gene effects. Hence, simple selection could be effective for improving this character.

Moderate genetic advance as % of mean with high or moderate heritability suggests the action of both additive and non-additive genes there by favorable influence of environment in the expression of the traits. The same was reported in case of days to first flowering, days to 50% flowering and days to first harvest. Moderate to low heritability coupled with low genetic advance as % of mean indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits, which was observed in case of number of primary branches per plant and days to last harvest. Hence, the breeder should adopt suitable breeding strategy to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programme.

4. CONCLUSION

Significant differences were observed among the 35 genotypes for all the characters indicating the presence of wide range of variability which helps to choose the potential genotype. Wide range of variability was observed for plant height, plant spread, fruit length, fruit diameter, number of fruits $plant^{-1}$, fruit weight, fruit yield $plant^{-1}$, fruit yield $plot^{-1}$, ascorbic acid, capsaicin and capsanthin content indicating the scope for selection of suitable initial breeding material from these genotypes for further improvement.

5. REFERENCES

Aparna, R., Singh, S.K., Vinay, S., Rakesh, P., 2014. Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research 38(2), 157–163.

Ashish, K., Anita, S., Akshay, C., Lalit, N., Rajeev, K.V., Mahesh, K.K., 2017. Variability and correlation study in tomato (*Solanum lycopersicum* L.). International Journal of Agriculture Sciences 9(29), 4391–4394.

Bahurupe, J.V., Sakhare, S.B., Kulwal, P.L., Akhare, A.A., Pawar, B.D., 2013. Genetic diversity analysis in chilli (*Capsicum annuum* L.) using RAPD markers. An International Quarterly Journal of Life Science 8(3), 915–918.

Burton, G.W., De vane, E.H., 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal 45, 478–481.

Cochran, W.G., Cox, G.M., 1957. Experimental designs (2nd edition), pp. 127-131. John Wiley and Sons, Inc., New York, N.Y.

Dias, G.B., Gomes, V.M., Moraes, T.M., Zottich, U.P., Rabelo, G.R., Carvalho, A.O., Moulin, M., Goncalves, L.S., Rodrigues, R., Da Cunha, M., 2013. Characterization of capsicum species using anatomical and molecular data. Genetics and Molecular Research 12(4), 6488–6501

Durust, N., Sumengen, D., Durust, Y., 1997. Ascorbic acid and element contents of foods of Trabzon (Turkey). Journal of Agricultural and Food Chemistry 45, 2085–2087.

El-Ghoraba, A.H., Javedb, Q., Anjumb, F.M., Hamedc, S.F., Shaabana, H.A., 2013. Pakistani bell pepper (*Capsicum annum* L.): chemical compositions and its antioxidant activity. International Journal of Food Properties 16(1), 18–32.

Farhad, M., Hasanuzzaman, M., Biswas, B.K., Ariifuzzaman, M., Islam, M.M., 2010. Genetic divergence in chilli (*Capsicum annuum* L.). Bangladesh Research Publications Journals 3(3), 1045–1051.

Hanson, C.H., Robinson, H.F., Comstock, R.E., 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. Agronomy Journal 8(4),

268–272.
Hasan, M.J., Kulsum, M.U., Ullah, M.Z., Hossain, M.M, Mahmud, E.M., 2014. Genetic diversity of some chilli (*Capsicum annuum* L.) genotypes. International Journal of Agricultural Research, Innovation and Technology 4(1), 32–35.
Isong, A., Balu. P.A., Ramakrishnan, P., 2017. Association and principal component analysis of yield and its components in cultivated cotton. Electronic Journal of Plant Breeding 8(3), 857–64.
Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in Soybean. Agronomy Journal 47(7) 314–318.
Khan, M.H., Rafii, M.Y., Ramlee, S.I., Jusoh, M., Mamun, A., 2020. Genetic variability, heritability, and clustering pattern exploration of bambara groundnut (*Vigna subterranea* L. Verdc) accessions for the perfection of yield and yield-related traits. Biomedical Research International Article ID 2195797.
Krishnamurthy, S.L., Madhavi Reddy, K., Mohan Rao, A., 2013. Genetic variation, path and correlation analysis in crosses among Indian and Taiwan presents in chilli. Vegetable Science 40(2), 210–213.
Lingaiah, N., Venkanna, V., Cheralu, C., 2019. Genetic vairability, heritability and genetic advance in rice (*Oryza sativa* L.). Frontiers in Crop Improvement 7(1), 72–73.
Lush, J.L., 1949. Heritability of quantitative characters in farm animals. Proceedings of the Eigth International Congress of Genetics. Hereditas 35(S1), 357–375.
Manjunathagowda, D.C., Anjanappa, M., 2021. Genetic variability studies for yield and yield contributing traits in onion (*Allium cepa* L.). Vegetos 34, 174–182.
Munshi, A.D., Behera, T.K., 2000. Genetic variability, heritability and genetic advance for some traits in chillies (*Capsicum annuum* L.). Vegetable Science 27, 39–41.
Pandiyaraj, P., Saraladevi, D., Juliet, H.S., Arindam, D., 2017. Genetic variability, heritability and genetic advance for quantitative and qualitative traits in chilli (*Capsicum annuum* L.). International Journal of Agriculture Science 9(14), 4081–4083.
Pidigam, S., Suchandranath, B.M., Srinivas, N., Narshimulu, G., Srivani, S.A., Hari, Y., Geetha, A., 2019. Assessment of genetic diversity in yardlong bean (*Vigna unguiculata* (L.) Walp subsp. *sesquipedalis* Verdc.) germplasm from India using RAPD markers. Genetic Resources and Crop Evolution 66, 1231–1242. https://doi.org/10.1007/s10722-019- 00782-w.
Pidigam, S., Thuraga, V., Munnam, S.B., Geetha, A., Gopal, K., Pandravada, S.R., Srinivas, N., Sudini, H.K., 2021. Genetic diversity, population structure and validation of SSR markers linked to *Sw-5* and *I-2* genes in tomato germplasm. Physiology and Molecular Biology of Plants 27, 1695–1710. https://doi.org/10.1007/s12298-021-01037-8.
Pradheep, K., Veeraragavathatham, D., 2006. Characterization of *Capsicum* spp. germplasm. Indian Journal of Plant Genetic Resources 19(2), 180–183.
Sabri, R.S., Rafii, M.Y., Ismail, M.R., Yusuff, O., Chukwu, S.C., Hasan, N.A., 2020. Assessment of agro-morphologic performance, genetic parameters and clustering pattern of newly developed blast resistant rice lines tested in four environments. Agronomy 10(8), 1098. doi: 10.3390/agronomy10081098.
Saidaiah, P., Pandravada, S.R., Sivaraj, N., Geetha, A., Lingaiah, N., 2021a. Understanding of yield stability in jack bean (*Canavalia ensiformis* L.) genotypes using AMMI and GGE bi-plot models. Legume Research. https://doi.org/10.18805/ LR-4548.
Saidaiah, P., Suchandranath, B.M., Srinivas, N., Geetha, A., Hari Kishan, S., Someswara Rao, P., Hari, Y., 2021b. Molecular characterization of Indian Dolichos bean (*Lablab purpureus* L. var. typicus Prain) accessions using RAPD markers. Indian Journal of Genetics and Plant Breeding 81(2), 322–326.
Saidaiah, P., Pandravada, S.R., Geetha, A., 2021c. *Per se* performance and variability in dwarf roselle germplasm for yield and yield attributing traits, 271–277. DOI: HTTPS://DOI.ORG/10.23910/1.2021.2203
Sandeep, Somanath, A., Mohan Kumar, H.D., 2013. Genetic variability, heritability and genetic advance for yield and its components in Byadgi Kaddichilli (*Capsicum annuum* L.) Accessions. Bioinfolet 10(1A), 50–53.
Sarma, R.N., Roy, A., 1995. Variation and character association in chilli (*Capsicum annuum* L.). Annals of Agricultural Research 16, 179–183.
Shah, A., Lal, S.D., Panth, C.C., 1986. Variability studies in chilli. Progressive Horticulture 18, 270–272.
Singh, D.V., Singh, A., 2011. Assessment of variability parameters and character association for quantitative traits in chilli (*Capsicum annuum* L.). Progressive Agriculture 11(1), 113–116.
Sivasubramanian, S., Menon, M., 1973. Heterosis and inbreeding depression in rice. Madras Agricultural Journal 60, 1139–1149.
Sran, T.S., Jindal, S.K., 2019. Genetic variability and character association analysis in chilli pepper (*Capsicum annuum* L.). Agricultural Research Journal 56(1), 24–32.
Sreelathakumary, I., Rajamony, L., 2004. Variability, heritability and genetic advance in chilli (*Capsicum annuum* L.). Journal of Tropical Agriculture 42(1-2), 35–37.
Vavilov, N.I., 1951. Origin, variation, immunity and breeding of cultivated plants. Chronoica Botanica 13, 4–364.