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Assessment of genetic variability of cucumber (*Cucumis sativus* L.) gene pool of Tamil Nadu through principal component analysis

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Abstract
Thirty cucumber genotypes collected across Tamil Nadu state were subjected to genetic variance and Principle Component Analysis. Wide variability was observed for the characters vine length (132-191 cm), fruit weight (114-242 g) and number of fruits per plant (4-15 nos.). In the PCA, the total variations were resolved with 14 axis and the first three component axis explained 75 percent variability. PC1 showed 55.55 per cent variability with Eigen value of 7.77 and PC2 and PC3 had Eigen value of 1.38 and 1.19 and exhibited 9.88 and 8.57% of total variation respectively. The traits marketable fruit yield per plant (Loading:0.319) number of fruits per plant (0.296), number of primary branches per plant (0.275), fruit weight, and ascorbic acid (0.285) had manifested high positive loadings. Selection and/or choosing the parents for hybridization based on variability in the aforesaid traits in cucumber will be rewarding for increasing yield. The local cultivars collected from Amaravathi, Aipatti, Orathanadu, Koradacherry, Vennamuthupatti and Periyakollapatti have contributed much for the variance of the traits studied.

Keywords: Cucumber (*Cucumis sativus* L.), PCA, variance, trait associations, high yield

Introduction
Cucumber (*Cucumis sativ*us L. 2n = 2x = 14) is the fourth most important vegetable crop after tomato, cabbage and onion in Asia (Tatlioglu *et al.* 1993) [14]. It is grown for its tender fruits, which are consumed either raw as salad, cooked as vegetable or as pickled in its immature stage besides utilisation in cosmetics and food industry because of its soothing, cleansing and softening properties (Wang *et al.* 2007) [15]. Although the crop is native to India, it remained unexploited as far as its genetic potential is concerned and so far only 10 varieties and hybrids have been released for commercial cultivation till 2015 (Singh *et al.* 2015) [12]. In Tamil Nadu the area under cucumber is progressing and it could be seen as an alternative and remunerative crop in the rice fallow system.

Cucumber is being cultivated in different parts of Tamil Nadu as local collections and so far the yield enhancement through genetic improvement has not been attempted extensively. The genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population and the knowledge on association of traits contributing to maximum variability.

Principal Component Analysis (PCA) helps to identify the most relevant characters, explaining maximum proportion of the genetic variation to the final yield. Moreover, PCA also helps the breeder in the genetic improvement of those traits that have low heritability, especially in early generations (Ahmadizadeh and Felenji, 2011) [1]. Principle component analysis (PCA) helps in identifying the most relevant characters that can be used as descriptors by explaining as much of total variation in the original set of variables as possible with as few components as possible and reducing the dimension of the problem. Therefore, an attempt has been made in the present investigation to access and analyze the extent of genetic diversity in the cucumber collections from Tamil Nadu through principle component analyses for yield improvement in cucumber.

Materials and Methods
The present study was carried out during summer 2017 at ICAR - Krishi Vigyan Kendra, Needamangalam, Tiruvarur district. It is located at 10.77º North latitude and 79.41º East longitude, representing Cauvery Delta Zone of Tamil Nadu, Experimental materials comprised

of 30 genotypes of cucumber acquired from the indigenous collections of local farmers from various regions of Tamil Nadu (Table 1).

Table 1: Details of cucumber genotypes used in the study.

S. No.	Genotypes	Source	District
1	G-1	Peramangalam Local	Perambalur
2	G-2	Uppiliyapuram Local	Perambalur
3	G-3	Karattampatti Local	Perambalur
4	G-4	Kuruvikarankulam Local	Perambalur
5	G-5	Musiri Local	Tiruchirappalli
6	G-6	Pattukottai Local	Thanjavur
7	G-7	Thirupovanam Local	Thanjavur
8	G-8	Kattur Local	Thanjavur
9	G-9	PonnavarayankottaiLoal	Thanjavur
10	G-10	Amaravathi Local	Thanjavur
11	G-11	Thillaiyambur Local	Thanjavur
12	G-12	Udaiyalur Local	Thanjavur
13	G-13	Orathanadu Local	Thanjavur
14	G-14	Iniyanur Local	Tiruchirappalli
15	G-15	Pirattiyur Local	Tiruchirappalli
16	G-16	Kalachery Local	Tiruvarur
17	G-17	Melamaravakadu Local	Tiruvarur
18	G-18	Koradachery Local	Tiruvarur
19	G-19	Kodavasal Local	Tiruvarur
20	G-20	Namanasamuthiram Local	Pudukottai
21	G-21	Aipatti Local	Pudhukottai
22	G-22	Vennamuthupatti Local	Pudhukottai
23	G-23	Vilavayal Local	Pudhukottai
24	G-24	Gandharvakottai Local	Pudhukottai
25	G-25	Paravai Local	Nagapattinam
26	G-26	Periyakollapatti Local	Virudhunagar
27	G-27	Pondi Local	Nagapattinam
28	G-28	Rasipuram Local	Erode
29	G-29	Sathyamangalam Local	Erode
30	G-30	Kallakurichi Local	Villupuram

The experiment was laid in Randomized Block Design (RBD) with two replications. All the genotypes were sown in 8m x 3m sized beds consisting of pits (1x1x1 ft) and 10 plants were maintained for each replication. The crops were grown with standard package of practices.

Observations were taken at five randomly selected plants at appropriate phenophases on 14 different characters namely Vine length (cm), Days to male flower anthesis, Days to female flower anthesis, Number of primary branches, Days to first harvest, Fruit length (cm), Fruit weight (kg), Flesh thickness (cm), Fruit diameter (cm), Number of fruits per plant, Marketable fruit yield per plant (kg), Total soluble solids (°Brix), Ascorbic acid (mg/100g) and Total chlorophyll content (g/100g) with procedure of A.O.A.C. (1984) [2]. The mean over five plants in each replication of each character were subjected to Principle Component Analysis using the software STAR Programme. The phenotypic and genotypic coefficient of variation for all the characters calculated using the formula of Burton (1952) [3].

Results and Discussion

Genetic Variability

Significant variance among the genotypes for all the characters as evident from table 2 manifests the presence of sufficient variability among the genotypes under study. The range values in yield attributing traits *viz*., fruit weight (114.1g – 241.8g), number of fruits per plant (3.65 – 14.80) was wider than the quality traits namely total soluble solids and ascorbic acids (Table 3.) which indicates that yield could be improved through pedigree breeding by selecting diversified parents. Such wide variations with respect to various horticultural characters were also reported earlier by Kumar *et al.* (2008) [8], Hanchinamani *et al.* (2008) [5], Yogesh *et al.* (2009) [16] and Hossain *et al.* (2010) [6] in cucumber. The PCV was higher than the GCV for almost all the characters studied implying that expression of traits observed in the study can be altered by GxE interaction. The genotypic coefficient of variation ranged from 6.12 (Days to first harvest) to 41.95 (Marketable fruit yield per plant) and the next maximum variation is attributed by number of fruits per plant. This reflects greater genetic variability among the genotypes for yield attributing characters for making further improvement by selection. Low GCV value was observed in vine length, days to first male flower anthesis, days to first female flower anthesis and days to first harvest shows the existence of narrow variability among the genotypes. Similar results were observed by Ahirwar *et al.*, (2018) [4], Shah *et al*., (2018) [11], Tamang *et al.*, (2018) [13].

Principle Component Analysis usually be deployed to standardize the variables when the variables are measured in different units and the PCA can be estimated from correlation or covariance matrix. In this study, the first three component axis out of fourteen have contributed for 74 percent of total variation with the eigen value more than one. The factors with Eigen values less than 1 were ignored by following "Guttamans lower bound Principle" (Kaiser, 1958) [7]. Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between Eigen values and principal component numbers. PC1 showed 55.55 per cent variability with Eigen value of 7.77 which then declined gradually. Semi curve line obtained after seven PC tended to become straight and showed upto PC10 in the graph (Fig 1.) leaving balance four PCs flat which got very meager Eigen values, PC2 and PC3 had eigen value of 1.38 and 1.19 and exhibited 9.88 and 8.57% of total variation respectively. Pal *et al.* (2018) [10] found eight PCs more than 0.5 Eigen values and showed 92.961% total variability in cucumber and PC1 showed 42.61 percentage (Table 4).

Table 2: Analysis of variance for different characters in cucumber genotypes.

Source of variation	Df	Mean sum of squares													
		VL (cm)	DFMFA	DFFFA	NPB	DFH	FL (cm)	FW (gm.)	FT (cm)	FD (cm)	NFP	TSS (°brix)	AA (mg/100g)	TC (mg/100g)	MYPP (Kg.)
Replication	1	0.91	72.16	44.20	1.93	45.44	46.99	0.008	0.08	15.68	2.41	0.008	0.03	0.001	0.02
Treatment	29	334.44**	21.24**	21.83**	2.36**	25.83**	21.47**	2314.27**	0.10**	0.94*	15.40**	0.77**	0.66**	0.13**	1.01**
Error	29	43.60	5.13	5.10	0.45	6.53	3.49	154.08	0.02	0.41	1.66	0.07	0.13	0.01	0.05

Table 3: Estimation of coefficient of variation and genetic parameter in cucumber.

S. No	Characters	General Mean	Range	Coefficient of variation		
				GCV	PCV	ECV
1.	Vine length (cm)	173.55	131.95 -191.05	6.95	7.92	3.81
2.	Days to first male flower anthesis	36.39	29.80 -40.35	7.80	9.98	6.23
3.	Days to first female flower anthesis	43.66	35.90 -47.65	6.62	8.40	5.17
4.	Number of primary branches	5.249	3.30 – 7.05	18.64	22.64	12.85
5.	Days to first harvest	50.72	43.75 – 56.25	6.12	7.93	5.04
6.	Fruit length (cm)	20.53	14.40 – 25.45	14.60	17.21	9.10
7.	Fruit weight (gm)	187.81	114.10 – 241.80	17.50	18.71	6.61
8.	Flesh thickness (cm)	1.53	1.03 – 2.04	13.23	16.76	10.29
9.	Fruit Diameter (cm)	5.06	3.92 – 6.12	10.15	16.24	12.68
10.	Number of fruits per plant	9.24	3.65 – 14.80	28.34	31.60	13.97
11.	Total soluble solids (^{0}Brix)	2.76	1.49 -3.72	21.48	23.63	9.86
12.	Ascorbic acid (g/100g)	5.37	4.26 – 6.44	9.56	11.78	6.89
13.	Total chlorophyll content (g/100g)	1.80	1.36 – 2.23	13.81	14.95	5.74
14.	Marketable fruit yield per plant (kg)	1.65	0.715 -3.11	41.95	44.25	14.07

Table 4: Eigen value and contribution of the principal component axes towards total genetic variation in cucumber germplasm

Principal component	Eigen value	Variability (%)	Cumulative variability
PC1	7.777	55.550	55.550
PC2	1.382	9.880	65.430
PC3	1.199	8.570	73.990
PC4	0.805	5.750	79.740
PC5	0.703	5.030	84.770
PC6	0.576	4.120	88.890
PC7	0.547	3.910	92.800
PC8	0.374	2.670	95.470
PC9	0.266	1.900	97.370
PC10	0.182	1.300	98.680
PC11	0.110	0.790	99.470
PC12	0.042	0.300	99.770
PC13	0.028	0.200	99.970
PC14	0.004	0.030	100.00

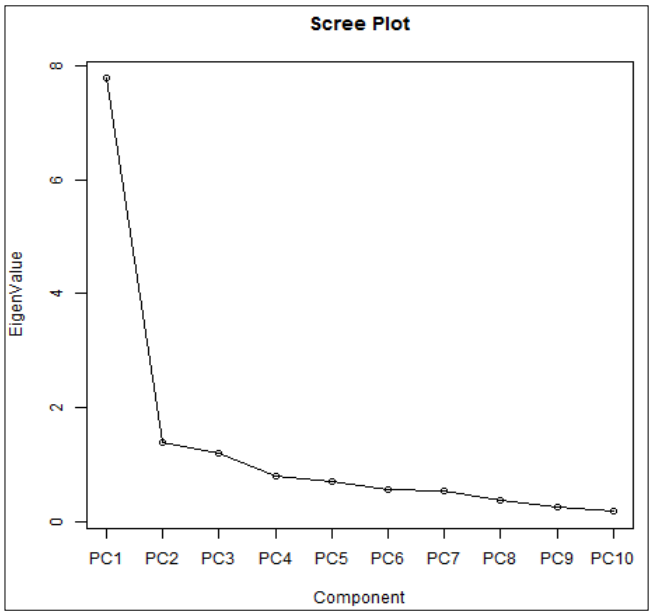

Fig 1: Scree plot of principal component analysis of cucumber germplasm between eigen value and principal components.

Rotated component matrix revealed positive contribution of the traits *viz*., marketable fruit yield per plant (Loading:0.319), number of fruits per plant (0.296), number of primary branches per plant (0.275), fruit weight (0.236), and ascorbic acid (0.285) for 55.5 percent of the total variability of the Principle Component1 (Table 5.). Hence, these traits were considered as important in separating the genotypes due to their high loadings.Therefore, while conducting selection and/or choosing the parents for hybridization in cucumber for increasing yield, a breeder has to give greater attention on these characters. The traits like days to first male flower anthesis, days to first female flower anthesis and days to first harvest showed negative contribution for component 2, the trait total soluble solids (0.580) contributed much for the 9.8 per cent variability. In PC2, negative contribution attributed to most of the traits like vine length, fruit weight, marketable fruit yield per plant, number of fruits per plant, fruit length, days to first male flower anthesis, days to first female anthesis and days to first harvest. Whereas, PC3 showed positive contribution to eight traits and negative contribution to six traits. Similar results have been reported by Zhang and cui (1993) [17] and Kumar *et al.* (2014) [9] in cucumber. It is also observed that the local cultivars collected from Amaravathi, Aipatti, Orathanadu, Koradacherry, Vennamuthupatti and Periyakollapatti have contributed much for the variance of the traits studied. The aforesaid genotypes can be utilized as parents for hybridization for better segregation.

Table 5: Contribution of different traits of cucumber towards the major principal components.

Traits	PC1	PC2	PC3
Vine length (cm)	0.203	-0.460	0.165
Days to first male flower anthesis	-0.331	-0168	-0.059
Days to first female flower anthesis	-0.316	-0.100	-0.064
Number of primary branches per plant	0.275	0.034	0.123
Days to first fruit harvest	-0.321	-0.152	-0.090
Fruit length (cm)	0.231	-0.190	0.017
Fruit weight (gm)	0.236	-0.341	-0.430
Flesh thickness (cm)	0.136	0.059	-0.644
Fruit Diameter (cm)	0.179	0.179	-0.503
Number of fruits per plant	0.296	-0.282	0.241
Total soluble solids (^{0}Brix)	0.220	0.580	0.147
Ascorbic acid (g/100g)	0.285	0.137	0.070
Total chlorophyll content (g/100g)	0.297	0.135	0.032
Marketable fruit yield per plant (kg)	0.319	-0.286	0.018

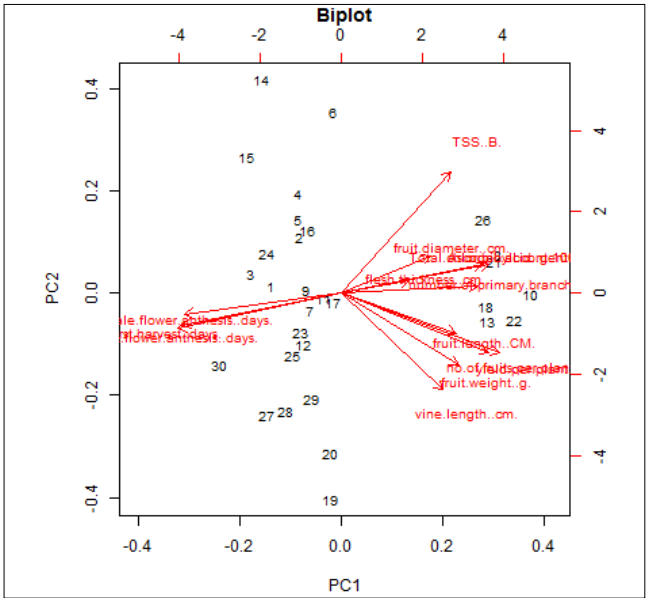

Fig 2: Distribution of germplasm accessions across first two components based on PCA

Conclusion

Wide variance among the cucumber genotypes studied is attributed by vine length, fruit weight and number of fruits per plant. The traits with positive high loadings *viz*., marketable fruit yield per plant number of fruits per plant, number of primary branches per plant, fruit weight, and ascorbic acid may be utilized for selection for higher yield and quality. The local cultivars from Amaravathi, Aipatti, Orathanadu, Koradacherry, Vennamuthupatti and Periyakollapatti could be utilized as parents for hybridization to exploit heterosis in cucumber

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