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GENETIC EVALUATION OF TWENTY DIVERSE GENOTYPES OF OKRA (*ABELMOSCHUS ESCULENTUS* L. MOENCH) IN HILLY REGIONS OF NORTH INDIA

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ABSTRACT

An experiment was conducted during the Monsoon season of 2020 to evaluate twenty genotypes of okra for agro-morphological traits collected from Krishi Vigyan Kendra (KVK) for yield and its contributing characters under field conditions at Jawali, District Kangra, Himachal Pradesh. High significance of analysis of variation showed the existence of large variability among the genotypes. The experiment was laid out in randomized block design with three replications and 10 plants/row. Highest GCV and PCV was found for 100 seed weight followed by days to first flowering node, yield per plant. While the lowest was observed for fruit girth, plant height and fruit length which determines the negligible influence of environment on the different traits. High broad sense heritability was observed for days to first flowering node and genetic advance was recorded highest for yield per plant. Average fruit weight, fruit length and fruit girth were in positive and significant relationship with yield per plant. Principal component analysis revealed the first four major principal components having Eigen value >1 which contributed 82.693% of the total variation. Cluster analysis suggested that the hybridization of cluster I with cluster II would be beneficial for developing varieties in different parts of India because of the variation present between both the clusters.

Keywords: Analysis of variance, Cluster analysis, Heritability, GCV, PCV, Principal component analysis.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench), also called as Ladies finger is the only significant vegetable crop of Malvaceae family. It was originated from Ehiopia and Sudan, North-eastern African countries. The plant is grown in tropical, sub-tropical and warm temperate regions all over the world (National Research Council, 2008). Okra can be grown on wide range of soil but it shows best result when grown in well-drained soil (Akinyele *et al*., 2007). Okra can be differentiated on into types, conventional and non-conventional types.

Okra is a good source of proteins, carbohydrates, vitamins, calcium, potassium, enzymes and total minerals. The chemical composition of okra are 67.5% a-cellulose, 15.4% hemicellulose, 7.1% lignin, 3.4% pectin matter, 3.9% fatty and waxy matter and 2.7% aqueous extract (Kumar *et al*., 2017). Rather than being rich in proteins, vitamins, minerals, high iodine content makes it helpful in playing a vital role in controlling goitre disease (Sindhumole *et al*., 2014).

India bags first position in the area and production of okra with an annual production of 61.26 lakh tonnes from an area of 5.14 lakh hectares with the productivity of 11.91 tonnes per hectare (FAOSTAT, 2018). Because of less availability of location specific varieties tolerant/resistant to various pests and diseases viz., fruit and shoot borer and YVMV resulted in loss of productivity and yield of okra (Reddy *et al*., 2012).

The information regarding concentration of variation present among the available breeding materials guides us to decides the characters for better selection of parents for further use in the breeding programme. Evaluation of genotypes was done to assess their genetic variability for yield and its contributing traits. Selection of genetically diverse parents is important for better results(Ranga *et al*., 2019; Joshi *et al*., 2004). After realizing the importance of high yielding genotypes, the present investigation was conducted to evaluate the genetic variability and diversity of agro- morphological traits of okra during the monsoon season of North India.

MATERIAL AND METHODS

Location and Climatic Conditions

The experiment was conducted in the local fields of a town Jawali, District Kangra of Himachal Pradesh during the monsoon season (May-August 2020). The geographic coordinates of the location are 32.15 N 76.01 E with an elevation of 625m (2051 ft.). The climate of the area represents sub-temperate condition.

Experimental material and agronomic traits studied

Twenty okra genotypes were grown in three replications with a spacing of 60 cm X 45 cm in randomized block

design (RBD). Table 1 represents the detail of genotypes used in the experiment. The germplasm were collected from Krishi Vigyan Kendra (KVK), Kangra, Himachal Pradesh, India and were evaluated at Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India. Five plants were selected randomly for observation. Various observations were recorded for different traits *viz.,* PH: plant height (cm), FL: fruit length (cm), FG: fruit girth (cm), FP: number of fruits per plant, FN: days to first flowering node,SF: number of seeds per fruit, DF: days to 50% flowering,SW: 100 seed weight (g), FW: fruit weight and YP: yield per plant (g).

Statistical Analysis

The mean values of different genotypes per replication were subjected for analysis of variance (ANOVA) in accordance with Panse and Sukhatme (1954) to check the presence of statistically significant differences among the genotypes for all the studied traits. Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation were calculated with the help of the formula given by Burton (1952) whereas genetic advance and heritability were calculated by using the formula given by Lush (1937) and Allard (1960). OP-STAT (Sheoran *et al*., 1998) and PAST (Hammer *et al.,* 2001) helped in calculating the genotypic correlation coefficient and Principal Component Analysis.Cluster analysis was performed with the help of PAST (Hammer *et al.,* 2001).

RESULT AND DISCUSSION

Mean Performance and Variability Parameters

The analysis of variance (ANOVA) was estimated and all the twenty genotypes were found highly significant for all the studied character which is represented in Table 2. High variability among the genotypes showed the presence of high significant differences among the genotypes used as genetic material. Sindhumole *et al*., (2014) also showed the same results as given above.

PCV was found greater than its respective GCV for all the studied characters, plant height, fruit length, fruit girth, number of fruits per plant, days to first flowering node, number of seeds per fruit, days to 50% flowering, 100 seed weight, fruit weight and yield per plant. Most of the traits showed high variability (>60) which proved that the studied traits would be beneficial for transferring their characters to their progenies and hence there would be greater chances for executing selection on the basis of the studied traits. Sood *et al*., (2017) and Azam *et al.,* (2013) also reported high magnitude of heritability and genetic advance.The greater magnitude of PCV and GCV were also observed in previous studies (Shanthakumar G and Salimath PM 2010 and Prakash *et al*., 2011). High estimates of heritability coupled with high genetic advance (>20%) were estimated in all the traits. This explains the pre-dominance of additive gene effects for the characters, thus we can consider the characters which showed high heritability for selection. Heritability is a good parameter for transferring the characters from parents to off-springs (Falconer, D.S. 1981). High broad sense heritability helps the breeder to indentify the appropriate characters for selection which would result in the selection of superior genotypes based on the phenotypic expression of the quantitative traits (Johnson *et al*., 1995).

Genotypic Correlation Coefficient Analysis

The correlation coefficient analysis was presented in Table 4 and graph depicting the correlation among all the twenty genotypes was presented in Figure 3. Fruit length showed highest positive correlation and significant behaviour for yield per plant (0.712**). Fruit girth was highly significant and in positive correlation with yield per plant (0.696**), average fruit weight (0.668**)and fruit length (0.514*). Days to first flowering node showed positive correlation and high significance only for days to 50% flowering (0.943**). Number of fruits per plant was non-significant but in positive correlation with fruit girth (0.177^{NS}), fruit length (0.197^{NS}), fruit weight (0.221^{NS}) and yield per plant (0.301^{NS}) respectively. Results for the remaining characters was showed in the Table 4. The overall effect of the segregating genes is known as correlation (Falconer, 1981). It is important to understand the inter-relationship among the characters to accumulate a combination of yield contributing characters in a single genotype (Jagan *et al*., 2013). Thus, it is necessary to associate such traits when rational improvement is done through selection. Correlation studies give focus on stability of various traits for indirect selection as selection of only one trait effects the correlated response of other traits (Neyhart *et al*., 2019).

Principal Component Analysis

Principal Component Analysis provides the information and importance of the largest contributing character to the total variation at each axis of differentiation. Table 5 showed the contribution of all the traits. Among all principal components, first four components showed Eigen value >1 which contributed to 82.693 of the total variation. In PC I, maximum variation was given by average fruit weight followed by fruit length, yield per plant, fruit girth and days to first flowering node respectively. In PC II, number of fruits per plant showed maximum variation which was followed by yield per plant, plant height, fruit girth respectively. In PC III, maximum variation was caused by plant height and days to 50% flowering. Seed weight showed maximum variation in PC IV.Thus, the use of these four traits would help in the identification and characterization of the genotypes of okra. Many workers have reported the high contribution of fruit length, 100 seed weight, number of seeds per plant and yield per plant

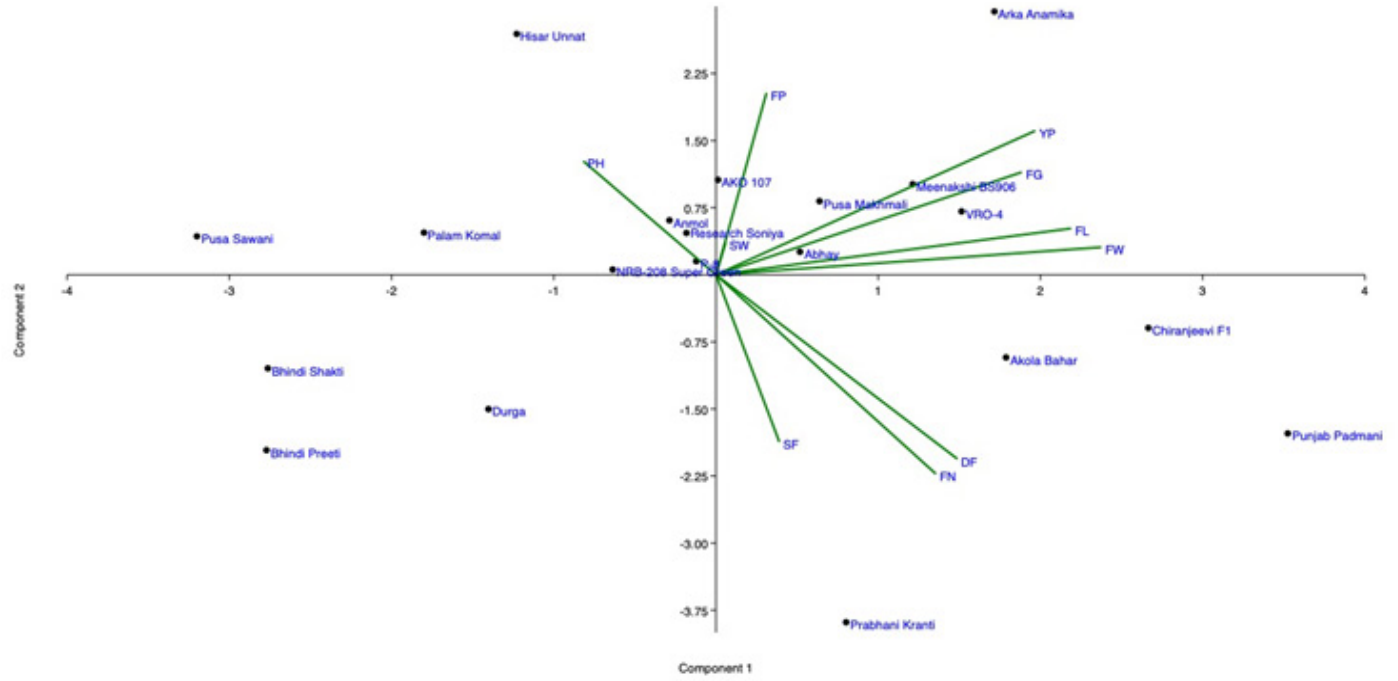

Fig. 1. Biplot between PCI and PC II showing contribution of various traits responsible for variability in okra.

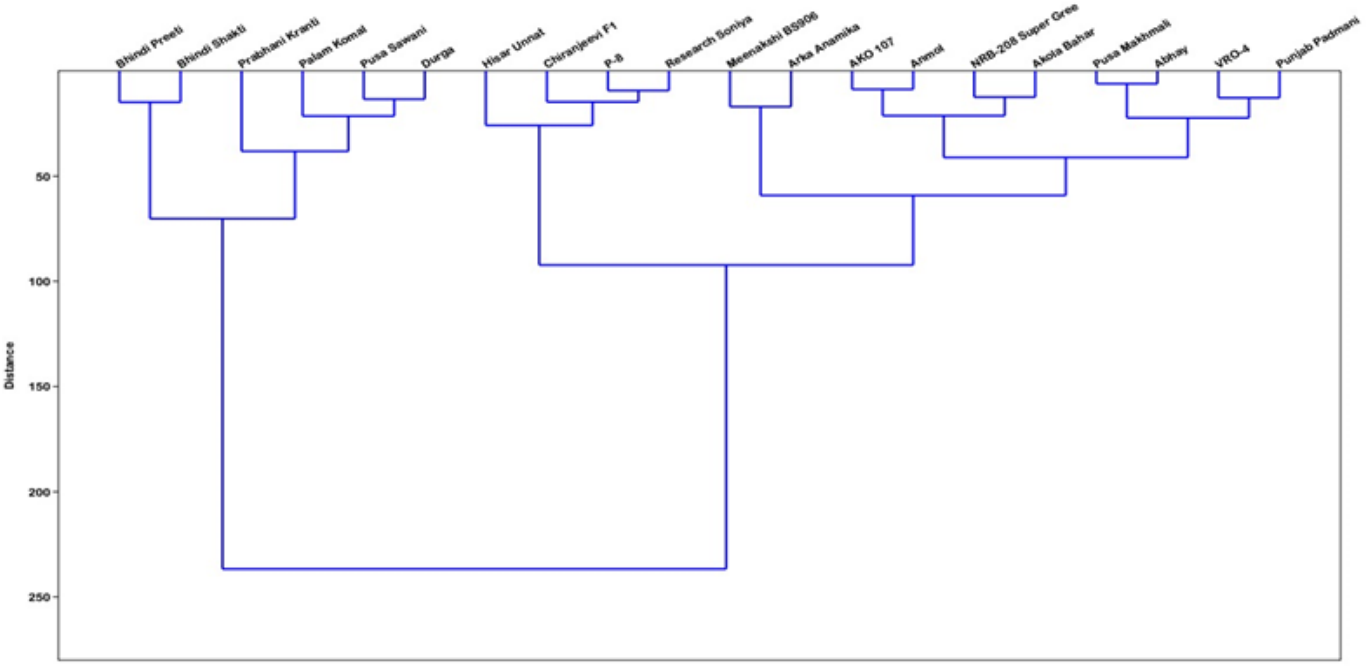

Fig. 2. Dendrogram showing genetic relationship among fifteen okra genotypes based on agro-morphological traits using Ward's method.

Table 1. List of okra genotypes used for evaluation

Sr. No.	Germplasm	Sr. No.	Germplasm
1	HisarUnnat	11	Meenakshi BS 906
2	Palam Komal	12	P-8
3	PusaSawani	13	Research Soniya
4	AKO 107	14	BhindiPreeti 21
5	PusaMakhmali	15	Chiranjeevi F1
6	Anmol	16	Bhindi Shakti
7	NRB-208 Super Green Research	17	Akola Bahar
8	PrabhaniKranti	18	VRO-4
9	Abhay	19	Punjab Padmani
10	ArkaAnamika	20	Durga

Table 2: Analysis of variance (ANOVA) for various characters of okra genotypes

Character	MSS of okra gentotypes		
	Replication (df=2)	Treatment (df=19)	Error df=38)
FL	1.713	15.596	3.174
FG	0.165	0.101	0.047
FN	0.090	74.114	0.114
FP	22.315	9.882	3.224
PH	292.015	84.966	18.077
DF	17.589	91.954	30.889
SW	0.411	22.488	0.563
SF	156.299	194.335	62.665
FW	39.158	83.719	44.752
YP	5.653	8182.582	27.194

Table 3: Estimates of variability parameters for various characters of okra genotypes.

Characters	Mean	Range	h^2	GCV	PCV	GA	Ga% of mean
FL	17.24	13.17-22.00	56.61	11.81	15.69	3.15	18.30
FG	2.01	1.70-2.50	27.42	6.61	12.62	0.14	7.13
FN	13.26	6.30-23.90	99.54	37.47	37.56	10.21	77.01
FP	12.49	7.80-32.50	40.77	14.18	22.20	1.96	18.65
PH	42.92	31.00-54.80	55.22	10.99	14.79	7.23	16.83
DF	47.07	38.40-62.00	39.72	9.58	15.21	5.86	12.44
SW	6.79	3.36-14.99	92.85	38.68	40.14	5.37	76.78
SF	58.82	46.83-82.20	41.19	11.26	17.55	8.76	14.89
FW	23.90	15.67-32.67	22.50	15.08	31.80	3.52	14.74
YP	160.44	48.33-225.17	99.01	32.50	32.66	106.87	66.61

Table 4: Genotypic correlation coefficient studies in okra genotypes.

	FL	FG	FN	FP	PH	DF	SW	SF	FW	YP
FL	1.000	**0.514***	0.309^{NS}	0.197^{NS}	-0.126^{NS}	0.413^{NS}	0.004^{NS}	-0.063^{NS}	0.670	0.712
FG		1.000	0.114^{NS}	0.177^{NS}	0.106^{NS}	0.173^{NS}	0.036^{NS}	-0.106^{NS}	**0.668****	**0.696****
FN			1.000	-0.370^{NS}	-0.261^{NS}	**0.943****	-0.045^{NS}	0.271^{NS}	0.352^{NS}	-0.079^{NS}
FP				1.000	-0.049^{NS}	-0.376^{NS}	-0.053^{NS}	-0.331^{NS}	0.221^{NS}	0.301^{NS}
PH					1.000	-0.241^{NS}	-0.106^{NS}	-0.597^{NS}	-0.290^{NS}	-0.094^{NS}
DF						1.000	-0.021^{NS}	0.185^{NS}	0.368^{NS}	-0.022^{NS}
SW							1.000	-0.181^{NS}	-0.076^{NS}	0.170^{NS}
SP								1.000	0.189^{NS}	-0.108^{NS}
FW									1.000	**0.735****
YP										1.000

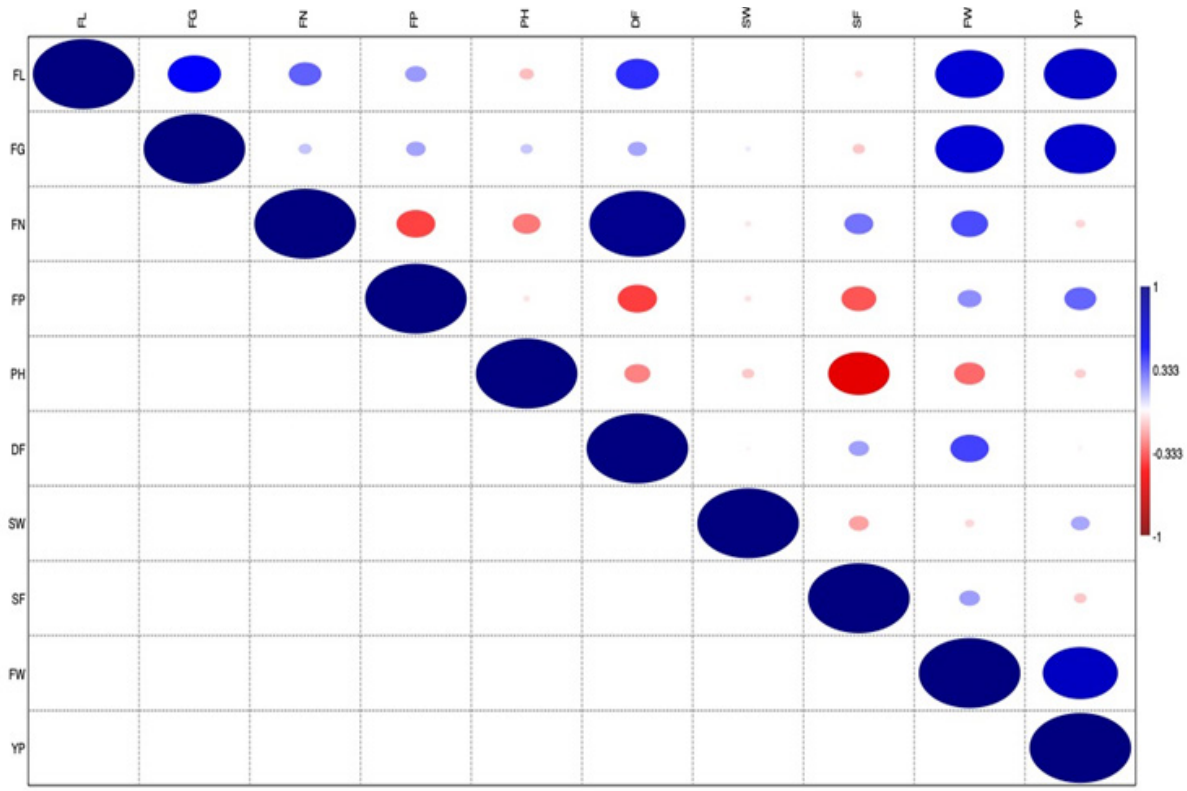

Fig. 3. Graph depicting correlation coefficient among twenty genotypes

Table 5: Principal component analysis among all the studied traits in okra

	PC I	PC II	PC III	PC IV	PC V	PC VI	PC VII	PC VIII	PC IX	PC X	Roots(Eigen Value)
FL	**0.458**	0.108	0.089	-0.021	-0.167	**0.657**	0.296	-0.329	-0.255	-0.224	3.345
FG	**0.394**	**0.240**	0.142	-0.059	**0.378**	**-0.556**	-0.037	**-0.543**	-0.069	-0.100	2.472
FN	**0.284**	**-0.466**	0.274	-0.010	-0.232	-0.195	0.101	0.144	**0.462**	**-0.540**	1.366
FP	0.065	**0.425**	-0.269	-0.142	**-0.665**	-0.322	**0.365**	-0.024	0.159	0.134	1.083
PH	-0.171	**0.266**	**0.626**	-0.239	0.264	0.017	**0.532**	0.282	0.068	0.116	0.774
DF	0.311	**-0.431**	**0.329**	0.016	-0.240	-0.067	-0.039	-0.099	-0.081	**0.727**	0.439
SW	0.013	0.076	0.069	**0.939**	0.005	-0.123	0.277	0.083	-0.097	-0.008	0.208
SF	0.082	**-0.391**	**-0.539**	-0.094	**0.389**	-0.017	**0.596**	-0.037	0.112	0.145	0.199
FW	**0.497**	0.065	-0.136	-0.114	0.064	-0.173	-0.065	**0.667**	**-0.479**	-0.071	0.078
YP	**0.412**	**0.337**	-0.100	0.125	0.225	0.261	-0.217	0.183	**0.655**	0.250	0.036
Total % Variation	**33.48**	**24.723**	**13.663**	**10.827**	7.743	4.389	2.078	1.985	0.784	0.359	

(Ahiakpa *et al*., 2013, Amoatey *et al*., 2015 and Denton *et al*., 2011). There are no instructions as how to explain the significance of a coefficient, i.e., Eigen vector (Duzyaman E. 2005 and Sokal *et al*., 1973). A bi-plot between PCI and PC II showed contribution of various traits which are responsible for variation in okra (Fig. 1).

Cluster Analysis

In cluster analysis, no prior information about the cluster membership for any object is given (Abonyi, J. Feil,B. 2007 and Sajad-Bokaei *et al*., 2008).Cluster analysis is used to differentiate genotypes into groups based on far or nearness among each other (Sokal, R.R. and Sneath, P.H.A. 1973). Twenty okra genotypes were taken into consideration using yield contributing characters under the study. The genotypes were grouped into two clusters and represented through a dendrogram using Ward's method (Ward, 1963). Cluster I comprised of six genotypes while the remaining fourteen came under cluster II (Fig. 2) The genotypes which were represented far away from each other showed more variation among themselves and therefore these genotypes are considered better for further use in crop improvement.

CONCLUSION

Twenty genotypes of Okra (*Abelmoschus esculentus* L. Moench) were collected from Krishi Vigyan Kendra (KVK) Kangra of Himachal Pradesh. The experiment

was conducted to estimate the genetic variability among all the genotypes. Highest GCV and PCV was calculated for 100 seed weight. Days to first flowering node showed highest broad sense heritability whereas it was lowest for fruit weight. The highest genetic advance as per cent mean was maximum for days to first flowering node. Yield per plant showed positive and significant correlation with fruit weight and fruit girth. Principal Component Analysis revealed that first four characters fruit length, fruit girth, days to first flowering node and number of fruits per plant contributed 80% to the total variation. BhindiPreeti and Punjab Padmani showed the highest variation among all the genotypes and can be further used for crop improvement programmes.

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CONFLICT OF INTEREST

All the authors declares that they do not have any conflict of interest and agree on all the parameters.

ABBREVIATIONS

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation.

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