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Morpho-agronomic characterization of cucumber (*Cucumis sativus* L.) germplasm through principal component analysis

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Abstract
The present experiment was carried out to determine the variability source structure for 24 morpho-agronomic traits of cucumber in the Experimental Farm of the Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Solan during *Kharif*, 2015. The results revealed that first four component axes had eigen values ≥1.0, representing a cumulative variability of 81.53%. PC1 explained the traits like days to first harvest, number of marketable fruits per plant, harvest duration, vine length, number of primary branches per plant, germination percentage, seed vigour index I and II, severity of anthracnose, downy mildew and powdery mildew. The traits *viz.*, average fruit weight, fruit length, fruit diameter, flesh thickness and seed cavity length were explained by PC2 and the remaining traits were explained by PC3 and PC4. Loading of different variables based on the first two principal components indicated that average fruit weight, fruit length and diameter, seed length, seed cavity length and breadth, harvest duration, hundred seed weight, seed vigour index I and II contributed greater proportion of the total variability. Therefore, while conducting selection or choosing parents for hybridization, breeders have to give special emphasis on these traits.

Keywords: cucumber, principal component analysis, PCA, yield and quality traits

Introduction
Cucumber (*Cucumis sativus* L.) is the second most widely cultivated cucurbitaceous vegetable after watermelon and according to Tatlioglu (1993) [1], it ranks fourth in the list of economic vegetables of Asia after tomato, cabbage and onion. It is valued for its tender fruits, consumed fresh as salad or pickling and mature fruits after cooking. It also one most suitable crop for protected cultivation to meet the year round domestic demands as well as for export. Although the crop is native to India, it remained unexploited as far as its genetic potential is concerned. As a result, there is an appreciable gap in the expected and the actual yield of this crop. This gap can be overcome by developing high yielding varieties/hybrids.

Genetic improvement is a continuous process and its success depends upon the availability of variability at the breeders' end. Cucumber, being a crop of Indian subcontinent, has got enormous variability with respect to different yield and quality traits. Even then the actual genetic potential of the crop is not fully exploited, possibly because of lack of sufficient evaluation and classification of data for various traits including yield. Although correlation studies help to find out the positive or negative effects of the independent variables on the dependant variable (*i.e.* yield), but with the inclusion of more number of independent variables, their association becomes more complex. Furthermore, two variables may show correlation as they are associated with a common variable. Yield, being a complex and dependant variable, association studies can give only a limited insight to improve it. Here, 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; Golparvar *et al.*, 2006) [2, 3]. Therefore, the present experiment was formulated to determine the dependence of yield towards several morpho-agronomic traits through Principal Component Analysis in cucumber.

Materials and Methods
The present study was conducted with experimental materials comprised of thirty indigenous genotypes of cucumber (Table 1) at the Experimental Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, during *Kharif* season of 2015.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at spacing of 125 cm × 50 cm. Standard cultural practices, recommended in Package and Practices of Vegetable Crops were followed for a healthy crop stand (Anonymous, 2013) [4]. The observations were recorded on 24 morphological characters *viz.*, node number bearing first female flower (NNBFF), days to first harvest (DFH), average fruit weight (AVGFW), fruit length (FL), fruit diameter (FD), flesh thickness (FT), total soluble solids (TSS), number of marketable fruits per plant (MFPP), harvest duration (HD), vine length (VL), number of primary branches per plant (PBBPP), seed cavity length (SCL), seed cavity breadth (SCB), seed length (SL), seed breadth (SB), hundred seed weight (HSW), germination percentage (GP), seed vigour index I (SV-I), seed vigour index (SV-II) and severity four economically important foliar diseases *viz.*, angular leaf spot (ANLS), anthracnose (ANT), downy mildew (SDM) and powdery mildew (SPM). For plant characters, data were recorded on five random plants in each replication at the end of flowering season. Fruit characters were noted from ten random fruits taken from the third harvest and seed characters were recorded from ten random self-pollinated seeds in each genotype. Seed germination was tested according to the standard method of International Seed Testing Association (Anonymous, 1985) [5]. Seed vigour index I and II were calculated as per formula given by Abdul-Baki and Anderson (1973) [6], where, seed vigour index I = seed germination percentage × seedling length (cm) and seed vigour index II = seed germination percentage × seedling dry weight (mg). The disease severity of angular leaf spot was recorded on modified 0-9 scale of Woltman *et al.* (2009) [7] where absence of disease symptom was taken as 0 and leaf damage of 87-100% was scored 9. Severity of anthracnose, downy mildew and powdery mildew was recorded by adopting 0-5 scale of Akem and Jovicich (2011) [8]. Here, absence of disease symptom was scored as 0 and leaf necrosis between 75-100 % was scored as 5. For all the four diseases, the observations were recorded 65 days after sowing from ten leaves in each plant, five such plants in each replication of each genotype. Percent Disease Index (PDI) was calculated by adopting the formula of McKinney (1923) [9],

$$\text{Disease severity} = \frac{\text{Sum of all disease ratings}}{\text{Total number of ratings} \times \text{maximum disease grade}} \times 100.$$

The data was subjected to analysis using SAS-JMPSW-12 statistical software. The Principal Component (PC) was used to determine the extent of genetic variation. Eigen values were obtained from PC, which were used to determine the relative discriminative power of the axes and their associated characters (Pradhan *et al.*, 2011) [10].

Table 1: List of 30 indigenous cucumber genotypes along with their sources

Genotype	Source	Genotype	Source
LC-1	Jampur, Hooghly, W.B.	LC-16	Uluberia, Howrah, W.B.
LC-2	Maheshwarpur, Hooghly, W.B.	LC-17	Mangalbaria, Sikkim.
LC-3	Sheoraphully, Hooghly, W.B.	LC-18	Allahabad, U.P.
LC-4	Champadanga, Hooghly, W.B.	LC-19	Varanasi, U.P.
LC-5	Bhanderhati, Hooghly, W.B.	LC-20	Hubli, Dharwad, K.N.
LC-6	Sibaichandi, Hooghly, W.B.	LC-21	Ettinagudda, Dharwad, K.N.
LC-7	Harit, Hooghly, W.B.	LC-22	Bhuira, Sirmour, H.P.
LC-8	Gopalpur, Nadia, W.B.	LC-23	Narag, Sirmour, H.P.
LC-9	Simurali, Nadia, W.B.	LC-24	Gohar, Mandi, H.P.
LC-10	Barasat, N-24 Parganas, W.B.	LC-25	Manali, Kullu, H.P.
LC-11	Amtala, S-24 Parganas, W.B.	LC-26	Sarkaghat, Mandi, H.P.
LC-12	Kamdebpur, N-24 Parganas, W.B.	LC-27	Deothi, Solan, H.P.
LC-13	Memari, Burdwan, W.B.	LC-28	Joharji, Solan, H.P.
LC-14	Diamond Harbour, S-24 Parganas, W.B.	LC-29	Bhojnagar, Solan, H.P.
LC-15	Paskura, West Medinipur, W.B.	K-75	UHF, Nauni, Solan, H.P.

Results and Discussion

We observed significant differences among all the genotypes for all the traits under study. The perusal of data as presented in Table 2 (Scree plot between component number and eigen values has been presented in Fig-1) clearly shows that approximately 95.61% of total variability present among the 30 studied cucumber genotypes was explained by first ten principal components. But out of these ten components, first four principal components had eigen value of 1 and above, representing a cumulative variance of 81.53%. Principal component one (PC1) had eigen value 10.2269 and contributed 42.612% of total variability, whereas, PC2, PC3 and PC4 with eigen values 5.6964, 2.1840 and 1.4608 showed 23.735%, 9.100% and 6.086% of total variation, respectively. We have taken the first four components having eigen values greater than 1 in the analysis. The factors with eigen values less than 1 were ignored by following "Guttmans lower bound Principle" (Kaiser, 1958) [11]. The first principal component (PC1) explained the traits *viz.*, days to first harvest, number of marketable fruits per plant, harvest duration, vine length, number of primary branches per plant, germination percentage, seed vigour index I and I, severity of anthracnose, downy mildew and powdery mildew. Out of these traits in PC1, all had positive contribution towards yield except for days to first harvest and severity of three economically important foliar diseases, which showed negative contribution to yield. The traits *viz.*, average fruit weight, fruit length, fruit diameter, flesh thickness and seed cavity length were explained by the second principal component (PC2) and the traits *viz.*, TSS, seed length, seed breadth and hundred seed weight were explained by the third principal component (PC3). All these traits had positive contribution to yield per plant. The remaining three traits *viz.*, number of primary branches per plant, seed cavity breadth and severity of angular leaf spot were explained by the fourth principal component (PC4). The former two traits in this component had positive whereas the later trait had a negative contribution to the final yield per plant (Table 3). So a breeder has to go for positive selection for those traits which showed positive contribution towards yield. Therefore, in order to improve yield in cucumber, negative selection can also be conducted for the traits which showed negative contribution towards yield.

Similar findings were also reported by Olfati *et al*. (2010) [12] and Chikezie *et al.* (2016) [13] in cucumber; Hayder *et al.* (2007) [14], Mondal *et al.* (2007) [15], Ahmadizadeh and Felenji (2011) [2], Pradhan *et al*. (2011) [10], Sattar *et al*. (2011) [16] and Lahoni *et al*. (2012) [17] in potato.

Table 2: Eigen value and contribution of the principal component axes towards total genetic variation in cucumber germplasm

Principal Component	Eigen value	Variability (%)	Cumulative Variability (%)
PC1	10.2269	42.612	42.612
PC2	5.6964	23.735	66.347
PC3	2.1840	9.100	75.447
PC4	1.4608	6.086	81.534
PC5	0.8554	3.564	85.098
PC6	0.7612	3.172	88.269
PC7	0.6189	2.579	90.848
PC8	0.5071	2.113	92.961
PC9	0.3399	1.416	94.377
PC10	0.2947	1.228	95.605
PC11	0.2749	1.145	96.750
PC12	0.1768	0.737	97.487
PC13	0.1565	0.652	98.139
PC14	0.1267	0.528	98.667
PC15	0.0878	0.366	99.033
PC16	0.0667	0.278	99.311
PC17	0.0476	0.198	99.509
PC18	0.0409	0.171	99.679
PC19	0.0318	0.132	99.812
PC20	0.0227	0.095	99.906
PC21	0.0099	0.041	99.948
PC22	0.0056	0.023	99.971
PC23	0.0046	0.019	99.990
PC24	0.0024	0.010	100.000

Table 3: Contribution of different morpho-agronomic traits of cucumber towards the major principal components

Traits	PC1	PC2	PC3	PC4
NNBFF	-0.196	0.046	0.035	0.490
DFH	-0.253	0.034	0.075	0.163
AVGFW	0.056	0.352	-0.206	-0.179
FL	0.092	0.337	-0.244	-0.182
FD	0.083	0.346	-0.179	0.105
FT	0.000	0.327	-0.042	0.189
TSS	-0.139	-0.071	0.468	-0.184
MFPP	0.252	-0.174	0.068	0.157
HD	0.252	0.080	-0.092	0.025
VL	0.223	-0.076	0.112	-0.170
PBBPP	0.289	0.010	0.138	-0.066
SCL	0.070	0.358	-0.201	-0.118
SCB	0.043	0.222	0.130	0.553
SL	0.096	0.287	0.320	-0.117
SB	0.131	0.199	0.421	-0.186
HSW	0.063	0.156	0.397	-0.022
GP	0.250	-0.203	-0.022	-0.034
SV-I	0.283	0.064	0.084	0.085
SV-II	0.288	0.089	0.118	0.082
ANLS	-0.238	0.141	-0.059	-0.336
ANT	-0.275	0.162	0.127	0.062
SDM	-0.245	0.144	0.184	-0.046
SPM	-0.256	0.169	0.130	-0.009
YPP	0.282	0.113	0.092	0.163

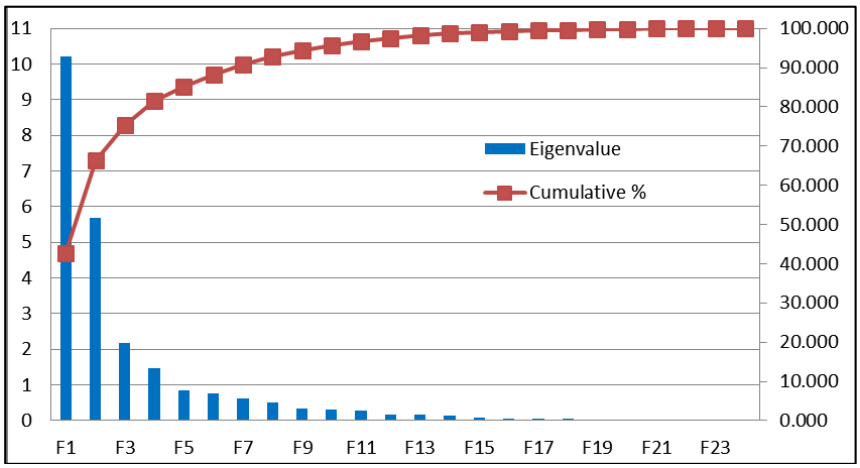

Fig 1: Principal scree plot between component number and corresponding eigen value.

Loading of different variables based on the first two principal components (Fig-2) indicated that, average fruit weight, fruit length and diameter, seed length, seed cavity length and breadth, harvest duration, hundred seed weight, seed vigour index I and II contributed greater proportion of the total variability, whereas, TSS contributed the least. Therefore, while conducting selection and/or choosing the parents for hybridization in cucumber for increasing yield and improving quality, a breeder has to give greater attention on these characters. Similar results have been emphasized by many researchers like Zhang and Cui (1993) [18] and Kumar *et al.* (2014) [19] in cucumber; Portis *et al.* (2006) [20] in peppers and Koutos *et al.* (2000) [21] in okra.

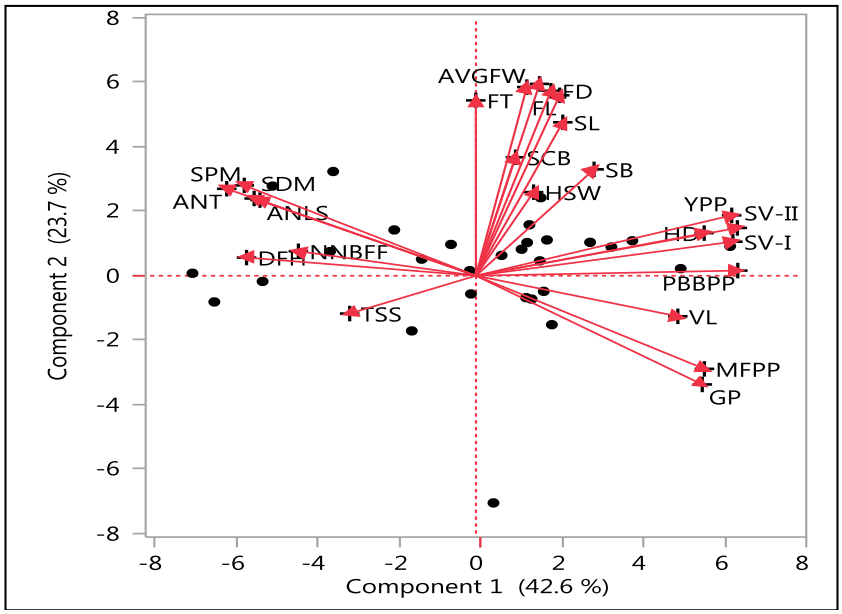

Fig 2: Loading of different characters based on the first two principal components.

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