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Assessment on the Genetic Diversity of Some Myanmar Cucumber (*Cucumis sativus* L.) Landraces

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Abstract

To access genetic diversity of some Myanmar cucumber landraces, 24 myanmar cucumber landraces were collected from three states and five divisions. The crops were grown and examined at the department of horticulture, Yezin Agricultural University, in November, 2004 (dry season). Randomized complete block design (RCB) was used with two replications.

All characters except leaf length to leaf width ratio and fruit diameter were highly and significantly different among accessions. High broad sense heritability estimates were found in days to male flowering, days to female flowering and days to first fruit harvest. Selection for early maturity would be beneficial. All clusters have considerable number of accessions for quantitative characters. These accessions were randomly distributed into different clusters with regardless of geographical regions. The selection of accessions for hybridization should be based on genetic diversity rather than on geographic diversity. Stem length, fruit length, fruit length to diameter ratio, table-use fruit weight, ripe fruit weight and number of days to female flowering were the most important characters for diversity analysis among these 24 cucumber accessions.

Introduction

Cucumber (*Cucumis sativus* L. 2n=14) is an important popular vegetable belonging to the family cucurbitaceae which consists of 90 genera and 750 species (Sitterly, 1972; Salunkhe and Kadam, 1998). It belongs to genus cucumis which includes 50 or more species from Asia and Africa (Salunkhe and Kadam, 1998). Cucumber is one of the oldest vegetable crops and has been found in cultivation for 3000-4000 years. It is a native of Asia and Africa. Some authorities claim that it originated in India and from there spread to Asia, Africa and Europe. Cucumber is the fourth most important vegetable crop after tomato (*Lycopersicon esculentum* mill), cabbage (*Brassica oleracea* var. capitata L.) and onion (*Allium cepa* L.) (Tatlioglu, 1993).

Plant genetic resources (PGRs) are the most valuable and essential basic raw materials to meet the current and future need of crop improvement programs. Information on characterization is specially valued by user as an indicator of usefulness of genetic resources. Reliable characteristic data are obtained from rational evaluation. In these regards, this attempt was organized with the following aims; to assess genetic variability of Myanmar cucumber landraces and its wild relatives based on morphological and agronomic characters.

The objectives of the study are as follows:
- To investigate correlation of geographical region with the genetic diversity of myanmar cucumber landraces, and
- To determine the important characters for genetic diversity analysis of myanmar cucumber landraces and its wild relative.

Materials and Methods

The field experiments were conducted at the Department of Horticulture, Yezin Agricultural University (YAU), in November, 2004. The soil texture was sandy loam and the soil ph was 6.59. A Randomized Complete Block (RCB) design with 2 replications was used. Twenty four cucumber accessions were collected from three States and five Divisions (Appendix1).

Vigorous and healthy fifteen days old (15 DAS) seedlings were selected and transplanted into prepared pits. The spacing of 4 x 5 square feet was used. The crops were allowed to grow on the ground naturally.

Quantitative and qualitative data presented in descriptors by IPGRI (1996) and additional required data were recorded. Quantitative data were subjected to analysis of variance and performed mean comparison by using IRRISTAT (version 4.1) computer software program. Ward's minimum variance clustering method was used to classify the accessions into discrete clusters with the help of computer soft ware program XLSTAT (version 4.3). The clusters resulted from the experiment were checked by Principle Component Analysis (PCA).

Results and Discussion
Descriptive Statistics

The high range was found in table-use yield per plant (6118.40 g), ripe yield per plant (4802.40 g), ripe fruit weight (1620.64 g), seeds per fruit (661.80 seeds), table-use fruit weight (628.64 g) and stem length (229.20 cm) respectively (Table 1). The characters with high range and high CV value implied that there was a great chance for breeders to select for those characters among these cucumber accessions.

Table1. Descriptive statistics parameters of seventeen quantitative characters for 24 cucumber accessions

No	Characters	Units	Mean	Max	Min	Range	Sd.	CV%
1	ITNL	cm	6.75	8.00	4.54	3.46	0.93	13.76 L
2	STL	cm	177.48	328.80	99.60	229.20	60.25	33.94 M
3	LL	cm	12.36	14.78	8.32	6.46	1.75	14.19 L
4	LW	cm	15.87	19.74	10.40	9.34	2.37	14.93 M
5	LLLW	ratio	0.78	0.86	0.72	0.13	0.04	4.64 L
6	DMFL	days	39.34	49.80	30.40	19.40	6.00	15.23 L
7	DFMFL	days	47.33	68.80	35.00	33.80	9.25	19.53 M
8	TFFH	days	72.04	103.60	55.20	48.40	11.22	15.57 M
9	TYDP	g	2765.55	6990.70	872.30	6118.40	1585.66	57.33 H
10	TWF	g	390.25	745.02	116.38	628.64	185.56	47.54 H
11	RYDP	g	2233.60	5349.00	546.60	4802.40	1244.56	55.71 H
12	RWF	g	778.03	1753.25	132.61	1620.64	490.83	63.08 H
13	FL	cm	21.24	44.74	9.66	35.08	9.28	43.69 H
14	FD	cm	9.55	25.80	5.70	20.10	3.93	41.17 H
15	FLD	ratio	2.50	5.38	1.02	4.37	1.22	48.70 H
16	FFT	mm	17.64	26.60	8.60	18.00	4.66	26.40 M
17	SDF	no.	410.20	809.40	147.60	661.80	216.40	52.75 H

L= low <14.83 %, M= medium 14.83-34.31% and H= high >34.31

ITNL= internode's length, STL= stem length, LL= leaf length, LW= leaf width, LLLW= leaf length to leaf width ratio, DMFL= days to male flowering, DFMFL= days to female flowering, TFFH= days to table-use

fruit first harvest, TYDP= table-use yield per plant, TWF= table-use fruit weight, RYDP= ripe yield per plant, RWF= ripe fruit weight, FL= fruit length, FD= fruit diameter, FFT= fruit flesh thickness, SDF= seeds per fruit.

Analysis of Variance

Analysis of variance showed that the effects of accessions were highly and significantly different for all characters except leaf length to leaf width ratio (LLLW) and fruit diameter (FD). The effects of accessions on leaf length to leaf width ratio (LLLW) and fruit diameter (FD) were not significantly different. Significant different effect of replication was observed in stem length (STL), number of days to male flowering (DMFL), number of days to female flowering (DFMFL) and table-use fruit weight (TWF). It revealed the efficient use of replication. In other words, the effect of replication could be excluded out of the residual. The coefficient of determination (R^2) value was high in DMFL (0.93), DFMFL (0.90), STL (0.85), TFFH (0.83), TWF (0.80) and FL (0.79) respectively. Comparatively low R^2 value was found in LLLW (0.26) and FD (0.30). Low R^2 value was implying that there were too much unknown factors for those characters and accomplished with not significant difference.

Cluster Analysis

On the basis of Ward's minimum variance clustering method, twenty four cucumber accessions were grouped into three different clusters (Table 2 and Figure 1). This indicated the existence of genetic diversity among the accessions. Maximum accessions were in cluster-I involving eleven accessions, followed by cluster-II with seven accessions and then cluster-III with six accessions. The accessions from different origins assembled into a cluster with other plants of close affinity. The accession 9 from Mandalay Division, 16 from Magway Division, 17 from Bago Division, 19 from Yakhaing State and 23 from Shan State formed cluster-III. On the other hand, three accessions: Acc21, Acc22, Acc23 collected from Shan State were distributed in different clusters: cluster-I, cluster-II and cluster-III respectively. These results showed that geographic diversity was not necessarily related with genetic diversity. It also implied that no natural selection pressure existed there and the accessions were randomly distributed by their natural dissemination. Similar finding has been reported by Tariqul Islam (2004) in bottle gourd. Therefore, the selection of accessions for hybridization should be based on genetic diversity rather than on geographic diversity. The tendency of accessions to occur in cluster cutting across geographic boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. This may be due to the wide soil and climatic differences in the region. Tariqul Islam (2004) presented that genetic drift and natural selection forces under diverse environmental conditions within a region could cause more considerable diversity than geographic isolation.

Table 2. Distribution of 24 cucumber accessions into different clusters by Ward's minimum variance method

Clusters	Total no. of accessions	Accessions
I	11	1,3,7,8,10,11,12,15,18,21,24
II	7	2,4,5,6,13,14,22
III	6	9,16,17,19,20,23

Intra and inter cluster distances were presented in Table 3. The average intra cluster distance ranged from 2.61 (cluster-I) to 3.38 (cluster-II) suggesting that the accessions in cluster-II

were relatively more diverse than the accessions in the other clusters. The maximum inter cluster distance was between cluster-I and cluster-II (5.13) followed by that between cluster-II and cluster-III (4.86), suggesting a large difference between these groups. On the other hand, the minimum distance between cluster-I and cluster-II (3.96) indicates a close relationship and the accessions of these clusters have the maximum of common gene complexes. The magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines. The greater the distance between two clusters, the wider the genetic difference between their accessions. Several researcher have suggested that selection of parents for hybridization should be done for two clusters with wider inter cluster distances in order to get more variability among the segregates. However, while considering genetic diversity among the parents to be included in hybridization programs, their yield potential should not be ignored.

Table 3. Average intra and inter-cluster distance of 24 cucumber accessions by Ward's minimum variance method

Clusters	I	II	III
I	2.61		
II	3.96	3.38	
III	5.13	4.86	3.16

The character means for different cluster were presented in Table 4. Cluster-I gave the lowest mean value for number of days to female flowering (42 days) and the lowest number of seeds per fruit (260 seeds), while cluster-II gave the lowest number of days to male flowering (34 days) and the lowest number of days to table-use fruit first harvest (68 days), the largest fruit diameter (12.38 cm) and the greatest table-use yield per plant (3782 g).

Table 4. Character means of different clusters for 17 characters of 24 accessions by Ward's minimum variance method

Characters	Units	Cluster I	Cluster II	Cluster III
ITNL	cm	6.89	5.88	7.51
STL	cm	137.00	185.37	242.50
LL	cm	13.14	10.38	13.23
LW	cm	16.71	13.15	17.52
LLLW	ratio	0.79	0.79	0.76
DMFL	days	38.38	34.29	47.00
DFMFL	days	42.55	44.00	60.00
TFFH	days	70.02	68.49	79.90
TYDP	g	1969.45	3782.07	3039.12
TWF	g	279.66	419.27	559.13
RYDP	g	1436.41	2706.80	3143.07
RWF	g	436.62	847.37	1323.07
FL	cm	15.64	22.28	30.28
FD	cm	7.60	12.39	9.82
FLD	ratio	2.06	2.36	3.45
FFT	mm	14.53	19.09	21.67
SDF	no.	260.42	560.29	509.70

But, cluster-III gave the longest internode's length (7.5 cm), stem length (422.5 cm), leaf length (13.23 cm), leaf width (17.52 cm), fruit length (30.28 cm), fruit flesh thickness

(21.66mm), the highest table-use fruit weight (559 g), ripe fruit weight (1323 g), and ripe yield per plant (3143 g). This character mean can be used in the selection of desirable characters. Selection should direct straight to the cluster which exists the superior value of desirable characters.

Principle Component Analysis

The cluster constellation pattern obtained by Ward's minimum variance clustering method was also confirmed by Principle Component Analysis (PCA). PCA analysis was carried out by calculating the first two PCA, which account for 58% of the total variation and the first four PCAs explain 77% of the total genetic variability (Table5).

The mean values of the first two PCAs for twenty four cucumber accessions were plotted on a two-dimensional graph in Figure 1. The scatter diagram of cucumber showed a distribution of accessions in cluster similar to that of Ward's method (Table3). The accessions were most heterogeneous in cluster-II and the accessions were comparatively close to each other in cluster-I (Figure 2).
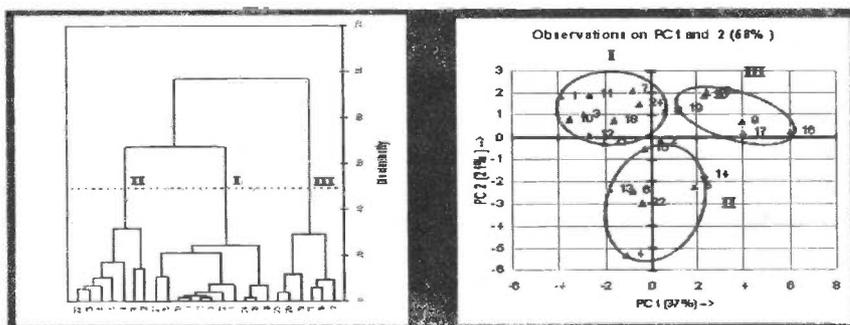

Figure 1. Dendrogram from cluster analysis for 24 collected cucumber accessions by Ward's minimum variance method

Figure 1. Twenty four cucumber accession were plotted on the basic of two principle dimension

Correlation between initial variables and principle factors were presented in Table 5. Stem length, days to male flowering, fruit length, fruit length to diameter ratio, table-use fruit weight, ripe yield per plant and ripe fruit weight were highly and positively correlated with principle factor one (PC1). Therefore, it can be interpreted that these characters were the most divergent among tested cucumber accessions.

Table 5. Eigenvalues, variation explained for important characters and correlation between initial variable and principle components

Principle components	PC1	PC2	PC3	PC4
Eigenvalues	6.36	3.49	1.88	1.39
% of variability	37.00	21.00	11.00	8.00
Cumulative %	37.00	58.00	69.00	77.00
ITNL	0.40	0.76	0.15	0.08
STL	0.79	0.08	0.13	0.04
LL	-0.05	0.91	-0.24	-0.12
LW	0.01	0.92	-0.03	-0.31
LLLW	-0.18	-0.18	-0.62	0.56
DMFL	0.57	0.44	-0.37	-0.36
DFMFL	0.84	0.17	-0.12	-0.14
TFFH	0.57	-0.03	-0.43	0.17
TYDP	0.35	-0.16	0.78	0.00
TWF	0.81	-0.12	0.25	0.13
RYDP	0.71	-0.16	0.33	-0.26
RWF	0.90	-0.09	-0.10	-0.01
FL	0.91	-0.01	-0.02	0.29
FD	0.12	-0.69	-0.28	-0.40
FLD	0.75	0.17	0.06	0.56
FFT	0.65	-0.18	-0.40	-0.20
SDF	0.50	-0.62	-0.18	-0.30

Conclusion

The study indicated that there is a great chance for breeders to select for quantitative characters as it posses a wide range of variations. All clusters have considerable number of accessions for quantitative characters. All these accessions were randomly distributed into different clusters with regardless of geographical regions. It indicated that the geographical region is not the only factor for cucumber genetic diversity. Therefore, selection of accessions for breeding should be based on genetic diversity rather than geographical region. Thus, the cross between the accessions of more diverse clusters; from cluster-I and cluster-III could be expected to obtain maximum heterosis and new recombinants with desired characters in cucumber.

Stem length, days to female flowering, fruit length, fruit length to diameter ratio, table-use fruit weight, ripe yield per plant and ripe fruit weight were the most divergent characters for dry season. Further research should be pursued in order to confirm the present finding and to support future cucumber improvement programs.

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Appendix 1. List of twenty four cucumber accessions collected from three States and five Divisions

1 PYINMANA(SINPHYUTAUNG)	13 SALIN(TAWSEINT)
2 YAMETHIN(YWQATAN)	14 MINBU(THAKHAMA)
3 YAMETHIN(NGAPYAUT)	15 PWINTPHYU(YWATHIT)
4 MADAYA(SAKYIN)	16 AUNGLAN(SHWEPANDAW)
5 MADAYA(THAKHWARSHAE)	17 PHYU(WAEDAUNGKHON)
6 MADAYA(THAKHWARLONE)	18 YANGON(MOTHAKHWAR)
7 KYAUKPADAUNG(NGAPYAUT)	19 YAKHING(YARTHAKHWAR)
8 MYINGYAN(SAKHA)	20 PYINOOLWIN(PYINOOLWIN)
9 MOGOK(KYATPYIN)	21 TAUNGGYI(AYETHAYAR)
10 KHINOO(MONHLA)	22 KALAW(BAWSAING)
11 SHWEBO(THEELON)	23 INLAY(INLAY)
12 DEPEYIN(PYAWBWE)	24 KACHIN(MOHNYIN)