Diversity in cucumber; An evaluation of diverse cucumber genotypes employing clustering and principal component analysis

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Abstract

The current experiment was carried out to identify the variability source structure in eleven phenotypic variables of 70 diverse cucumber genotypes. The findings showed that the first three-component axes provided a bigger share of the total variability, with eigenvalues of more than one depicting a cumulative variability of 73.75%. Cluster VII and cluster XII had the greatest intercluster distance showing a significant genetic diversity between the two clusters followed by clusters VII and cluster VIII. Principal Component Analysis (PCA) verified that all the investigated traits contributed to the observed genetic divergence, suggesting that these traits may be amenable to phenotypic selection. The number of fruits per vine contributed the most to genetic divergence, according to the relative contribution of characteristics to divergence. Therefore, breeders must place a special emphasis on these qualities when undertaking selection or selecting parents for hybridization.

Keywords: principal component analysis, cluster analysis, yield attributes, and cucumber (*Cucumis sativus* L.)

Introduction

The cucumber (*Cucumis sativus* L.) is the second most extensively cultivated cucurbit vegetable after the watermelon, and it ranks fourth on the list of Asian economic vegetables after tomato, cabbage, and onion, as per Tatlioglu(1997). It is prized for its delicate fruits, which are eaten fresh as salads or pickled, as well as mature fruits upon cooking. Moreover, it is among the most promising crops for protected farming to meet domestic and international needs year-round. Although the vegetable is indigenous to India, its genetic potential has been untapped. As a result, there is a substantial disparity between the projected and true yield of this crop. This gap can be filled by breeding high-yielding varieties/hybrids.

Genetic advancement is an ongoing process wherein efficacy is determined by the existence of variability on the breeders' part. The cucumber, as an Indian subcontinent crop, exhibits tremendous diversity in terms of yield and quality attributes. Even so, the crop's true genetic potential is not being completely utilized, probably due to a lack of adequate evaluation and classification for various aspects such as yield. Although association studies aid in determining the positive or negative impacts of independent factors on the dependent factor (yield), their link becomes more intricate as the number of independent variables increases. Likewise, two or more variables may exhibit correlation if they are linked by a mutual attribute. Since yield is a heterogeneous and dependent variable, correlation studies only offer finite insight into how to enhance it. In this case, Principal Component Analysis (PCA) assists in identifying the most relevant features, which explain the greatest proportion of the genetic variance to the final yield. Additionally, PCA aids breeders in the genetic improvement of traits with low heritability, particularly in early generations Ahmadizadeh and Felenji; Golparvar*et al.*(2011, 2006). Hierarchical cluster analysis is a popular method for forming clusters and revealing similarities and differences among genotype pairs, wherein agglomerative hierarchical clustering was formed by grouping cases into bigger and bigger clusters until all cases were members of a single cluster. Principal component analysis (PCA) is a data reduction technique for quantitative data that converts a set of multi-correlated variables into an uncorrelated variable Kalagare*et al.* (2022). As a result, the current experiment was designed to assess the yield reliance on different yield-attributed traits in cucumbers using Principal Component Analysis and to assess the genetic diversity by cluster analysis.

Materials and methods

The current study was conducted at the College Orchard, Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore from February 2021 to May 2022, A total of 70 cucumber genotypes (Table 6) were raised in a Randomized Block Design (RBD) with two replications using a standard set of procedures. For data collection, five plants were chosen at random and tagged in each replication of the treatment. Data on growth, flowering behavior, physical parameters of fruit, and yield were collected (pooled data furnished in Table 5). The level of genetic variation was calculated using the Principal Component (PC) analysis method. For this purpose, PC was used to derive Eigenvalues, which were then utilized to rank the axes and characters according to their discriminatory ability Pradhan *et al.*(2011). The unweighted pair group method with arithmetic averages (UPGMA) was used to calculate the Euclidean distance between the genotypes, and XLSTAT Version 2014.5.0 software was used to perform PCA (Principal Component Analysis) and cluster analysis for standardized mean data.

Results and Discussion

Using quantitative traits, Principal Component Analysis (PCA) based on standardized phenotypic means was performed to determine which of them accounted for the most diversity while also being the most discriminant among genotypes. For all the traits examined, we found substantial variations within genotypes. The statistics reported in Table 1 (Scree plot between component number and eigenvalues shown in Fig.1) clearly show that the first six principal components (PC) accounted for around 93.97% of total variability present among the 70 evaluated cucumber genotypes. However, the first three of these six PC had eigenvalues of one or greater, suggesting a total variance of 73.75 percent. PC1 had an eigenvalue of 5.4355 and accounted for 49.41 percent of the total variance, while PC2 and PC3 had eigenvalues of 1.6765 and 1.0006 as well as accounted for 15.24 percent and 9.09 percent of the total variance, respectively. The analysis considered PC1, PC2, and PC3 because their eigenvalues were greater than one. The factor loading of PC analysis revealed that PC1 accounted for the highest variability for most of the traits, including days to first male flower, days to first female flower, days to first fruit harvest, fruit length, and fruit girth, while PC2 apprehended other traits such as vine length, node number for first male flower and node number for first female flower, and PC3 recorded the trait average fruit weight and

yield per vine (Table 2). PCA factor loading analysis revealed that the largest variability accounted for by PC1 was strongly associated with most yield-attributing variables. PC2 demonstrated the highest factor loading for vine length, node number for the first male flower, and node number for the first female flower. Since PC3 caught the most variation for average fruit weight and fruit yield per vine, the genotypes lying under this component can be selected for crop improvement for the aforementioned traits. PCA findings are typically presented as a biplot, where the axes refer to the new coordinate system (Fig. 2). The orientation of the arrow indicates the greatest amount of change, and the length may be related to the changing rate. Acutevector angles between traits or the principal component axis and trait indicate a positive correlation among these traits, whereas obtuse angles ($>90^0$) establish a negative association and right angles ($=90^0$) show no association at all Govindaraj *et al.*,(2020). The loading of various variables based on the first two principal components (Fig. 2) uncovered that node number for the first male flower, node number for the first female flower, and days to first fruit harvest contributed a greater proportion of the total variability, whereas fruits per vine and average fruit weight had the least impact. *Kumar et al.* (2015)observed similar findings for cucumbers. As a result, when conducting selection and/or identifying the parents for hybrid development in cucumber to increase yield and ameliorate quality, a breeder must pay special attention to these attributes. Kumar *et al.* (2015)and Ahirwar *et al.*,(2017) have reported identical results in cucumber.

Seventy genotypes were clustered into twelve groups. Cluster II contained the most genotypes (forty-three), followed by cluster I with (twelve) genotypes, cluster VIII with (four) genotypes, and cluster VI with (three) genotypes. The remaining clusters III, IV, V, VII, IX, X, XI, and XII which had only one genotype, indicated that these genotypes are completely distinct from the other accessions used in this study. The clustering pattern showed that the materials were prevalent with a certain amount of variability.

The intracluster distance was found to be lower than the inter-cluster distance (Table 3). Cluster I had the greatest intra-cluster distance, followed by clusters IX, VII, and cluster II, while intra-cluster distance was observed as zero for clusters III, IV, V, VI, VII, X, XI, and cluster XII, which had only one genotype. Cluster VII and cluster XII had the greatest intercluster distance showing a significant genetic diversity between the two clusters followed by clusters VII and cluster VIII, cluster VII and cluster IX, and cluster VII and cluster XII. Cluster VIII and cluster IX had the smallest intercluster distance showing a close relationship between the accessions examined. followed by cluster III and cluster IV.

Table 4 depicts the cluster mean value of seventy cucumber genotypes. Cluster IV and Cluster XI had the highest cluster mean value for average fruit weight and yield per vine for monoecious and gynoecious cucumber genotypes. Cluster III and Cluster X had the highest mean value for fruits per vine for monoecious and gynoecious cucumber genotypes. The cluster with the highest mean value for fruit length among monoecious cucumber genotypes was Cluster VII, followed by Cluster III, and the cluster with the highest mean value for the gynoecious line was Cluster XII. Cluster VI had the highest mean value for fruit girth for monoecious cucumber genotypes, followed by cluster III, while cluster XII had the highest mean value for the gynoecious cucumber line. This indicates that accessions in clusters III, IV, VII, IX, X, and XII have the genetic potential to contribute more effectively to cucumber genotype yield maximization. This conclusion is in agreement with the findings of Hasan *et al.*(2015).

Table 5 and Fig 3 show the relative contribution of characteristics to divergence. Among the independent traits studied, the number of fruits per vine (14.135%) contributed the most to genetic divergence, followed by node number for the first male flower (10.51%) and node number for the first female flower (9.90%). Days to first fruit harvest (4.25%), followed by days taken for the first female flower (4.96%), contributed the least to genetic divergence. The findings reported here are consistent with previous research on cucumbers conducted by Ahirwar (20147); Hasan(2015); and Zhang (1993)

CONCLUSION:

According to the current study's Agglomerative Hierarchical Analysis, Clusters VII and XII are genetically distinct from one another, highlighting the significance of these genotypes for subsequent breeding programs that will employ heterosis through hybridization and selection. Clusters III, IV, XI, and XII were discovered to have one or more features that were superior. The production of superior segregants in advanced generations with high yield potential and improved quality can therefore be suggested using a multiple crossing program containing features from these clusters. The attributes with the highest levels of variation identified by PC3 were average fruit weight and fruit yield per vine; it is possible to select genotypes from this component to enhance crops for these traits.

AUTHORS' CONTRIBUTION

Perception of research (RT and VR); Experimental design (RT and VR); Contribution of experimental materials (RT and VR); Field/lab experiment execution and data acquisition (RT and VR); Data analysis and interpretation (RT and VR); Manuscript preparation (RT and VR).

DECLARATION

The authors declare that they have no conflicts of interest.

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Table 1: Eigenvalues and estimated percentages of variability that the principal component analysis accounts for

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalue	5.4355	1.6765	1.0006	0.9400	0.8276	0.4568	0.3055	0.2603	0.0722	0.0183	0.0066
Variability (%)	49.4139	15.2409	9.0961	8.5458	7.5238	4.1529	2.7772	2.3661	0.6561	0.1667	0.0604
Cumulative %	49.4139	64.6548	73.7509	82.2967	89.8205	93.9734	96.7506	99.1167	99.7728	99.9396	100.0000

Table 2: Factor loading of three important principal components of cucumber genotypes for yield and yield-attributing traits

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11
VL	-0.8334	0.0717	0.1265	-0.1204	0.1504	-0.1811	0.3919	-0.2461	-0.0148	-0.0003	-0.0005
NMF	-0.1673	0.8375	0.2971	-0.0505	-0.0046	0.3557	0.1561	0.1644	0.0417	0.0006	-0.0023
NFF	0.0960	0.8613	0.1558	0.1345	0.1547	-0.3400	-0.2321	-0.1130	-0.0176	0.0001	0.0019
DMF	0.8809	0.0242	0.0483	-0.3617	0.2468	0.0012	0.0465	0.0543	-0.1315	-0.0833	-0.0060
DFF	0.9207	0.0422	0.0110	-0.3268	0.1534	0.0020	0.0511	0.0111	-0.0809	0.1034	0.0110
DFH	0.8768	-0.0324	-0.0379	-0.3572	0.2156	-0.0781	0.0131	-0.0538	0.2129	-0.0112	-0.0057
FL	0.2466	-0.3583	0.4561	0.4954	0.5907	0.0914	-0.0015	0.0087	0.0091	0.0059	0.0010
FG	0.3888	-0.2357	0.7207	-0.0640	-0.4475	-0.2377	0.0452	0.1041	0.0103	-0.0010	-0.0005
FPV	-0.8822	-0.0687	-0.0568	-0.1771	0.2491	-0.2095	-0.0179	0.2710	-0.0001	0.0204	-0.0476
AFW	-0.7046	-0.1604	0.3636	-0.4184	0.0160	0.2482	-0.2461	-0.2180	-0.0146	0.0062	-0.0189
YPV	-0.9081	-0.1009	0.0725	-0.2893	0.1967	-0.0736	-0.0761	0.1484	0.0183	-0.0100	0.0619

Table 3: Crop yield and yield-attributing attributes in cucumber genotypes, estimated using the D^2 technique, with intra-cluster (diagonal bolded) and inter-cluster (non-diagonal) distances presented.

Clusters	Cluster1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12
Cluster 1	**29.85**	25.62	52.68	67.60	43.74	60.11	79.11	155.15	138.34	64.78	160.19	152.45
Cluster 2		**25.21**	38.06	54.78	50.83	38.51	79.29	133.22	116.70	42.66	139.75	130.98
Cluster 3			**0**	20.41	71.56	26.05	96.87	106.57	90.51	45.41	113.37	103.30
Cluster 4				**0**	81.74	36.80	105.77	97.06	81.54	56.30	104.70	92.173
Cluster 5					**0**	74.05	43.82	166.09	151.64	88.70	178.41	156.90
Cluster 6						**0**	97.60	100.08	83.85	35.64	108.75	96.85
Cluster 7							**0**	176.84	165.68	111.42	194.91	164.69
Cluster 8								**24.10**	19.90	102.74	36.04	27.71
Cluster 9									**25.46**	85.69	32.96	34.75
Cluster 10										**0**	105.57	106.91
Cluster 11											**0**	57.70
Cluster 12												**0**

Table 4: Cluster means of cucumber genotypes and proportional contribution of characteristics to overall yield and yield-attributing trait divergence by D^2 approach

Class	VL	NMF	NFF	DMF	DFF	DFH	FL	FG	FPV	AFW	YPV
Cluster 1	123.98	3.65	4.79	53.43	56.50	62.69	17.97	11.08	5.67	133.74	0.75
Cluster 2	141.84	4.35	5.93	43.04	46.64	53.15	18.86	11.34	6.25	139.93	0.86
Cluster 3	169.48	3.67	8.50	53.17	56.83	61.00	21.85	18.92	7.17	158.44	1.17
Cluster 4	183.69	3.50	8.17	58.17	60.17	69.00	19.10	10.28	6.00	164.01	1.01
Cluster 5	141.15	7.17	9.67	56.50	58.17	65.50	11.27	7.62	6.67	94.95	0.65
Cluster 6	173.91	7.83	8.83	38.83	45.67	50.67	8.68	20.95	4.00	154.36	0.62
Cluster 7	156.50	5.33	8.50	48.83	50.83	59.00	35.92	5.74	7.67	64.73	0.49
Cluster 8	253.65	1.78	2.67	28.44	30.33	41.61	18.50	9.93	16.83	206.98	3.49
Cluster 9	235.78	5.54	4.83	31.67	34.00	42.00	14.54	7.44	13.79	205.37	2.86
Cluster 10	158.66	2.33	5.50	31.50	33.33	39.50	14.29	7.03	19.17	168.64	3.25
Cluster 11	238.54	11.50	8.50	31.17	33.17	38.17	15.97	6.81	17.50	236.94	4.12
Cluster 12	263.16	6.50	11.50	34.50	38.50	44.50	17.27	8.64	10.83	186.38	1.97
Percent contribution	7.76	10.51	9.90	5.50	4.96	4.25	6.08	8.22	14.13	6.65	22.03

VL: Vine length, NMF: Node for first male flower, NFF: Node for first female flower, DMF: Days to first male flower, DFF: Days to first female flower, DFH: Days taken for first fruit harvest, FL: Fruit length, FG: Fruit girth, FPV: Number of fruits per vine, AFW: Average fruit weight YPV: Yield per vine

Table 5: Pooled mean performance of cucumber genotypes for growth, flowering, and yield characters.

Sl.no	No. of Genotype (70)	VL (cm)	NMF	NFF	DMF	DFF	DFFH	FL	FG	FPV	AFW (g)	YPV (g)
Max		238.8317	11.5	11.555	59.7517	61.4617	70.47	37.3217	22.165	19.7067	241.6283	4350.6899
Min		93.2517	1.33	2.00	27.1933	28.3983	34.1533	9.4783	6.2083	4.3333	69.66	558.6517
Mean		152.5305	4.3844	5.8939	45.3647	48.3405	55.0837	19.8263	12.2013	8.1026	150.4593	1290.1395
C.V.		6.5699	4.6347	5.5575	4.8737	4.5727	2.7679	3.2224	12.4270	14.9549	4.1138	16.2082
S.E.		4.0911	0.0830	0.1337	0.9026	0.9024	0.6224	0.2608	0.6190	0.4947	2.5269	8.53683
C.D. 5%		11.3796	0.2308	0.3720	2.5106	2.5101	1.7313	0.7255	1.7218	1.3760	7.0287	237.4561

Table 6. Particular of genotypes used in the present study

Sl.no	Genotype name	Place of collection
G-1	Gandharvakottai Local	Department of Vegetable Science, TNAU Coimbatore
G-2	Kattur Local	Department of Vegetable Science, TNAU Coimbatore
G-3	Aiapatti	Department of Vegetable Science, TNAU Coimbatore
G-4	Sathyamangalam	Department of Vegetable Science, TNAU Coimbatore
G-5	Paravai Local	Department of Vegetable Science, TNAU Coimbatore
G-6	Amaravathi	Department of Vegetable Science, TNAU Coimbatore
G-7	Piraittur	Department of Vegetable Science, TNAU Coimbatore
G-8	Iniyanur	Department of Vegetable Science, TNAU Coimbatore
G-9	Udaiyanur	Department of Vegetable Science, TNAU Coimbatore
G-10	Rasipuram	Department of Vegetable Science, TNAU Coimbatore
G-11	Peramangalam	Department of Vegetable Science, TNAU Coimbatore
G-12	Melmaravakadu	Department of Vegetable Science, TNAU Coimbatore
G-13	Karratampatti	Department of Vegetable Science, TNAU Coimbatore
G-14	Kuruvikarankulam	Department of Vegetable Science, TNAU Coimbatore
G-15	Kagahpuram	Department of Vegetable Science, TNAU Coimbatore
G-16	Kodaivasal	Department of Vegetable Science, TNAU Coimbatore
G-17	Uppliyapuram	Department of Vegetable Science, TNAU Coimbatore
G-18	Namanasamuthiram	Department of Vegetable Science, TNAU Coimbatore
G-19	Vennamuthupatti	Department of Vegetable Science, TNAU Coimbatore
G-20	Orathanadu	Department of Vegetable Science, TNAU Coimbatore
G-21	Kordachery	Department of Vegetable Science, TNAU Coimbatore
G-22	Pattukottai	Department of Vegetable Science, TNAU Coimbatore
G-23	Kollidam	Department of Vegetable Science, TNAU Coimbatore
G-24	Kallakuruchi	Department of Vegetable Science, TNAU Coimbatore
G-25	Pondicherry	Department of Vegetable Science, TNAU Coimbatore
G-26	Thirupuvanam	Department of Vegetable Science, TNAU Coimbatore
G-27	Karur Local	Department of Vegetable Science, TNAU Coimbatore
G-28	Ponnavarayankottai	Department of Vegetable Science, TNAU Coimbatore
G-29	Thillaiyampuram	Department of Vegetable Science, TNAU Coimbatore
G-30	Periyakollapatti	Department of Vegetable Science, TNAU Coimbatore
G-31	Sankakiri	Department of Vegetable Science, TNAU Coimbatore
G-32	Ramanad Local	Department of Vegetable Science, TNAU Coimbatore
G-33	Sathur	Department of Vegetable Science, TNAU Coimbatore
G-34	Musiri	Department of Vegetable Science, TNAU Coimbatore
G-35	Kalachery	Department of Vegetable Science, TNAU Coimbatore
G-36	Namakkal	Department of Vegetable Science, TNAU Coimbatore
G-37	Dharwad green	Dharwad, Karnataka
G-38	Kerala Local	Kerala

G-39	Kanchipuram	Department of Vegetable Science, TNAU Coimbatore
G-40	Gujarat Local	Gujarat
G-41	Guntur long type	Guntur, Andhra Pradesh
G-42	Guntur round type	Guntur, Andhra Pradesh
G-43	Mudicole	Thrissur, Kerala
G-44	Ranibennur Local	Tumkur, Karnataka
G-45	White type	Mysore, Karnataka
G-46	Haryana Local-1	Rewari, Haryana
G-47	Haryana Local-2	Bhiwani, Haryana
G-48	Haryana Local-3	Bhiwani, Haryana
G-49	Akola Local	Nagpur, Maharashtra
G-50	Dharwad Local	Dharwad, Karnataka
G-51	Yaganti	Department of Vegetable Science, TNAU Coimbatore
G-52	Mysore Local	Mysore, Karnataka
G-53	Sirsi Local	Sirsi, Karnataka
G-54	Delhi Local	Delhi
G-55	Pudukottai Local	Department of Vegetable Science, TNAU Coimbatore
G-56	NS-404	Namdhari seeds
G-57	Cucumber white kakri	Bangalore, Karnataka
G-58	Green long	Bangalore, Karnataka
G-59	Emerald green	Bangalore, Karnataka
G-60	Chikkaballapura	Chikkaballapura, Karnataka
G-61	KPHC-1	Kerala
G-62	Pusa seedless	IARI, New Delhi
G-63	Parthenocarpic cucumber-2	Department of Vegetable Science, TNAU Coimbatore
G-64	Parthenocarpic cucumber-3	Department of Vegetable Science, TNAU Coimbatore
G-65	Multi star-RZ	Department of Vegetable Science, TNAU Coimbatore
G-66	AVCU-1202	Department of Vegetable Science, TNAU Coimbatore
G-67	AVCU-1203	Department of Vegetable Science, TNAU Coimbatore
G-68	AVCU-1205	Department of Vegetable Science, TNAU Coimbatore
G-69	AVCU-1206	Department of Vegetable Science, TNAU Coimbatore
G-70	AVCU-1303	Department of Vegetable Science, TNAU Coimbatore

Fig 1: Principal scree plot between component number and corresponding eigenvalue.

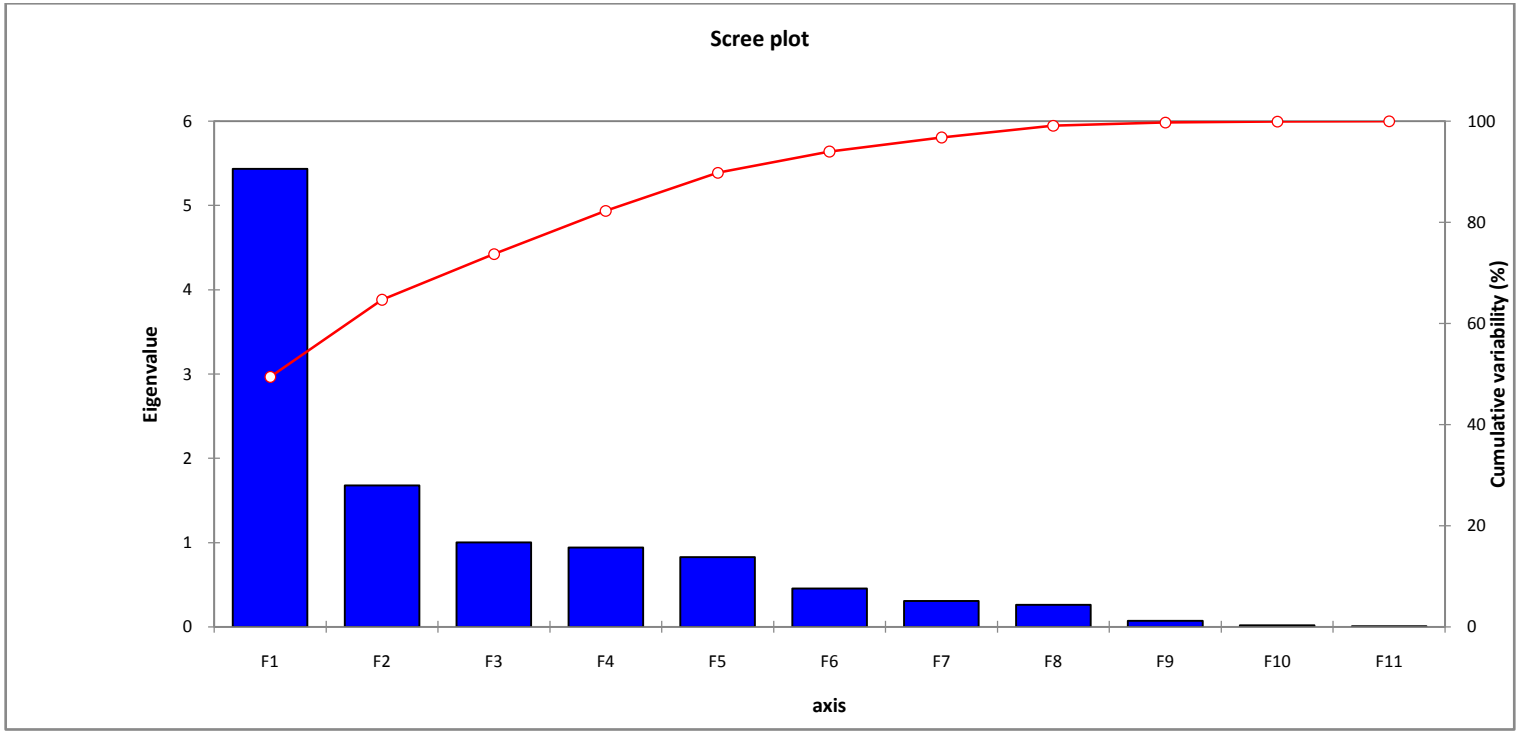

Fig 2: Biplotrepresenting the relationship between yield and yield attributing traits of cucumber genotypes on the first two principal components

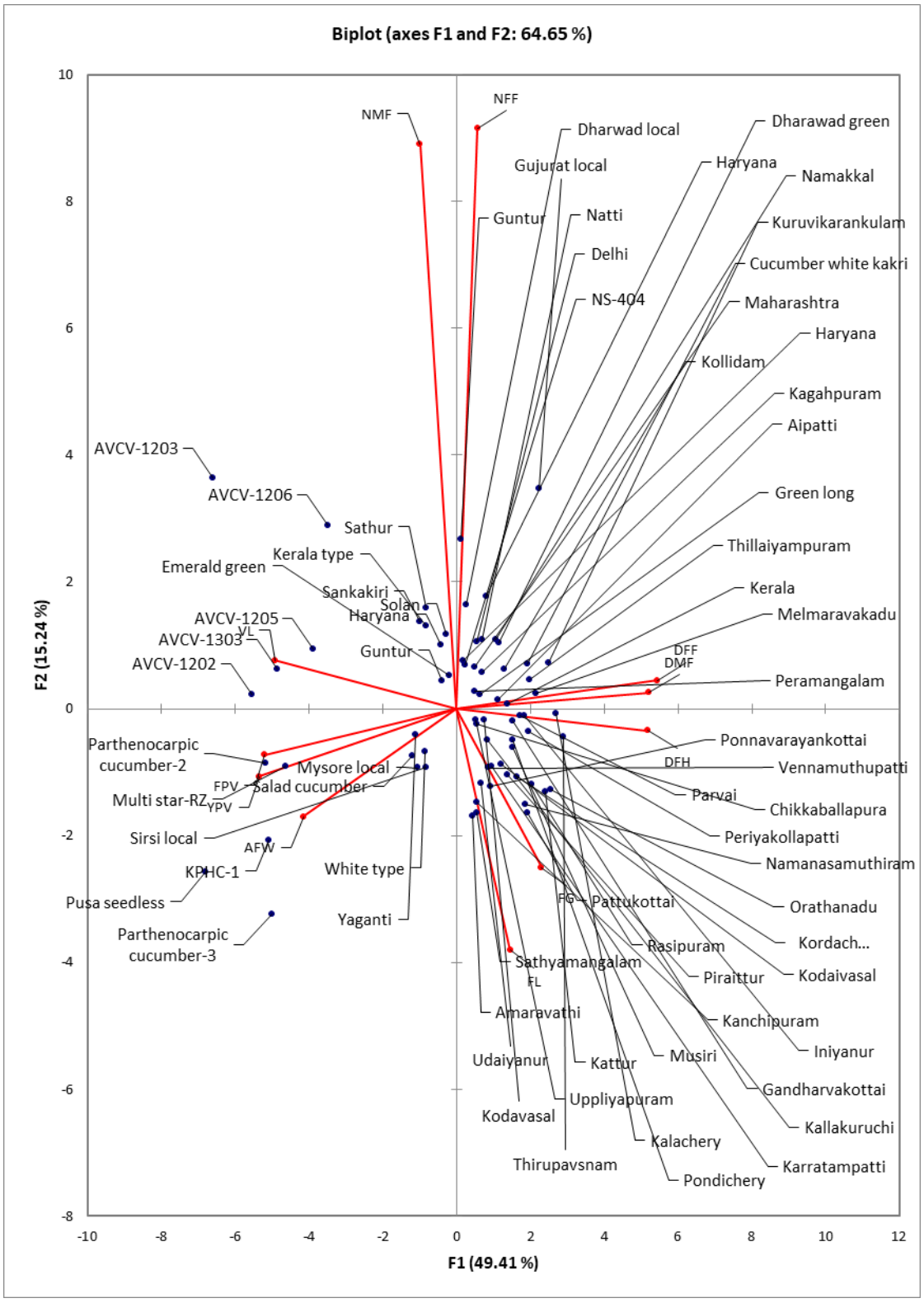

Fig 3: Trait contribution (%) toward genetic divergence