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Research Article

Genetic Diversity, Heritability Estimate and Correlation among Quantitative Traits in Thirty *Capsicum annum* L. Genotypes

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ABSTRACT

In this study, a genetic diversity study was carried out on thirty hot chilli (*Capsicum annum*) genotypes to know the extent of genetic variation present in the germplasm materials, to estimate the variance components, and to study the association among the quantitative traits. The thirty genotypes were planted under a fertigation system in three replicates using a complete randomized design (CRD). Eight quantitative traits, which include vegetative and yield traits, were collected at different stages of planting. Data analysis, which includes analysis of ANOVA, correlation coefficient, variance components, and principal component analysis (PCA), was carried out to see the pattern of diversity and associations. From the analysis, it was observed that the effect of genotypes on the expression of all the traits was highly significant except for plant height at the age of 6-12 weeks. A positive association was observed between fruit yield and other quantitative traits. The differences between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low for traits like yield, fruit length, and leaf area, indicating high effect of genotype on the expression of these traits. A high broad sense heritability value of more than 60% was observed in most of the traits. Cluster analysis based on the quantitative traits groups the 30 chili genotypes into eight distinct groups at a coefficient of 4.09. Some chilli genotypes such as CA813, CA904, CA905, and CA203 have been identified as potential high-yielding materials that are suitable to be used as parents during hybridization programme.

Keywords: Genetic diversity; Genetic erosion; Principal component analysis; Selection gain; Vegetable

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INTRODUCTION

Capsicum annum (2n=24) is one of the most valuable members of Solanaceae family. It is regarded as one of the oldest and commercially viable vegetable and spices crops due to its domestic and industrial uses (Miranda *et al.,* 2023; Saha *et al.,* 2010). Chilli is a short height vegetable crop, which was said to have originated from South America. It has been widely cultivated in tropics and sub-tropical regions of the world with China and Turkey being the world largest producer (Yaldiz *et al.,* 2010).

Capsicum annum, being a vegetable and spices crop, contains a high amount of β-carotene, giving it red colour and this makes it to become an important part of human food. Also the significance of this plant as a therapeutic and medicinal plant due to its analgesic, antiseptic carminative and counter irritant properties as been reported. These makes it to be suitable in treating, arthritis, itching, rheumatism, neuralgia diseases (Faisal and Mustafa, 2025; Joshi *et al.,* 2024; Yaldiz *et al.,* 2010). Also, capsaicin concentration and other capsaicinoid contents are important factors that affect the flavour and pungency of the chilli.

In many countries, including Malaysia, the importance of chilli cannot be overemphasized. The fruits and vegetative parts of this crop are consumed as vegetables and spices. This plant is an important economic crop that serves as a source of income for the rural dwellers. However, the production and cultivation of this important vegetable crop have been under threat as a result of several factors. These include problems of low yield, pest invasion, and attack by disease, low soil fertility, and inadequate knowledge of the required agronomical practices to bring about optimum yield (Sam-on *et al.,* 2024).

Furthermore, for improvement in production and sustainability in the growth and yield of chilli, rational breeding of improved varieties through conventional and modern approach is needed to be established (Younas *et al.,* 2024). Similarly, establishment of rational breeding is needed to produce crop varieties which will be tolerant to the fast changing climatic conditions and simultaneously high yielding to cater for the rapid growing human population (Ibrahim, 2012). The presence of genetic variability plays an important role in the breeding and improvement program of any crop (Arolu *et al.,* 2017; Rafii *et al.,* 2012) . Genetic variability which is the study of the variation in growth and yield performance due to differences in genetic origin or composition (Allard, 1960; Arolu *et al.,* 2012).

Additionally, several methods have been designed to study the genetic variation and diversity patterns in any germplasm populations (Bernardo, 2002). These methods include agro-morphological, biochemical, physiological, and molecular markers. Agro-morphological traits have been used extensively in studying genetic diversity and heritability estimates in vegetable and spice crops (Rêgo *et al.,* 2010). Heritability estimate and other variance components serve as important parameters through which progress and advances made in breeding and improvement programmes could be measured. Therefore, this research aims to study the genetic variation in 30 elite chilli genotypes using agro-morphological traits. This work equally studied the heritability pattern and estimate other variance components as a yard stick through which progress or advances in breeding could be measured.

MATERIALS AND METHODS

Plant Materials

This experiment was carried out at the rain shelter in Agrotech unit, Universiti Putra Malaysia, Serdang, Selangor by using the fertigation system. The seed of thirty genotypes of *C. annuum* were collected from the Asian Vegetable Research and Development Center (AVRDC) in Taiwan.

Experimental design and agronomical practices

The study was conducted using a complete randomized design (CRD) with 30 accessions replicated three times. The spacing used was 75 × 150cm. Firstly, the seeds were germinated for 14 days in the Agrogene Bank, Faculty of Agriculture after which they were sow in the seedling tray at rate of one seed/stand before finally transplanted to rain shelter. Fertigation system containing stock solution of calcium nitrate and ferum ions (solution A) and (solution B) which has KNO_3, KH_2PO_4, $MgSO_4$, $MnSO_4$, $CuSO_4$, $ZnSO_4$, boric acid, ammonium molibdate were used as the fertilizer. Malathion was used to control aphid, Leaf miner and other pest of chill to ensure the chilli are safe pest damage.

Data Collection

Data on quantitative traits measured include days to flowering, days to maturity, plant height, fruits yield, fruit length, number of fruits per plant, disease score and leaf area using leaf area meter.

Data Analysis

Analysis of variance (ANOVA) was calculated for all the data of phenotypic traits using Statistical Analysis Software (SAS) version 9.1 (SAS Institute Inc., 2005) to determine the diversity in the genotypes. The mean, range, coefficient of variation (CV) standard deviation were equally calculated for each trait. Mean comparison was done using Least Significant Difference (LSD), whereas the heritability and variance components were calculated following the method of Falconer and Mackay (1996). Expected genetic advance as a percentage of the mean (GAM) was calculated using the method of Assefa et al. (1999), where the selection intensity (K) was assumed to be of 5%.

a. σ^2_G (Genotypic variance) = $(MS_G - MS_E)/r$, where MS_G = mean square of accession, MS_E = mean square of error, and r = number of replications

b. $\sigma_E^2 = MS_E$

c. σ^2_P (Phenotypic variance) = $(\sigma_G^2 + \sigma_E^2)$

d. PCV (Phenotypic coefficient of variation) = $\sqrt{\sigma^2_P} / \bar{X} \times 100$, where σ^2_P = phenotypic variance and $\bar{X}$ = mean of the trait

e. GCV (Genotypic coefficient of variation) = $\sqrt{\sigma^2_G} / \bar{X} \times 100$, where σ^2_G = genotypic variance and $\bar{X}$ = mean of the trait

f. h^2_B (Broad sense heritability) = $\frac{\sigma^2_G}{\sigma^2_P}$, where σ^2_G = genotypic variance and σ^2_P = phenotypic variance

g. Genetic advance, assuming selection intensity of superior accessions is 5% =

$$K \times \sqrt{\sigma^2 p} \times h^2{}_B$$

h. Genetic gain (GG) = $K \times \sqrt{\sigma^2{}_P} / \overline{X} \times h_B{}^2 \times 100$, where K =2.06, $\sqrt{\sigma^2{}_P} / \overline{X}$ is the phenotypic standard deviation, $h^2{}_B$ is the heritability, and X refers to the mean of the trait being evaluated.

Correlation coefficient used to measure the degree of association among different traits was calculated using PROC CORR of Statistical Analysis Software (SAS) version 9.1 (SAS Institute Inc., 2005).

Clustering analysis was carried out using NTSYS-PC version 2.1 (Rohlf, 2005) to group the accessions that are similar together, while the 2-dimentional principal component analysis was done to show the displacement of the accession from one another.

RESULTS

Genetic variability among the vegetative and yield traits

Great variability was observed in the yield and vegetative performance of the chilli plants (Table 1). The highest plant height recorded in week 2, 4, 6, 8, and 10 are 16.3, 36.8, 68.7 and 81.0 cm, respectively while the least height was recorded during these weeks were 9.8, 20.7, 37.7, 46.0 and 47.7 cm. The plant leaf area ranges from 440.9 (AC202) - 3668.6 cm^2 (AC012) with mean of 1917.1 cm^2. In days to flowering, the accession AC902 has the least while longest days to flowering was found in accession AC406 with 41.5 days and 33 days was found to be the mean. Similarly, days to maturity ranged from 74.7 days in AC304 to 84 days in accession AC703 with 77.5 days as the mean. Fruit yield per plant ranges from 592.3 g (AC813) to 8.3 g (AC002) with mean value of 207.2 g. In addition to this number of fruit per plant also varies from 76 in accession AC005 to 2 fruits/ plant in accession AC002. Percentage of disease score also ranged from 93% in AC202 to 29% in A0204.

Furthermore, analysis of means square for the phenotypic traits reveals that, effect of replicate was highly significant for all the traits measured (Table 2). This table equally revealed the effect of genotypes to be highly significant for all the phenotypic or morphological traits except for plant height at week 6 to 12 where the effect of genotypes was not significant.

Correlation analysis among the quantitative traits

Moreover, correlations among the quantitative traits varied significantly from negative to positive association (Fig.1). Plant heights recorded at different period of plant growth associated positively with one another. However, days to flowering and maturity period had no any relationship between each other. Fruit yield per plant associated positively with all other traits except for plant height at early stage where no relationships was observed and disease score which had highly significant negative association with the yield. Also, percentage disease score has a negative relationship with fruit length, number of fruits per plant and leaf area. Leaf area had positive and significant association with others except for days to maturity, days to flowering and plant height at 2 and 4 weeks.

Heritability estimate of vegetative and yield in *Capsicum annum* germplasm

From Table 3, it could be observed that wide differences were present between genotypic and phenotypic variance. Genotypic variance ranges from 2.06 (plant height at two weeks) to 565973.97 in leaf area, together with phenotypic variance which ranges 4.54 in plant height at 2 weeks to 825515.07 in leaf area. Most of the traits have moderate to large broad sense heritability value of more than 35% to 73.15% except for plant height from 6 till 12 weeks of age, days to maturity and numbers of fruit. Plant height at 8 and 10 weeks of age were found to have the least value of heritability (13.66%) while fruit length was found to have the largest heritability value of 73.15%. Low differences were observed between the phenotypic and genotypic coefficient of variation for most of the traits. These suggest that effect of environmental factors on the expression of these quantitative traits is low. The Genetic advance and genetic gain as expressed by the mean percentage of the genetic advance possessed high value which ranges from 30.39% -66.94% in traits like yield, number of fruits, fruit length, leaf area and disease score. Low genetic gains were observed in plant height, days to flowering and maturity.

Table 1: Mean value of quantitative traits for 30 *Capsicum annuum* genotypes

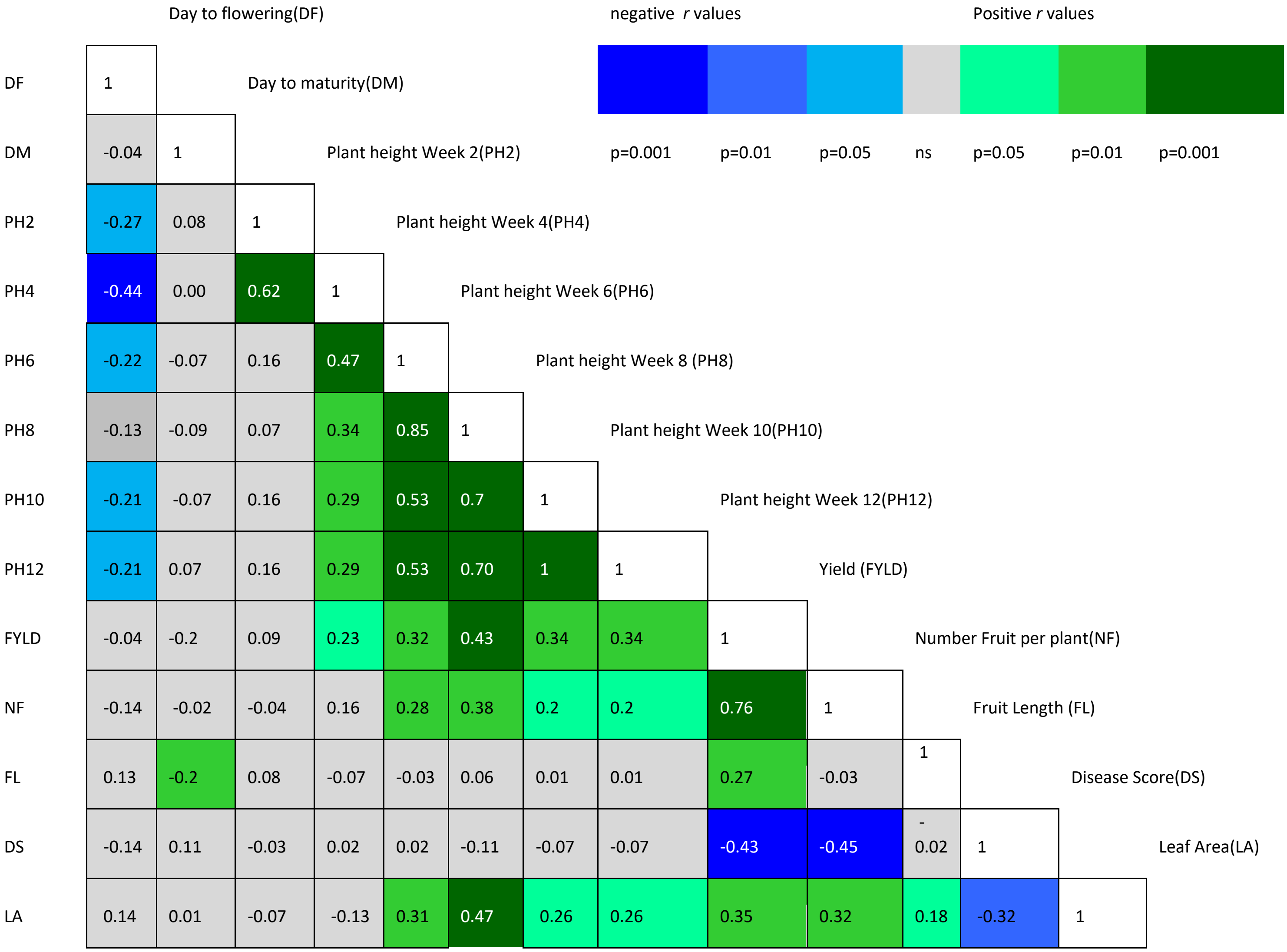
No.	Accessions	DF (days)	DM (Days)	PH W2 (cm)	PH W4 (cm)	PH W6 (cm)	PH W8 (cm)	PH W10 (cm)	PH 12 (cm)	Yield (g)	NF	FL (cm)	DS (%)	LA (cm2)
1	AC002	33.3	60.7	14.2	28.8	46.7	51.0	55.7	55.7	8.3	1.7	6.4	85.3	599.6
2	AC005	33.0	82.5	10.8	27.5	54.3	63.5	71.5	71.5	220.0	76.0	11.8	49.0	2603.3
3	AC010	32.3	77.7	12.1	29.7	46.7	55.3	64.3	64.3	166.7	47.3	9.5	73.0	677.7
4	AC012	35.0	86.3	16.1	32.7	54.0	62.7	72.0	72.0	328.0	70.7	13.0	53.7	3668.6
5	AC013	32.3	78.7	14.5	32.8	55.0	54.3	56.0	56.0	153.7	30.3	11.3	70.0	853.9
6	A0102	34.7	76.0	13.5	29.3	44.7	52.7	55.7	55.7	190.0	24.7	12.7	62.3	2456.9
7	A0201	31.7	76.7	15.0	29.3	44.0	49.0	73.7	73.7	70.0	11.3	10.7	72.0	612.6
8	A0202	33.0	80.0	11.8	30.3	48.0	50.3	59.7	59.7	160.7	17.0	12.8	93.0	440.9
9	AC203	32.0	76.3	12.8	33.0	60.3	68.7	72.7	72.7	460.0	52.7	17.4	92.3	2099.9
10	AC303	31.0	76.3	16.3	32.2	49.7	55.3	63.7	63.7	211.7	11.0	17.5	86.0	2126.2
11	AC304	34.0	74.7	10.4	21.0	37.7	46.3	58.3	58.3	148.9	18.3	13.0	61.7	2492.2
12	AC406	41.5	76.5	9.8	20.8	40.5	51.0	54.0	54.0	200.0	12.0	16.0	69.5	2540.3
13	AC510	34.7	76.7	13.2	27.8	43.7	49.0	55.0	55.0	119.3	16.0	14.6	57.0	1855.3
14	AC606	36.0	76.7	10.8	20.7	42.5	50.7	56.7	56.7	291.0	21.0	15.0	70.7	2680.8
15	AC607	34.0	79.3	12.2	26.0	49.0	50.7	54.3	54.3	145.5	31.0	12.0	60.7	1611.7
16	AC702	32.0	76.0	14.1	29.8	44.7	51.3	61.3	61.3	207.3	47.3	11.7	40.7	2233.5
17	AC801	30.7	74.3	15.2	31.0	50.7	53.7	61.7	61.7	195.0	19.0	13.4	80.7	1547.5
18	AC804	33.7	78.3	16.5	30.3	44.3	46.7	47.7	47.7	206.7	11.7	13.7	29.0	1982.8
19	AC805	33.3	78.0	11.5	28.7	59.0	65.3	59.0	59.0	186.2	49.3	10.0	54.7	3332.2
20	AC904	33.3	76.3	15.0	36.8	52.7	62.0	69.0	69.0	449.7	67.3	12.9	46.0	2452.4
21	AC909	33.0	80.0	13.0	32.1	43.0	46.0	55.5	55.5	161.5	12.0	16.2	73.5	1103.9
22	AC701	32.7	79.7	12.4	29.2	51.0	56.7	63.7	63.7	171.3	45.7	12.0	75.3	2296.2
23	AC703	30.3	84.0	14.0	28.8	52.7	62.7	67.7	67.7	56.9	10.3	12.3	78.0	2849.3
24	AC805	33.3	76.7	13.5	29.5	52.7	55.3	56.0	56.0	175.7	17.3	15.5	65.0	1195.2
25	AC806	31.0	76.5	14.4	31.5	45.0	52.5	59.0	59.0	69.5	8.0	13.8	85.5	1722.5
26	AC810	32.3	79.0	13.2	31.0	46.0	53.3	62.0	62.0	71.2	6.7	10.3	68.3	1148.7
27	AC813	32.3	75.0	14.8	35.2	53.0	62.5	81.0	81.0	592.3	65.3	9.7	42.0	1813.9
28	AC901	33.7	80.3	12.6	30.7	50.7	53.0	54.3	54.3	53.7	12.7	7.6	90.0	2264.5

29	AC902	30.0	80.0	15.6	36.3	52.0	54.3	65.7	65.7	226.9	36.7	12.4	82.0	1833.4
30	AC905	32.7	76.3	13.7	29.2	54.7	60.3	73.0	73.0	459.3	47.7	13.4	35.7	2517.3
	mean	33.0	77.5	13.5	29.8	49.1	54.9	62.1	62.1	207.2	30.1	12.5	66.6	1917.1
	CV (%)	7.4	12.4	15.8	14.5	15.5	16.1	18.7	18.7	86.6	103.9	23.1	33.0	47.7
	Standard error	0.3	1.0	0.2	0.5	0.8	1.0	1.2	1.2	19.4	3.4	0.3	2.4	98.6
	LSD (p=0.05)	3.2	17.5	2.7	4.2	n.s	n.s	n.s	n.s	227.6	41.7	2.8	26.4	861.3

Note: DF= day to flowering, DM= day to maturity, PHW= plant height week, NF= number fruit per plant, FL= fruit length, DS= disease score, LA= leaf area, ns= not significant

Table 2: Mean squares of all phenotypic traits for 30 accessions *C. annuum*

Source of variation	**d.f**	**Day to flowering (days)**	**Day to maturity (days)**	**Plant height Week 2 (cm)**	**Plant height Week 4 (cm)**	**Plant height Week 6 (cm)**	**Plant height Week 8 (cm)**	**Plant height Week 10 (cm)**	**Plant height Week 12 (cm)**	**Yield (g)**	**Number Fruit per plant**	**Fruit Length (cm)**	**Disease Score (%)**	**Leaf Area (cm2)**
Blocks	2	1.98**	294.32**	0.65**	20.80**	75.25^{ns}	5.61^{ns}	83.58^{ns}	83.58^{ns}	102650.55**	6283.39**	2.60**	1359.95**	171001.51**
Genotypes	29	10.76**	51.30**	8.66**	42.00**	2405.12^{ns}	101.90^{ns}	171.24^{ns}	171.24^{ns}	53649.96**	1295.66**	19.21**	870.34**	1957463.49**
Error	54	3.63	106.76	2.48	6.03	45.66	68.88	116.13	116.13	18121.51	609.23	2.76	243.34	259541.09



negative *r* values | Positive *r* values

p=0.001	p=0.01	p=0.05	ns	p=0.05	p=0.01	p=0.001

	Day to flowering(DF)	Day to maturity(DM)	Plant height Week 2(PH2)	Plant height Week 4(PH4)	Plant height Week 6(PH6)	Plant height Week 8 (PH8)	Plant height Week 10(PH10)	Plant height Week 12(PH12)	Yield (FYLD)	Number Fruit per plant(NF)	Fruit Length (FL)	Disease Score(DS)	Leaf Area(LA)
DF	1												
DM	-0.04	1											
PH2	-0.27	0.08	1										
PH4	-0.44	0.00	0.62	1									
PH6	-0.22	-0.07	0.16	0.47	1								
PH8	-0.13	-0.09	0.07	0.34	0.85	1							
PH10	-0.21	-0.07	0.16	0.29	0.53	0.7	1						
PH12	-0.21	0.07	0.16	0.29	0.53	0.70	1	1					
FYLD	-0.04	-0.2	0.09	0.23	0.32	0.43	0.34	0.34	1				
NF	-0.14	-0.02	-0.04	0.16	0.28	0.38	0.2	0.2	0.76	1			
FL	0.13	-0.2	0.08	-0.07	-0.03	0.06	0.01	0.01	0.27	-0.03	1		
DS	-0.14	0.11	-0.03	0.02	0.02	-0.11	-0.07	-0.07	-0.43	-0.45	-0.02	1	
LA	0.14	0.01	-0.07	-0.13	0.31	0.47	0.26	0.26	0.35	0.32	0.18	-0.32	1

Fig. 1: Correlation coefficient of vegetative and yield traits for 30 accessions of *C. annuum*

Note: r= correlation coefficient (i.e. the number in each box)

Table 3: Heritability component and broad sense heritability

Phenotypic traits	mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	$h^2_{B\,(\%)}$	GA	GG (%)
Day to flowering (days)	33	2.38	6.01	4.67	7.43	39.57	2.00	6.06
Day to maturity (days)	77.5	6.55	19.27	3.30	5.66	33.99	3.07	3.97
Plant height Week 2 (cm)	13.5	2.06	4.54	10.63	15.78	45.37	1.99	14.75
Plant height Week 4 (cm)	29.8	11.99	18.02	11.62	14.24	66.54	5.82	19.53
Plant height Week 6 (cm)	49.1	12.43	58.09	7.18	15.52	21.39	3.36	6.84
Plant height Week 8 (cm)	54.9	11.01	79.89	6.04	16.28	13.78	2.54	4.62
Plant height Week 10(cm)	62.1	18.37	134.50	6.90	18.68	13.66	3.26	5.26
Plant height Week 12(cm)	62.1	18.37	134.50	6.90	18.68	13.66	3.26	5.26
Yield (g)	207.2	11119.14	29917.37	50.89	83.48	37.17	132.44	63.92
Number Fruit per plant	30.1	211.17	841.92	48.28	96.40	25.08	14.99	49.80
Fruit Length (cm)	12.5	4.71	6.44	17.36	20.30	73.15	3.82	30.59
Disease Score (%)	66.6	209.00	452.34	21.71	31.93	46.20	20.24	30.39
Leaf Area (cm2)	1917.1	565973.97	825515.07	39.24	47.39	68.56	1283.22	66.94

Note: σ^2g= Genotypic variance, σ^2p= phenotypic variance, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, h^2_B (%) = Broad sense heritability, GA = Genetic advance (measured in unit of each trait), GG (%) = Genetic gain

Clustering analysis

Cluster analysis using the phenotypic data grouped the 30 accessions into eight major groups at the genetic distance of 4.07 (Fig. 2). Cluster V, has the highest members of 17 accessions, followed by cluster III cluster VIII and cluster II with four, three and two membership accessions respectively. The other clusters comprise of one accession each (Table 4 and 5). Cluster IV, had the highest mean yield (460 g), followed by cluster III (457.33 g), while the cluster with least mean yield of *C. annum* was found to be cluster I with 8.33g as the mean yield per plant (Table 6). Cluster IV also got the highest mean fruit length (17.43 cm), followed by cluster VIII (14.67 cm) and cluster VII (13.7 cm) respectively. In terms of disease infestation percentage, cluster IV had highest (85.33%), followed by cluster I (85.33%) while cluster VII had the least disease infestation percentage of 29%.

Principal component analysis

From the principal component analysis (Table 6), the first three components contributed a total of 68.1%. Variables such as yield, number of fruits and leaf area and plant height from the age of 6 to 12 weeks contributed positively to the first principal components while disease score contributed negatively to this component. Also, at the second principal, plant height from the age of 2 to 4 weeks, days to maturity and disease score contributed positively while days to flowering, number of leaves, number of fruits, yield and leaf area contributed negatively. In the third principal component, days to maturity, plant height at 2 and 4 weeks of age, number of leaves and yield contributed negatively to this component, while all other variables except for plant height at 10 and 12 weeks contributed positively. In the third principal component, days to flowering and maturity, plant height at 2 and 4 weeks, number of fruits and leaf area contributed negatively while number of leaves and disease score contributed positively to this component.

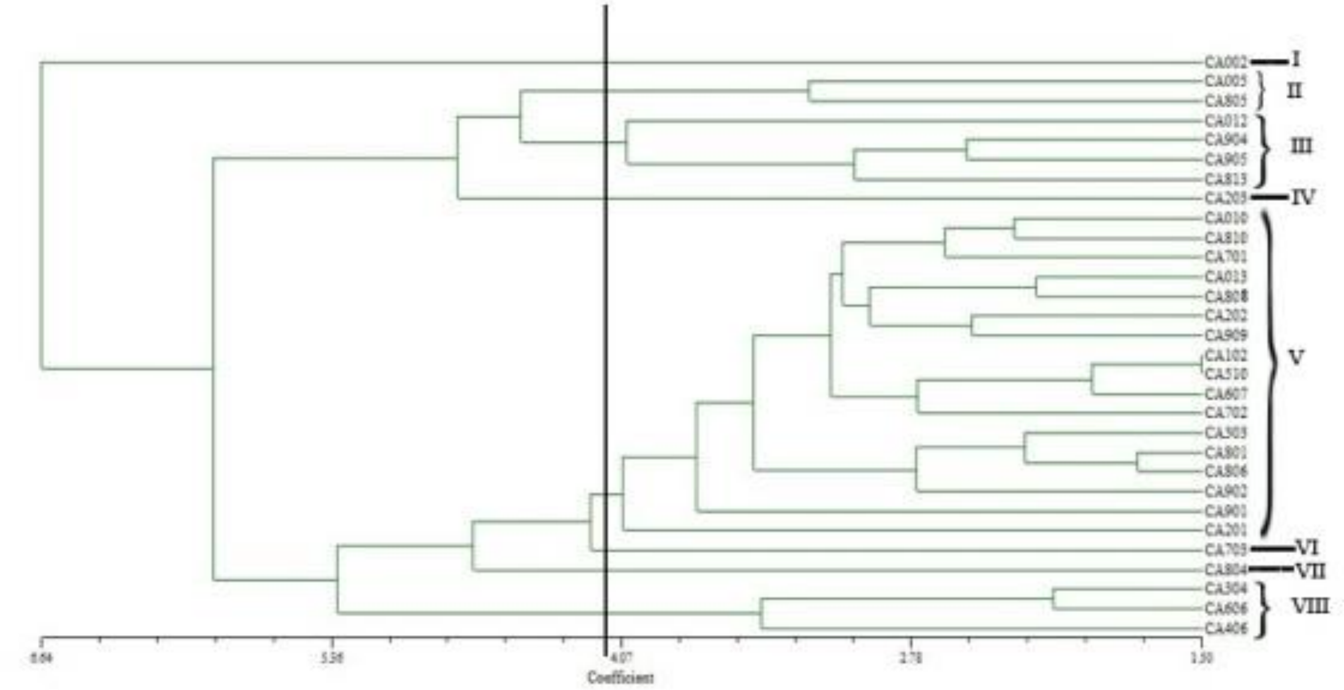


Fig. 2. Dendrogram showing clustering patterns 30 *C. annuum* accessions based on quantitative traits

Table 4: Cluster number and the members of the clusters

Cluster	Number	Accessions
I	1	AC002
II	2	AC005, AC805
III	4	AC012, AC904, AC905, AC813
IV	1	AC203
V	17	AC010, AC810, AC701, AC013, AC808, AC202, AC202, AC909, AC102, AC510, AVPP0607, AC702, AC303, AC801, AC806, AC902, AC901, AC201
VI	1	AC703
VII	1	AC804
VIII	3	AC304, AC606, AC406

Table 5: Mean value of quantitative traits for each cluster

Traits	I	II	III	IV	V	VI	VII	VIII
Day to flowering (days)	33.33	33.17	33.33	32.00	32.49	30.33	33.67	37.17
Day to maturity (days)	60.67	80.25	78.50	76.33	77.87	84.00	78.33	75.94
Plant height Week 2 (cm)	14.23	11.13	14.88	12.83	13.68	14.00	16.47	10.33
Plant height Week 4 (cm)	28.83	28.08	33.46	33.00	30.51	28.83	30.33	20.81
Plant height Week 6 (cm)	46.67	56.63	53.58	60.33	48.02	52.67	44.33	40.23
Plant height Week 8 (cm)	51.00	64.42	61.88	68.67	52.52	62.67	46.67	49.33
Plant height Week 10 (cm)	55.67	65.25	73.75	72.67	60.09	67.67	47.67	56.33
Plant height Week 12 (cm)	55.67	65.25	73.75	72.67	60.09	67.67	47.67	56.33
Yield (g)	8.33	203.08	457.33	460.00	149.98	56.87	206.67	213.30
Number Fruit per plant	1.67	62.67	62.75	52.67	23.18	10.33	11.67	17.11
Fruit Length (cm)	6.43	10.89	12.23	17.43	12.59	12.27	13.70	14.67
Disease Score (%)	85.33	51.83	44.33	92.33	72.65	78.00	29.00	67.28
Leaf Area (cm2)	599.59	2967.73	2613.03	2099.85	1528.26	2849.27	1982.84	2571.11

Table 6: Principal component analysis and percentage variation

Variables			PC1	PC2	PC3	PC4
Variation (%)			37.9	19.0	11.4	
Days to flowering			-0.183	-0.474	0.112	-0.026
Days to maturity			-0.005	0.208	-0.593	-0.103
Plant height @ week 2			0.158	0.371	-0.353	-0.307
Plant height @ week 4			0.277	0.388	-0.195	-0.121
Plant height @ week 6			0.352	0.092	0.207	0.178
Plant height @ week 8			0.389	-0.084	0.237	0.228
Plant height @ week 10			0.390	0.019	0.000	0.120
Plant height @ week 12			0.390	0.019	0.000	0.120
Yield			0.331	-0.270	-0.296	0.012
Number of fruits			0.368	-0.225	0.119	-0.155
Number of leaves			-0.047	-0.185	-0.476	0.516
Disease score			-0.127	0.320	0.163	0.690
Leaf area	0.151	-0.410	0.136	-0.026		

DISCUSSION

The presence of genetic variability in yield and vegetative plant traits as observed in this experiment is essential for successful breeding and improvement program. Its presence will give wide room for genetic exploitation, selection, introduction of desirable genes into the germplasm. This observation follows suite to what was earlier observed in Ethiopia as reported by Marame *et al.* (2009) in his genetic diversity study on 78 genotypes of *C. annuum* using seven quantitative traits. He reported that wide variabilities and highly significant differences were observed in all these traits (days to maturity, fruit length, single fruit weight and dry fruit yield per plant) except for number of branches per plant in which non-significant different was observed. This result, that is presence of variabilities in yield and vegetative traits was also supported by finding from previous research in Bangladesh, India and Turkey on chili improvement program (Alam *et al.,* 2024; Aktas *et al.,* 2006; Singh *et al.,* 2009). Additionally, variabilities in the flavonoids and carotenoids contents of chilli have been reported (Naseem *et al.,* 2024). This occurred as a result of differences in genotypes and developmental stages of the plant.

The presence of positive and significant relationship among the yield components traits (numbers of fruit, fruit weight, fruit length etc.) suggests that, improvement on any of these traits will bring about simultaneous improvement in other quantitative yield traits. This observation is in line with finding of Safavi (2011) and Suraj *et al.* (2024) in their study on different genotypes of poplar clones and chili germplam respectively. It was observed that selection based on blade length will automatically improve Plant height. Similar observation was reported by Zeng *et al.* (2007) in their study on the improvement of cotton yield. This phenomenon implies that, continuous improvement in fruit weight will bring about greater yield compensation. High broad sense heritability as seen in some quantitative traits in this study implies that, these characters can be passed from one generation to another (Imani *et al.,* 2021; Zewdu *et al.,* 2024). High heritability and genetic advance are vital and important attributes for realizing high selection gain in any plant breeding and improvement program. In India, high broad sense heritability of more than 90% for plant height, numbers of fruit, fruit length, seed weight in different genotypes of chilli (Sreelathakumary and Rajamony, 2004). In addition, Ben-chaim *et al.* (2000) also observed high narrow sense and broad sense of about 95 in fruit length, fruit diameter fruit weight in *C. annum* inbred lines. Narrow differences between phenotypic and genotypic coefficient of variation for some of the traits like fruit length, leaves area, disease score showed that influence of biotic and abiotic environmental factors on the expression of these traits is low. This low difference increases the chance of high selection gain. This observation agreed with the finding of Kole *et al.* (2008) in their study conducted on genetic variability of mutants of aromatic non-basmati rice. The presence of moderate to high broad sense heritability and high genetic advance as a percentage of mean (genetic gain) as reported in this research suggest high additive gene effect and this will bring about high and effective selection.

Clustering analysis based on quantitative traits that grouped 30 accessions into eight clusters as showed in the dendrogram. The dendrogram tends to grouped some of the accessions with similar morphological traits into the same cluster. No differentiation based on geographical background of these accessions was observed. Lahbib *et al.* (2012) has reported that no classification as a result of geographical origin was observed when eleven accessions of land race *C. annum* clustered into three groups in his study on genetic diversity of pepper collected from different environment in Tunisia. Also, Bozokalfa *et al.* (2009) observed that no classification based on geographical origin during the clustering analysis of 48 genotypes of chilli based on 67 agro-morphological traits.

Furthermore, it has been reported that the first two principal component axes accounted for 84.32% of the total variation observed in germplasm comprising 45 Chilli genotypes (Farhad *et al.,* 2010). Traits such as plant height, seed fruits, and number of secondary branches are responsible for the divergence in the first axis, while variability in the second axis where caused by days to flowering and plant height, respectively.

CONCLUSION

In conclusion, chili genotypes such as CA813, CA904, CA905, and CA203 from cluster III and IV, respectively, have been identified as potential high-yielding materials based on their quantitative traits. These materials are recommended for further field evaluation before the commencement of the selection and hybridization programme.

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