Genetic diversity analysis of transplanting responsiveness in Pigeonpea (*Cajanus cajan* (L))

* DHANDAPANI M[1], SATHYA P[1], GEETHANJALI S[2], SALINI A P[3], SANGEETHA M[4], NELSON NAVAMANIRAJ K[5], SHANMUGAM A[1] AND SUBRAHMANIYAN K[1]

[1]Tamil Nadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai, INDIA
[2]Centre for Plant Molecular Biology, Tamil Nadu Agricultural University, Coimbatore, INDIA
[3]Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, INDIA
[4]Regional Research Station, Tamil Nadu Agricultural University, Paiyur, INDIA
[5]Seed Centre, Tamil Nadu Agricultural University, Coimbatore, INDIA

Abstract: Principal component analysis, genetic variability studies were performed in pigeon pea germplasm lines to study the genotypic responses, characters associations and environmental interactions towards transplanting responsiveness for yield and yield attributing traits. Short duration (120-145 days) photo insensitive types did not show significant differences on seed yield and attributing traits. Medium duration types (above 145 days) showed moderate to poor responses. Even in long duration types, perennial vegetable types, vegetable types showed greater levels of adaptation followed by grain types. Yield attributing traits like plant height, number of branches, number of pods, and number of seeds were highly associated with seed yield under transplanting responsiveness.

Keywords: Transplanting, Genetic variability, Seedling vigour, G × E interactions

Received: June 24, 2022. Revised: January 25, 2023. Accepted: February 27, 2023. Published: April 3, 2023.

1. Introduction

Pigeonpea (*Cajanus cajan* (L) ssp typicus & flavus) is the important and sole source of vegetable protein for the entire Indian sub continent consisting of 36 provincial states without exceptions. Pigeon Pea dhal is rich in protein (20%), iron, calcium, phosphorus and carbohydrates. It serves as a cheaper source of important nutritional components viz., protein to the lower income group of the nation. It is part of daily diet in Indian households invariably across the geographical regions. Annual production is 3.5 million tonnes from an area of 4.0 million hectares with average productivity of 800 Kg/ ha. But annual requirements as per the consumption pattern of Indian populations both from urban and rural areas range from 4.5-6.0 million tonnes for the entire nation. To meet out the short falls in supply, India is importing larger quantities of pigeon pea grains from countries like Kenya, Malawi, Tanzania, Myanmar and Australia. Yield increase is static over the past several decades and it is always subjected to instabilities mainly due to rainfall patterns. Both deficit and excess rains affect the yield drastically. Poor source to sink ratio also causes yield imbalances (Shivangangavva et al., 2016) . Genetic gains through selection have been considerably very low, as the Genotype x Environment interactions play a major role and are always a complex phenomenon. Genetic diversity analysis has always been carried out for the yield and yield attributing traits in pigeon pea. Pigeonpea has richer sources of genetic resources throughout the nation. Seed yield is highly influenced by proportion of flowers converted into pods followed by seed filling which are again affected by poor source to sink ratio.

Imbalances in source to sink causes flower dropping, higher percentage of sterility and poor seed filling. Genetic diversity on flowering and seed setting revealed the complex G x E interactions regulating the component traits vis., flowers dropping, pollination, pod set, and seed filling. Pigeonpea poly bag transplanting is emerging as a reliable and high yielding technique and it was introduced in northern Karnataka by KVK, Bidar (SA Patil, 2002). Yield and yield attributing traits were increased drastically and seed yield 3000 Kg/ha recorded. Main reasons for phenomenal yield increase were due to initial seedling growth (25-45 days) supported under optimized conditions viz., continuous water supply, balanced nutrients supply, regulated temperature under shade net conditions which resulted in increased shoot and root growth responsible for early seedling vigour. Early seedling vigour contributes to the increased levels of yield and yield attributing traits which resulted in increased yields. But when it comes to yield responses only vegetable types and dual types with longer durations responded. Hence, it is assumed that responsiveness for transplanting ability is genetically controlled traits and genetic analysis should be performed for the understanding of traits contributing to the transplanting responsiveness. In this research study, seedling parameters viz., root length, shoot length, seedling vigour, and number of nodules were analysed by raising the genotypes in poly bags and diversity analysis was performed.

2. Materials and Methods

Sowing of seeds and raising poly bag nursery

Poly bags (6''x2'') were filled with pot mixture (red soil: compost: fine sand) in 1:1:1 ratio. Bottom of the covers were punctured with punching machine to have holes on both sides. Cylindrical shaped bags were arranged for each selected genotype and labeled. Poly bags were filled with water till saturation and allowed for complete wetting of pot mixtures. Middle of the surface of the soil in the bag was made a small hole using finger and two seeds were sown per bag. Hole was covered with soil and watered properly. The poly bags sown with seeds are covered with shade net and watered once in three days. Seeds germinated on 5-7 days after sowing. After 10 days of sowing, poly bags with two seedlings were thinned by removing one seedling and allowed only one seedling per bag. Seedlings were maintained in 50% shade net house for growth and development by regular watering and maintenance free from weeds. Seedlings were maintained till 25 days from germination and transplanted on 3rd leaf stage to main field.

Transplanting of seedlings

The main field was previously transplanted with finger millet variety, Paiyur2 and after the ear head harvest, the stubbles were incorporated. This is to provide nitrogen deficient conditions in soil for screening. 25 days old seedlings were used for transplanting. Field was ploughed twice to attain tilth conditions and after leveling, beds and channels were formed. Spacing of 150 x 90 cm was followed. A small pit was dug using spade to the depth of 15 cm and seedlings with pot mixtures intact with root were carefully removed from polybags by excisions with sharp blade and planted into the pit. Flood irrigation was done immediately at sufficient levels for each plot. Standard weeding, and plant protection measures were followed. No soil and foliar application of nutrients was done to ensure the deficient conditions in the soil to study the nutrients mobilization capabilities under transplanted conditions.

Experimental design and statistical analysis

Totally 120 genotypes with different duration group from grain and vegetables types were used in this study. 8 checks were used for taking the experiment using augmented design II (Table 1) Totally 8 blocks comprising twenty genotypes (12 lines + 8 checks) for each block raised. Randomisation was done accordingly. The yield and yield contributing traits were recorded in the all the blocks utilized for data analysis. The traits *viz.*,days to fifty percent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, root length, shoot length, number of nodules per plant, 100-seed weight and seed yield was recorded. The TNAUSTAT software (Manivannan, 2014) was used to analyse the variability.

3. Results and Discussion

Variability analysis

The effectiveness of selection depends on the existence of genetic variability within the population. Heritability estimates are used to determine the amount of genetic variation present in the population (Yadav et al., 2012). The choice of genetically diverse parents for hybridization is an important feature of crop improvement programme for getting desirable segregants (Rajamani et al., 2020; Anuradha et al., 2020). In other words, the knowledge of genetic variability for characters of economic importance and their heritability and genetic advance is of utmost importance in planning future breeding programmes (Singh *et al.,* 2007, Chandana et al., 2013). High heritability along with high genetic advance denotes the presence of additive gene action and selection will be effective for such characters (Sharma et al., 2018; Anuradha et al., 2019; Patil et al., 2019).

Phenotypic and genotypic coefficient of variation

The presence of variability in crop is important for genetic studies and consequently used for improvement and selection. Genetic variability is more reliable for selecting the successful breeding method, while phenotypic variation is used to estimate the environmental effect. Heritable portion of phenotypic variance is heritability. Heritability estimation coupled with genetic advance as per cent of mean was more useful in assessing the gain under selection than predicted heritability alone. The results are presented in Table 2, Fig 1 and Fig 2.

In this population the traits *viz.,* root length, number of nodules per plant, number of branches per plant, number of pods per plant and seed yield per plant recorded high phenotypic and genotypic coefficient of variation. Similar results were reported by Hemavathy *et al.* (2019), Vanniarajan *et al*. (2021) and Sharma *et al.* (2021). The remaining traits *viz.,* days to fifty per cent flowering, days to maturity, shoot length, plant height, number of seeds per pod and hundred seed weight recorded moderate PCV and GCV. Moderate heritability for these traits were already reported in similar studies (Pushpavalli *et al*., 2018; Ramesh et al., 2017). None of the traits recorded low phenotypic and genotypic variation. These results indicated the occurrence of wider variability in this population.

High heritability accompanied with high genetic advance as percent of mean was observed for the traits *viz.,* days to fifty per cent flowering, days to maturity, root length and plant height. Ranjani *et al.* (2018) and Hemavathy *et al.* (2019) reported the similar findings. The traits *viz.,* number of nodules per plant, number of branches per

plant and seed yield per plant recorded low heritability accompained with high genetic advance as percent of mean. Similar results were reported by Tiwari *et al.* (2015) and Mallesh *et al.* (2017). The traits had high heritability and genetic advance and low heritability and high genetic advance are appropriate for further selection due to the presence of additive gene action. Low heritability may be due to the environmental influence (Sreelakshmi et al., 2010; Rupika et al., 2014;).

4. Principal component analysis - Conclusions

The results of PCA were presented in Table 3 and Table 4. The total variation was divided into 10 principal components. The first five principal components showed eigen values more than one explaining 70 per cent of the total variation. The scree plot showing contribution of each principal component towards total variance is given in Fig 3. The traits *viz.,* days to fifty percent flowering (0.46), days to maturity (0.51), number of nodules per plant (0.31) and plant height (0.35) contributed highly to PC 1, whereas the trait number of nodules per plant (0.38) and number of seeds per pod (0.46) recorded higher contribution to PC 2. Root length (0.54) contributed higher contribution to PC 3, the trait days to fifty percent flowering (0.51) and days to maturity (0.41) contributed high to PC 4 and the seed yield per plant (0.76) recorded higher contribution to PC 5. Biplot depicts the fact that, the genotypes close to the origin are close to the average value for a particular trait. However, those away from the origin are outliers. The genotypes which are present in close proximity with each other in the biplot are less divergent, whereas those present in different quadrants are more divergent.

The loading plot represents the relationship of the quantitative trait with the principal components considered between the traits (Hartmann *et al.,* 2018; Hussain et al., 2021). The loading plot for first two principal components is given in Fig 4. The orientation of the vector with the principal component axis explains its contribution to the principal component. The traits *viz.,* days to fifty percent flowering, days to maturity and hundred seed weight are oriented with the axes of PC1, indicating their higher contribution to PC1 than PC2. The traits *viz.,* number of nodules per plant and number of seeds per pod were directed towards axes of PC2, hence contributed more to PC2 than PC1. Longer the vector in the loading plot, higher variability of the variables is explained by the two principal components. The shorter vectors are explained better in other dimensions. The quantitative traits *viz.,* days to fifty percent flowering, days to maturity, number of nodules per plant and number of seeds per pod, plant height and shoot length were contributed more to the variability of PC1 and PC2. The traits with smaller angles between them are positively correlated and those with opposite angles are said to have negative correlation. The traits which are at right angle to each other are negatively related. The traits in the same quadrant are closely related and distantly related with those in the different quadrant.

References

[1]. Anuradha, N. and Patro, T.S.S.K., 2019. Genetic variability, heritability and correlation in advanced red gram genotypes. *International Journal of Chemical Studies*, *7*(3), pp.2964-2966.

[2]. Anuradha, N., Patro, T.S.S.K., Triveni, U., Rao, P.J. and Rajkumar, S., 2020. Estimation of genetic variability in red gram advanced breeding lines. *Journal of*

Pharmacognosy and Phytochemistry, *9*(1), pp.1617-1619.

[3]. Chandana, K.C., Prasanthi, L., Sekhar, M.R. and Reddy, B.B., 2013. Studies on genetic diversity in redgram genotypes using rapd markers. *Electronic Journal of Plant Breeding*, *4*(3), pp.1219-1227.

[4]. Hartman, K., Krois, J. and Waske, B., 2018. E-Learning Project SOGA: Statistics and Geospatial Data Analysis. Department of Earth Sciences. *Correlation*.

[5]. Hemavathy, A.T., Bapu, J.R. and Priyadharshini, M., 2019. Genetic variability and character association in pigeonpea [Cajanus cajan (L.) Millsp.] core collection. *Indian Journal of Agricultural Research*, *53*(3), pp.362-365.

[6]. Hussain, M.E., Sharma, S., Joel, A.J., Ravikesavan, R., Senthil, N. and Senthil, A., 2021. Genetic variability of agronomic traits in extra-early maturing Introgression Lines (ILs) of pigeonpea [Cajanus cajan (L.)]. *Electronic Journal of Plant Breeding*, *12*(2), pp.507-514.

[7]. Mallesh, P., Nanda, H.C., Durgaraju, C.H., Sameer Kumar, C.V., Mohan, N. and Lee, J., 2017. Variability, Heritability and Genetic Advance for Quantitative Traits in Pigeonpea (Cajanus cajan (L.) Mill sp.). *International Journal of Pure & Applied Bioscience*, *5*(5), pp.25-28.

[8]. Manivannan, N., 2014. TNAUSTAT-Statistical package.

[9]. Patil, S.S., Patil, H.E., Jagtap, P.K. and Patel, S.R., 2019. Framing a pigeon pea improvement program through genetic analysis, character association and genetic diversity: A review. *IJCS*, *7*(4), pp.889-895.

[10]. Pushpavalli, S.N.C.V.L., Yamini, K.N., Kumar, G., Rani, C.S., Sudhakar, C., Saxena, R.K., Varshney, R.K. and Kumar, C.V., 2018. Genetic variability and correlation in pigeonpea genotypes. *Electronic Journal of Plant Breeding*, *9*(1), pp.343-349.

[11]. Rajamani, S., Saxena, R., Ramana, M.V., Chapara, R., Sreekanth, M. and Varshney, R.K., 2020. Identification of genetic diversity in pigeonpea [Cajanus cajan (L) Mill sp.] varieties through molecular markers. *International Journal of Chemical Studies*, *8*(1), pp.2754-2761.

[12]. Ramesh, M., 2017. Genetic diversity and characterization of pigeonpea germplasm. *J. Genet, Genomics, Plant Breed*, *1*(1), pp.32-35.

[13]. Rupika, K. and Bapu, J.K., 2014. Assessment of genetic diversity in pigeonpea germplasm collection using morphological characters. *Electronic Journal of Plant Breeding*, *5*(4), pp.781-785.

[14]. Sharma, P., Singh, I. and Singh, S., 2018. Studies on genetic diversity and inheritance of fertility restoration in pigeonpea [Cajanus cajan (L) Millsp.]. *Journal of Food Legumes*, *31*(3), pp.135-138.

[15]. Sharma, P., Singh, I., Khosla, G., Singh, G., Singh, S., Dhaliwal, S.K. and Singh, S., 2021. Variability and association studies for yield and yield related traits in pigeonpea [Cajanus cajan (L.) Millsp.]. *Legume*

Research-An International Journal, *1*, p.6.

[16]. Shivagangavva, P.D. and Reddy, B.S., 2016. Factors determining supply of pulses in India. *Indian Journal of Economics and Development*, *4*(6), pp.1-6.

[17]. Sreelakshmi, C., Shivani, D. and Kumar, C.V.S., 2010. Genetic divergence in redgram (Cajanus cajan L.). *Journal of Research ANGRAU*, *38*(3/4), pp.76-79.

[18]. Tiwari, A., Sharma, R.N., Nanda, H.C. and Sarawgi, A.K., 2015. Genetic variability analysis for plant selection in pigeonpea [Cajanus cajan (L.) MILLSP.]. *Annals of Plant and Soil Research*, p.524.

[19]. Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S.M., Ramya, K.R. and Monisha, K., 2021. Assessment of Genetic Variability and Traits Association in Pigeonpea [Cajanus cajan (L.) Millsp.] Germplasm. *Legume Research-An International Journal*, *1*, p.8.

[20]. Yadav, K., Yadav, S.K., Yadav, A., Pandey, V.P. and Dwivedi, U.N., 2012. Genetic diversity of Pigeonpea (Cajanus cajan (L.) Millsp.) cultivars and its wild relatives using randomly amplified polymorphic DNA (RAPD) markers. *American Journal of Plant Sciences*, *3*(3), pp.322-330.

Table 1. List of accessions used in this study

S. No	Accession name	S. No	Accession name	S. No	Accession name
1	88	27	IC15048	53	IC9922
2	3R16	28	IC215535	54	ICP10266
3	AC601	29	IC2454474	55	ICP10788
4	AC611	30	IC33716	56	ICP11292
5	AC9060	31	IC523438	57	ICP11743
6	AF284	32	IC525409	58	ICP11873
7	AS36	33	IC525426	59	ICP12168
8	AS46	34	IC525427	60	ICP12212
9	Bennur Local	35	IC525429	61	ICP122822
10	BRG4	36	IC525431	62	ICP13576
11	BRG4	37	IC525437	63	ICP13918
12	BRG4	38	IC525449	64	ICP14041
13	BRG4	39	IC525452	65	ICP2185
14	BRG4	40	IC525456	66	ICP2455325
15	BRG4	41	IC525458	67	ICP245-535
16	BRG4	42	IC525460	68	ICP4765
17	BSMR	43	IC525462	69	ICP52505
18	C11	44	IC52547	70	ICP525409
19	CO-8	45	IC525473	71	ICP5254611
20	EPRS120	46	IC525475	72	ICP73799

21	GL-11-39	47	IC525477	73	ICP7674
22	GRG-131	48	IC525514	74	ICP7731
23	Guliyal red	49	IC5255413	75	ICP9162
24	IC12196	50	IC5255507	76	ICP92047
25	IC12325	51	IC526430	77	ICP9260
26	IC14304	52	IC73999	78	ICP9419
S. No	**Accession name**	**S. No**	**Accession name**	**S. No**	**Accession name**
79	ICP9662	93	PYRRG-16-02	107	PYRRG-16-16
80	ICP9922	94	PYRRG-16-03	108	PYRRG-16-17
81	ICPL-14-1588039	95	PYRRG-16-04	109	PYRRGV-16-01
82	ICPL90047	96	PYRRG-16-05	110	PYRRGV-16-02
83	ICPL900747	97	PYRRG-16-06	111	PYRRGV-16-03
84	ICPR2363	98	PYRRG-16-07	112	PYRRGV-16-04
85	ICPR2431	99	PYRRG-16-08	113	PYRRGV-16-05
86	ICPR2447	100	PYRRG-16-09	114	PYRRGV-16-06
87	ICPR525585	101	PYRRG-16-10	115	RVKT-261
88	Katti beja	102	PYRRG-16-11	116	T5
89	PP2183	103	PYRRG-16-12	117	TS-3
90	PPP2-183	104	PYRRG-16-13	118	TT401
91	PUSA992	105	PYRRG-16-14		
92	PYRRG-16-01	106	PYRRG-16-15		
S. No	**Check name**	**S. No**	**Check name**	**S. No**	**Check name**
1	CO 6	4	BRG 2	7	PYR 1614
2	CRG 10-01	5	LRG 41	8	PYR 1615
3	BRG 1	6	TTB7		

Table 2. Variability parameters of yield and yield attributes in redgram

Characters	PCV	GCV	h^2	GAM
DFF	17.52	17.48	99.62	35.95
DM	14.08	13.04	85.75	24.88
SL	18.14	10.47	33.32	12.45
RL	35.37	32.14	82.60	60.18
NNPP	98.66	39.10	15.70	31.92
PH	16.27	13.31	66.92	22.43
NBPP	44.80	22.82	25.93	23.94
NP	74.47	40.37	29.38	45.08
NSPP	12.40	10.13	66.67	17.03
HSW	16.84	12.68	56.67	19.66
SYPP	81.05	37.40	21.29	35.55

Table 3. Eigen values and contribution of 11 quantitative characters towards divergence.

Principal component	Eigenvalue λ	Variance percent towards divergence	Cumulative percent variance towards divergence
PC 1	2.84	25.8	25.8
PC 2	1.38	12.5	38.3
PC 3	1.28	11.6	49.9
PC 4	1.16	10.6	60.5
PC 5	1.07	9.7	70.2
PC 6	0.82	7.4	77.6
PC 7	0.76	6.9	84.6
PC 8	0.65	5.9	90.5
PC 9	0.52	4.7	95.2
PC 10	0.47	4.3	99.5

PC - Principal component.

Table 4: Per cent contribution of 11 quantitative characters towards principal components.

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10	PC 11
DFF	0.46	0.00	0.17	0.51	-0.01	0.12	-0.12	-0.06	-0.04	-0.03	0.68
DM	0.51	0.01	0.14	0.41	0.03	0.10	-0.11	-0.01	-0.07	0.03	-0.73
SL	0.27	0.28	-0.08	-0.35	0.26	-0.18	-0.65	-0.17	0.40	0.05	0.03
RL	0.19	0.27	0.54	-0.16	0.19	-0.23	0.42	0.43	0.31	-0.20	0.02
NNPP	0.31	0.38	0.04	-0.45	-0.05	0.16	0.04	0.05	-0.71	0.15	0.06
PH	0.35	-0.22	0.03	-0.25	-0.34	-0.09	0.39	-0.40	0.29	0.49	0.03
NBPP	0.28	-0.42	-0.01	-0.34	-0.37	0.16	-0.12	0.06	0.02	-0.67	-0.01
NP	0.21	-0.44	-0.21	0.01	0.21	-0.71	-0.04	0.28	-0.29	0.11	0.05
NSPP	0.12	0.46	-0.49	0.16	-0.11	-0.34	0.32	-0.32	0.00	-0.42	-0.02
HSW	0.22	0.05	-0.61	-0.01	0.04	0.37	0.14	0.57	0.27	0.18	0.04
SYPP	0.11	-0.26	-0.08	-0.13	0.76	0.29	0.29	-0.35	-0.05	-0.16	0.01

PC - Principal component

Fig 1. Phenotypic and genotypic coefficient of variation of given population.

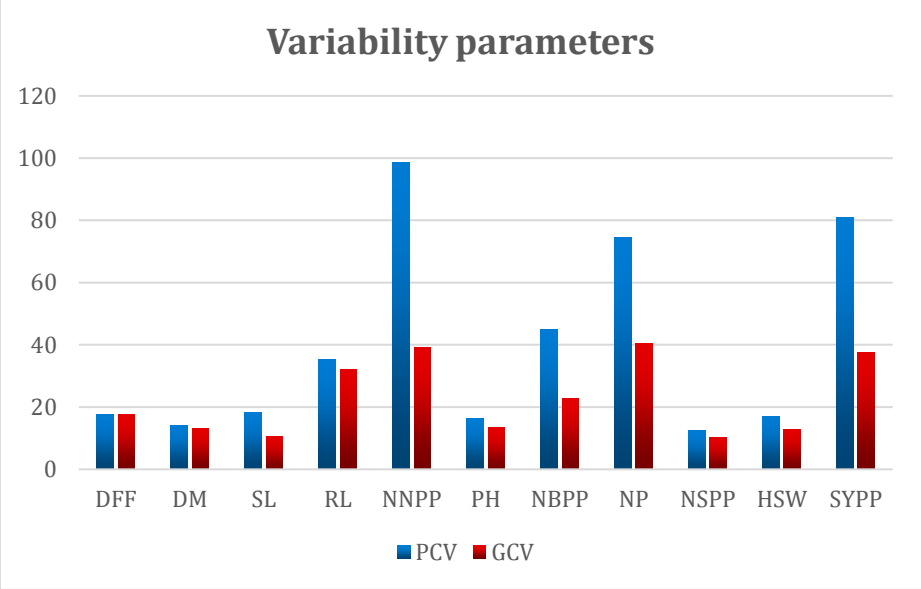

Fig 2. Heritability and genetic advance as percent ofmean of given population.

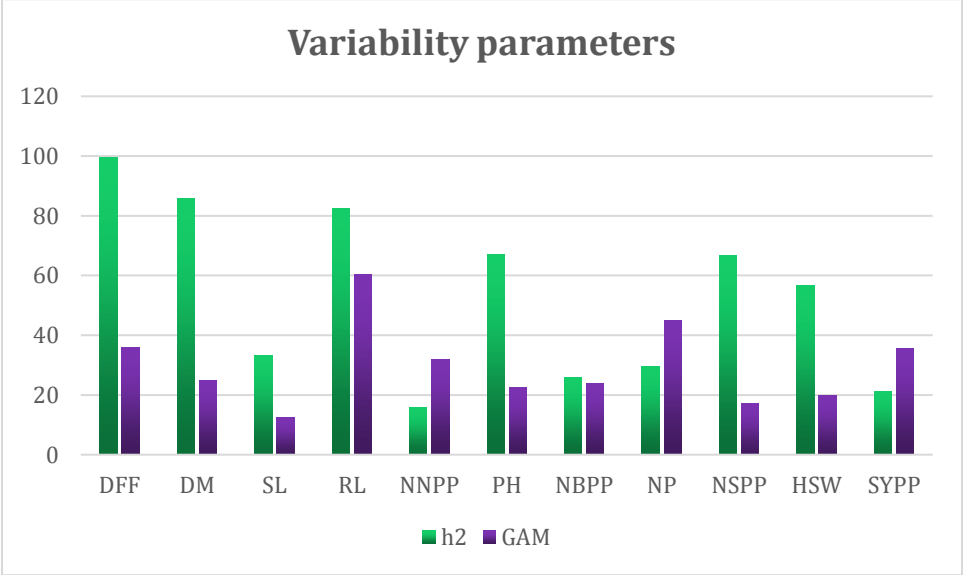

Fig 3. Scree plot showing contribution of various principal components towards divergence.

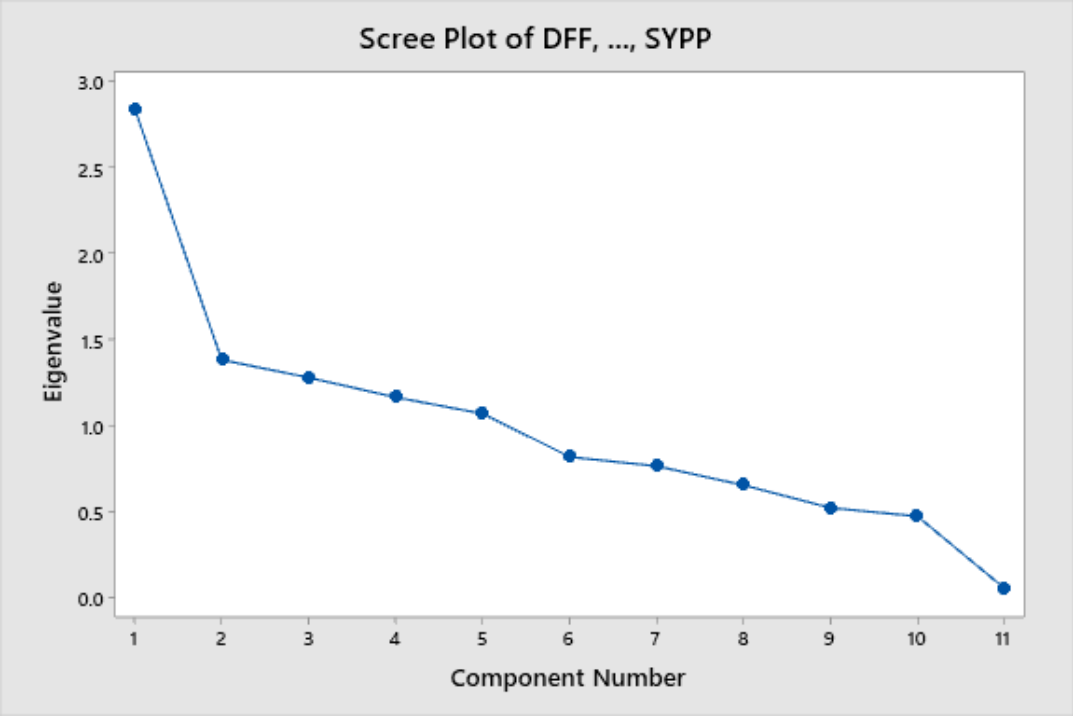

Fig 4. Loading plot of 11 quantitative characters based on PC 1 and PC 2.