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ABSTRACT

The experiment was carried out at Woramit horticultural research and training sub-center using thirty six hot pepper local land race of Ethiopia for morphological characterization. Data were collected for seven qualitative traits of each genotypes. Based on the hierarchical centriod linkage cluster analysis method for qualitative characters, the genotypes got grouped into five clusters at different per cent level of similarity. Accordngly, the 36 hot pepper genotypes including a standard check fell into the first three clusters. Half of the hot pepper genotypes (50%) were grouped in cluster II. Further, the two dimensions were identified using corresponding analysis that explained 27.55% and 22.81%, respectively, of the observed variability for seven qualitative traits. Both cluster and multiple correspondence analysis indicating the narrow genetic base of these germplasm for the qualitative characters considered. Characterization of the hot pepper land races was done based on the mean values to the different scales of the respective character.

Keywords: Characterization, Cluster analysis, Correspondance analysis, Hot Pepper, Qualitative Traits.

INTRODUCTION

Pepper is one of the important cultivated vegetable crops in the word which belongs to the *Solanaceae* family like as tomatoes, potatoes and eggplants (Ashilenje, 2013). It is believed that pepper has originated from tropical American countries such as Peru, Boliva and Mexico and it rapidly spreads to Europe and then to other parts of the world such as African countries (Ashiblenje, 2013; Zonneveld *et al.*,2015).

C.annuum, *C.baccatum*, *C.chinense*, *C.frutescens* and *C.pubescens* are the only five cultivated species in the genus *Capsicum*, although there are about 22-27 wild species ((Bosland and Votava, 2000; CPEC/ CEDA, 2004). These species are grown in the tropical and temperate regions across the continents. In Africa, they are generally considered together as *C. annuum*. *L* (Grubben and Tahir, 2004).*C. annuum*. *L* has grown widely in tropical agro climate conditions of Ethiopia (Berhanu Yadeta *et al.*, 2011). It is the most important crop uses as spice and food vegetable in the world (Amare Tesfaw, 2013).

In addition, *Capsicum species* have been used as medicines and lachrymatory agents. In Ethiopia, it is a high value crop due to its high pungency which serve as food consumption and source of cash earning for smallholder farmers/ or producers in both green and dry form (Amare Tesfaw, 2013).

Genetic diversity assessment and estimation of relationship among accessions are very helpful for germplasm improvement. So, analysis of genetic diversity is important to examine differences between individuals of the same species and is also used to compare the genetic composition of members of different species over a wider taxonomic range (Dale and Schatz, 2002). According to Peeraullee and Sanmukhiya (2013) description establishing the morphological and agronomic traits has been used to characterization and evaluation of crop germplasm. However, the expression of qualitative traits appeared less influenced by environment and so they are considered more important for characterizing plants (Berg et al.,

1993). Qualitative genetic variation is characterized by differences in a trait, which are small in number or non-continuous classes or values.

These variations are governed by allelic differences at one or few numbers of interacting gene loci and the genotypic differences could be easily identified from the trait's expressions. Usually the classification using qualitative traits could be applied for any year, location or environment (Briggs and Knowles, 1967). But, quantitative traits are highly influenced by environment and that is why quantitative descriptors are impediment to their use for genetic diversity assessment (Dagnoko et al., 2013). In Ethiopia, generating information on the degree and pattern of genetic diversity of the hot pepper genotypes using morphological qualitative characters were so far limited evaluation scientifically. Hence, a total of 36 hot pepper landraces were studied to determine their genetic variability as well as genetic relationship among or within individual accessions using qualitative traits

MATERIAL AND METHODS

Experimental Site Description

The field experiment was conducted at Woramit horticultural research and training sub-center. It is located at 563km far from Addis Ababa in the Northwestern part of Ethiopia at Bahir Dar. Geographically, the area lies within 11°38' N latitude and 37°10' E longitude. The altitude of the study area is 1800 m.a.s.l with annual rainfall of about 800 to 1250 mm. Monthly mean minimum and maximum temperature is 6.2°C in January and 29.5°C in April, respectively. The soil at this experimental site is Nitosol with moderately acidic (pH 6.4) (Habtamu Tegen et al., 2014).

Experimental Materials

The experimental materials of tested hot pepper genotypes were obtained from the Assosa Agricultural Research Center. The study consisted of 36 genotypes and they are local landraces which were collected from different areas of Assosa. List of the experimental materials are given in Table 3.1.

Entry #	Code	Accession Name	Entry # Code		Accession Name	
1	1	AS 052/13	19 19		AS 037/13	
2	2	AS 110/13	20	20	AS 031/13	
3	3	AS 056/13	21 21		AS 042/13	
4	4	AS 104-2/13	22 22		AS 057/13	
5	5	AS 094/13	23	23	AS 023/13	
6	6	AS 138-2/13	24	24	AS 142/13	
7	7	AS 039/13	25	25	AS 043/13	
8	8	AS 105/13	26	26	AS 047/13	
9	9	AS 040/13	27	27	AS 058-2/13	
10	10	AS 119/13	28	28	AS 075/13	
11	11	AS 139/13	29	29	AS 063/13	
12	12	AS 058-1/13	30	30	AS 005/13	
13	13	AS 054/13	31	31	AS 015/13	
14	14	AS 060/13	32	32	Melka Zala (check)	
15	15	AS 024/13	33	33	AS 087/13	
16	16	AS 078/13	34	34	AS 017/13	
17	17	AS 059/13	35	35	AS 008/13	
18	18	AS 050/13	36	36	AS 138-1/13	

 Table2.1. List of hot pepper genotypes and their codes.

Field Experimental Design and Trial Management

The field experiment was laid out in a 6 x 6 simple lattice design. The genotypes were grown under rain fed condition in 2016/2017. Transplanting was done to the open fields when the seedling attained 15-20 cm height. The plot

size was 2.4 m long and 3 m wide (7.2 m^2) with 0.6m and 0.3m inter row and between plants spacing, respectively. Each incomplete block and replication was spaced 0.6 and 0.75 meters, respectively. There were four rows per plot, out of which the first and fourth rows of each plot were used as border rows. Fertilizer in the forms

of Urea and DAP, hand weeding and all other agronomic practices were applied uniformly to the entire plots as recommended of EIAR (2015) for hot pepper production during the growing season to raise a healthy seedling. data were scored on ten randomly selected plants in the middle two rows of all plots. The ten samples were selected at the seedling stage and tagged, which helps to avoid biasness during data recorded.

Data Collection

Data collections for all qualitative traits were based on descriptor from IPGRI (1996). The

 Table2.2. List of qualitative characters considered with their codes and descriptions as per IPGRI Capsicum annum descriptor

Ser.	Character	Description and codes		
no.				
1.	Plant growth habit	Prostrate (3), Compact (5) and Erect (7)		
2.	Leaf color	Yellow (1), Light green (2), Green (3), Dark green (4), light		
		purple (5), Purple (6)		
3.	Branching habit	Sparse (3), Intermediate (5), Dense (7)		
4.	Fruit color	Orange (6), Light red (7), Red (8), Dark red (9), Purple		
		(10), Brown (11), Black (12)		
5.	Fruit shape	Elongate (1), Almost round (2), Triangular (3), Campanulate		
		(4), Blocky (5)		
6.	Fruit shape at pedicle	Acute (1), Obtuse (3), Truncate (5), Cordate (7), Lobate (9)		
7.	Fruit shape at blossom end shape	Pointed (3), Blunt (5), Sunken (7),		

Stasstical Analysis

The associations among the accessions were examined by hierarchical cluster analysis of observations with Euclidean distance and Centroid linkage method using the Minitab (version 14) software package (Minitab Inc., 1998). Then each cluster was characterized for its special feature based on the mean values of all traits. Further, the data was subjected to multiple correspondence analysis in order to identify the pattern of morphological qualitative variation of genotypes using JMP version 13.1 Software (SAS, 2013).

RESULTS AND DISCUSSION

Cluster Analysis

The clustering of 36 hot pepper accessions based on qualitative characters has been classify into five different groups which fells at different similarity coefficient cutting edge (Figure 2).



Figure1. Dendrogram of 36 hot pepper genotypes based on Centriod linkage cluster analysis method for eight qualitative traits

Accordingly, the genotypes were distributed in such a way that five genotypes grouped in to cluster I (13.8%), 18 genotypes into II (50%),

seven genotypes into III (19.4%), four genotypes into IV (11.11%) and two genotypes into V (5.6%) (Table3.1). Distribution of

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genotypes into five clusters implies the prevalence of genetic variation, even if it was

bare minimum, among genotypes for most of the traits under consideration.

Table3.1. The distribution of accessions on five clusters of qualitative traits for 36 hot pepper accessions tested at Woramit.

Clusters	No. of acc.	Accessions
Ι	5	AS052/13, AS182-8/13, AS 008/13, AS13913, AS 181-1/13
II	18	AS110/13, AS023/13, AS1104-2/13, AS105/13, AS015/13, AS039/13, AS005/13,
		AS024/13, AS078/13, MelkaZala, AS087/13, AS050/13, AS037/13, AS057/13,
		AS017/13, AS043/13, AS047/13, AS063/13
III	7	AS056/13, AS042/13, AS058-1/13, AS060/13, AS059/13, AS039/13, AS054/13
IV	4	AS094/13, AS031/13, AS142/13, AS036/13
V	2	AS075/13, AS063/13

The unique characteristics relevant to each cluster can be easily determined by comparing the mean values to the different scales of the respective character. Accordingly from this study, clusters consisted unique features genotypes. For example, cluster I for compact growth habit with sparse branching nature with obtuse fruit shape at pedicle, cluster II intermediate branching habit with truncate fruit shape at pedicle, cluster III for dark green leaf color with truncate fruit shape at pedicle, cluster VI for almost sunken fruit shape at pedicle shape and cluster V for campanulate fruit shape.

Table3.2. Cluster centriods and mean values for the five clusters of seven qualitative traits in hot peppers.

Characters	Ι	II	III	IV	V
LC	3.000	3.278	3.714	3.000	3.000
GH	4.600	6.444	7.000	5.000	7.000
ТС	3.000	4.778	3.857	3.500	6.000
FSP	4.600	5.333	3.280	4.500	6.000
FSH	1.400	1.000	1.000	2.000	2.000
FSB	3.000	3.667	4.715	5.500	7.000
FC	8.600	8.056	8.286	9.000	8.000
Cluster Centriods	2.656	2.289	2.419	2.289	4.211

Where, LC = leaf color, GH = plant growth habit, TC = Tillering capacity, FSP = Fruit shape at pedicle, FSH = Fruit shape at blossom end shape and FC = Fruit color

In addition, cluster I and II had green leaf color with obtuse fruit shape at pedicle with blunted fruit shape at blossom end. Cluster IV for sunken fruit shape at the blossom end and V comprised erect plant growth habit with blunt fruit shape at blossom end shape where as all clusters had genotypes with red fruit color except cluster I and IV (they had dark red fruit color) (Table 3.2).



Figure3. Map of the two dimensions of 36 hot pepper genotypes for seven qualitative traits using multiple correspondance analysis.

Multiple Correspondence Analysis

The multiple correspondence analysis (MCA) with two factorial dimensions explained 27.55% and 22.81%, respectively for seven qualitative traits of 36 hot pepper genotypes. The MCA dimensions of the hot pepper landraces depicts that the variables and the genotypes are overlapped and distributed on the plot quadrants. From this graph, the genotypes that are close together are perceived being resemblance while the genotypes that are further apart are more different. Hence, most of the genotypes are close to each other except some genotypes like 11(AS139/13), of the 20(AS031/13), 28(AS075/13), 25(AS043/13), 21(AS042/13), 3AS(056/13) and 12(AS058/13) are separated from each other on two dimensions (F1 and F2). The first dimensions was mainly associated with compact growth habit (GH-Compact), blocky fruit shape (FSH-Blocky), sparce tillering capacity (TC- Sparce), pointed fruit shape at blossom end (FSB-Pointed), dark fruit color (FC-Dark Red), green leaf color (LC-Gren) and cordate fruit shape at pedicle (FSP-Cordate).

In the second factorial deminsions, erect growth habit (GH-Erect), dark green lef color (LC-Dark Green), elongated fruit shape (FSH-Elongate), red fruit color (Fc-Red), intermidiate tillelering capacity (TC-Intermidiate), blunted fruit shape at blossom end(FSB- Blunt) and cordate fruit shape at pedicle (FSP-Cordate) were principally related. Such distribution pattern of genotypes and qualitative traits on two dimensions showed the prevalance of genetic variability among hot pepper genotypes.





Genotype AS058-1/13 (Cluster III)





Genotype AS 110/13 (Cluster II)

CONCLUSIONS

The result of this study has provided a clue for the existence of variability in the characters under study in hot pepper land races. Based on the above result, it may be possible to state that in general, the variation among tested hot pepper accessions for qualitative characters appeared to be minimum. This could be seen from the fact that most of the accessions (50%) were grouped in the same cluster (cluster II),

which showed that no distinctive variation existed in majority of the accessions. The distribution of the rest accessions into four clusters reflected the presence of variation among that accession. Moreover, the multiple correspondence analyses for 36 hot pepper genotypes revealed most of the genotypes are close together which indicated the narrow genetic base of these germ plasm for the qualitative characters considered.

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