Research Article

Biodiversity Estimation in Chilli (*Capsicum frutescens*) Germplasm through Morphological Traits

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Abstract | *Capsicum frutescens,* one of the domesticated species of pepper grown around the globe, is considered to be highly valued horticultural crop due to high productivity and intense aroma. The present study was carried out to evaluate genetic diversity among 78 selected genotypes of *Capsicum frutescens* through morphological attributes. The diversity assessment based on morphological attributes indicated maximum fruit weight was gained in genotype AZRI-Selection-10-B (2.82 ± 0.26 g), maximum fruit length was observed in genotype Super-Hot F1 (6.79 ± 0.52 cm), however maximum fruit diameter was recorded in genotypes 36563 (26.42 ± 1.93 mm), maximum pedicle length was measured in genotype KP Local (4.27 ± 0.82 cm), maximum plant height was gained in genotypes AZRI-Selection-06-1C (71.35 ± 4.63 cm), while maximum yield per plant was calculated in genotypes Sky Line 2 (325.95 ± 19.48 g), maximum number of leaves per plant were counted in genotypes AZRI-Selection-02-A2 (516.91 ± 22.29), however maximum leaf area was recorded in genotypes Kot Sultan (62.24 ± 2.14 cm^2), the maximum time took to flower was observed in genotype 37032 (66.0 ± 2.50 days), while maximum time took to ripen fruit was observed in genotypes CKD 2204 (57.0 ± 2.00 days), the maximum relative leaf chlorophyll content (SPAD value) was measured in genotypes Zenia F1 (45.88 ± 0.92) and maximum number of stomata per unit area (mm^2) was counted in 32344 (41.00 ± 0.16). The data based on morphological traits was analyzed in multivariate analysis. Cluster analysis indicated that 78 genotypes were grouped into five clusters where cluster-I comprised of (19) genotypes, cluster-II contain (8) genotypes, cluster-III contain (21) genotypes, cluster-IV contain (6) genotypes and cluster-V contain (24) genotypes. PCA analysis based on first two components for morphological attributes of *Capsicum frutescens* genotypes explained (39.62 %) variability.

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Introduction

Capsicum peppers are considered one of the oldest domesticated plants in the world (Kraft *et al.*, 2014). *Capsicum* has its use since the beginning of civilizations. The name *Capsicum* may have been derived from Greek word "Kapso" meaning to bite, in reference to its spiciness, or from the Latin "Capsa"

referring to the fruit pod (Govindarajan, 1985). The taxonomists used the word *Capsicum* for the genus, the term "pepper" originated from "red pepper". This name was given by Columbus for a colorful red fruit named "aji" by the inhabitants of the New World. He found that this product was much stronger compared to the black pepper of Asia. He brought fruit samples, returned to Spain and called it "red pepper" (Govindarajan, 1985). These are native to South and Central America and belong to family Solancaeae. Spanish and Portuguese traders distributed the *Capsicum frutescens* and *Capsicum annuum* in the sixteenth century from the New World to other continents; afterwards these became the essential food part of various countries (Gurnani *et al*., 2016). The wild and primitive species have thin flesh, seeded fruit and small in size that helped in dissemination by birds and animals (Lippert *et al*., 1966).

The genus *Capsicum* consist of 25 wild and 5 domesticated spp. (*Capsicum annuum, Capsicum pubescens, Capsicum baccatum, Capsicum frutescens* and *Capsicum chinense*) containing more than 200 varieties (Conforti *et al*., 2007). Varieties are named on the basis of location and type, so common names of pepper are chilli, red pepper, bell pepper or only pepper (Faustino *et al*., 2007). For grouping and categorization of different pepper genotypes various morphological characters are used such as plant height, fruit shape, fruit weight and flower color (Fonseca *et al*., 2008). Phenotypic characterization is important trait for grouping the germplasm in every characterization program (Tyler *et al*., 2014). However, studies have revealed that the morphological characterization of *Capsicum* is simple and common method of identifying differences among genotypes, but highly affected by environmental factors and is not capable to differentiate closely related genotypes (Gilbert *et al*., 1999; Saqib and Anjum, 2021). Therefore, Oh *et al*. (2012) reported that morphological characterization with molecular markers has been confirmed to be independent of environmental factors.

Materials and Methods

These studies were conducted during 2017-20 at the experimental field of Department of Horticulture, Faculty of Agricultural Sciences and Technology (FA and ST), Bahauddin Zakariya University (BZU), Multan, Pakistan. The seedlings were transplanted every year for crop establishment. Diversity was assed among 78 genotypes (Table 1) of *Capsicum frutescens* based on following morphological attributes.

Table 1: *Genotypes of Capsicum frutescens and their origin.*

Genotypes	origin
Shakti, Sky Line 2, Hot pepper Sky Red, Hot Red, D91, Hot Queen F1, Amber F1, Red Giant F1, Hot Queen, Rainbow, Advanta 509, Sky Star 4 F1, Sky Red, Sky Line 3, CKD 2204, 1130 F1, High Fly 2, Super-Hot F1, Chandar Mukhi, HHP-091A, Zenia F1, HHP-082B, ARI S2, BSS-410	Vegetable seed market Multan
AZRI-Pr-20530-01, AZRI-Selection-06-1C, AZRI-Selection-10-B, AZRI-AVPP-9704-4, AZRI-AVPP-1346-D, AZRI-Selection-02-A2, AZRI-Selection-05-C-01B, AZRI-Selection-09, AZRI-Selection-03-03B, AZRI-Pr-16162-A, AZRI-Selection-09-B, AZRI-Selection-01-B2, AZRI-I-A-20B, AZRI-Selection-04-C1, AZRI-Selection-07-A1	PARC AZRI ,Umerkot
DG 2	DG khan
Ghotki	Ghotki
Tota Pari	Multan
Talhari	Talhar
KP local	Kahror Pacca
HIS-74, IHS 64, IHS 75	Institute of Horticultural Sciences, UAF
LD 1	Lodhran
BWP-01	Bahawalpur
Koth sultan	Kot sultan
32332, 36648, 32350, 37028, 32324, 36560, 33830, 36569, 32319, 32395, 32344, 36698, 32330, 33828, 32336, 32355, 36558, 32385, 32326, 32390, 32405, 32333, 36563, 32328, 37032, 32335, 32331, 30880	PGRI, PARC, Islamabad

The studies were laid out under Randomized Complete Block Design (RCBD) with five replications. After washing and surface sterilization seeds of each genotype were sown in pots, filled with mixture of sand and silt (1:1) as described by Gungor and Yildirim (2013). After completion of germination, the seedlings were supplemented with 2% NPK (20-20-20) solution (Islam *et al*., 2015). The selected area for transplanting the seedlings was prepared by deep ploughing and rotavator for fine soil texture. After final preparation of land, the ridges were prepared with a tractor driven ridger, maintaining 60 cm distance between the ridges (Islam *et al*., 2015). The seedlings of 45 days were uprooted carefully from the pots, before uprooting of seedlings, light irrigation was applied to avoid damage to roots of seedlings. The roots of the seedlings were dipped in 2% solution of carbendazim for five minutes and transplanted on top of ridges in standing water conditions. As regards the planting geometry, 30 cm plant to plant and 60 cm ridge-to-ridge distances were maintained during transplanting. Ten plants of each genotype were transplanted in each replication. For the morphological characterization following parameter were studied fruit weight (g), fruit length (cm), fruit diameter (mm), pedicle length (cm), plant height (cm), yield per plant (g), leaf density, leaf area (cm^2), time of flower (days), time to ripe fruit (days), relative leaf chlorophyll content (SPAD value) was measured with digital chlorophyll meter and number of stomata per unit area (mm^2) as explained by (Ngouajio *et al*., 2003; Hallidri, 2001; Padrón *et al*., 2016). The data based on morphological traits were analyzed in multivariate analysis.

Results and Discussion

The genus *Capsicum* includes around 38 described species, with great morphological variation, mainly in terms of fruit color, size and shape. In current study, 78 genotypes of *Capsicum frutescens* were evaluated on basis of following morphological traits fruit weight (g), fruit length (cm), fruit diameter (mm), pedicle length (cm), plant height (cm), yield per plant (g), leaf density, leaf area (cm^2), time of flower (days), time to ripe fruit (days), relative leaf chlorophyll content (SPAD value) and number of stomata per unit area (mm^2). The minimum fruit weight was measured in genotype 32385 (0.77 ± 0.12 g) while maximum fruit weight gained in genotypes AZRI-Selection-10-B (2.82 ± 0.26 g) as mentioned in Table 2. The findings of current study are in line with those of Obidiebube *et al*. (2012) who found the maximum fruit weight (1.9 g) in "Magura" among other five genotypes of Capsicum frutescens. Fourteen genotypes of Capsicum annuum were collected from Malaysia and Taiwan to estimate biodiversity, there was significant variation among the genotypes on the basis of fruit weight (Ridzuan *et al*., 2019). In another study, 38 genotypes were used for characterization on the basis of morphological attributes including fruit weight; the average value of fruit weight ranged from 0.85 to 8.30 g (Khan *et al*., 2020). The minimum fruit length was measured in genotype 32385 (1.21 ± 0.14 cm), while maximum fruit length was observed in genotype KP Local (4.27 ± 0.82 cm). Constantino *et al*. (2020) used 22 genotypes of *Capsicum baccatum* for evaluation based on morphological, biochemical and molecular traits. Among morphological attributes, fruit length was highly divergent which ranged from 1.66 to 11.10 cm. Morphological characters of 90 *Capsicum frutescens* genotypes were investigated by Yamamoto and Nawata (2004) who grouped all the genotypes in four clusters on the basis of fruit length. The average fruit length was diversified in each cluster with maximum fruit length of 42.38 ± 1.45 mm.,

Minimum fruit diameter was measured in genotype Hot Queen F1 (10.89 ± 0.74 mm) while maximum was in genotype, 36563 (26.42 ± 1.93 mm). Yumnam *et al*. (2012) estimated genetic diversity among 56 genotypes based on morphological and molecular attributes. In their findings, the fruit diameter ranged from 0.6 to 4.54 cm. However, minimum pedicle length was measured in genotype 32385 (1.21 ± 0.14 cm), while maximum was in genotype KP Local (4.27 ± 0.82). Eight genotypes were studied for morphological characterization; pedicel length ranged from 1.5 to 3.8 cm among the genotypes (Costa *et al*., 2019)

Short statured plants were observed in genotype D91 (23.69 ± 0.34 cm), however maximum plant height was observed in genotype AZRI-Selection-06-1C (71.35 ± 4.63 cm). These findings are in accordance with Chowdhury *et al*. (2015) who used four cultivars (Magura, Kajoli, Vaduria and Bogra Morich) of chilli and found that Magura cultivar had the maximum height of 92.5 cm. The maximum red fruit of chilli was obtained in genotype Sky Line 2 genotypes (325.95 ± 19.48 g), while genotype 32331 yielded (85.86 ± 5.58 g) per plant. The fruit yield per plant ranged from

195 to 993.33 g in CHIVAR-8 genotype (Barche and Nair, 2014).

Table 2: *Summery of morphological characters.*

Parameters	Genotypes	Mean value
Fruit weight (g)	32385	0.77 ± 0.12
	AZRI-Selection-10-B	2.82 ± 0.26
Fruit length (cm)	AZRI-Selection-06-1C	2.29 ± 0.17
	Super-Hot F1	6.79 ± 0.52
Fruit diameter (mm)	Hot Queen F1	10.89 ± 0.74
	36563	26.42 ± 1.93
Pedicle length (cm)	32385	1.21 ± 0.14
	KP Local	4.27 ± 0.82
Plant height (cm)	D91	23.69 ± 0.34
	AZRI-Selection-06-1C	71.35 ± 4.63
Yield per plant (g)	32331	85.86 ± 5.58
	Sky Line 2	325.95 ± 19.48
Leaf density (number)	Kot Sultan	97.31 ± 12.33
	AZRI-Selection-02-A2	516.91 ± 22.29
Leaf area (cm^2)	AZRI-Selection-03-03B	6.71 ± 0.45
	Kot Sultan	62.24 ± 2.14
Time of flower (days)	32319	42.0 ± 1.00
	37032	66.0 ± 2.50
Time to ripe fruit (days)	36698	37.0 ± 2.00
	CKD 2204	57.0 ± 2.00
Relative leaf chlorophyll content (SPAD value)	D91	11.18 ± 0.61
	Zenia F1	45.88 ± 0.92
Number of stomata per unit area (mm^2)	32330	3.67 ± 0.24
	32344	41.00 ± 0.16

Lowest number of leaf was counted in genotype Kot Sultan (97.31 ± 12.33), however maximum number of leaves were counted in genotype AZRI-Selection-02-A2 (516.91 ± 22.29). Bhargava *et al.* (2019) evaluated diversity among 13 genotypes of vegetable chenopodium. Based on morphological and qualitative attributes, they concluded that significant variation regarding number of leaves per plant existed and leaf number ranged from 10.20 to 28.94 per plant. The maximum leaf area was observed is genotype Kot Sultan (62.24 ± 2.14 cm^2), while smaller leaf area exhibited in genotypes AZRI-Selection-03-03B (6.71 ± 0.45 cm^2). Time of flowering is very important farmer point of view, earliest flowering was observed in genotype 32319 (42.0 ± 1.00 days) while late flowering was exhibited in genotype 37032 (66.0 ± 2.50 days). The maximum number days took to ripe fruit was recorded in genotype CKD 2204 (57.0 ± 2.00 days), while minimum days too to fruit was recorded in genotype 36698 (37.0 ± 2.00 days).

Capsicum frutescens genotypes were evaluated on the basis of relative leaf chlorophyll content (SPAD value), results depicted that highest relative leaf chlorophyll content was recorded in genotype Zenia F1 (45.88 ± 0.92 SPAD value), while minimum in genotype D91 (11.18 ± 0.61 SPAD value). The maximum number of stomata per unit area (mm^2) were counted in genotype 32344 (41.00 ± 0.16), while minimum number of stomata were counted in genotype 32330 (3.67 ± 0.24). Usman *et al.* (2015) among 36 genotypes of *Capsicum annuum*, based on morphological and biochemical attributes. Results indicated that leaf chlorophyll content ranged from 4.54-11.93 SPAD value.

Cluster analysis based on quantitative analysis

Dendrogram (Ward linkage, Pearson distance) was constructed based on morphological characters of 78 genotypes of *Capsicum frutescens*, which divided these genotypes into five major clusters while truncated at 0.24 (24 %) similarity (Figure 1). According to dendrogram clustering pattern, Cluster 1 consisted of 19 genotypes (D91, Ghotki, Hot Red, 36563, Sky Line 3, Sky Line 2, Hot Pepper Sky Red, Zenia F_1, Sky Red, Sky Star 4 F1, 1130 F_1, Adventa 509, 32350, 32385, 32326, AZRI-I-A-20B, 30880, Red Gaint F_1 and CKD 2204) which represented 24.23% of the total gene pool. In cluster 1, two genotypes 32385 and 32326 were very close to each other as maximum similarity was observed in their morphological attributes. Cluster one was divided into two groups i.e. group 1 consisted of D91, Ghotki, Hot Red, 36563, Sky Line 3, Sky Line 2 and Hot Pepper Sky Red genotypes, while group 2 comprised of Zenia F_1, Sky Red, Sky Star 4 F1, 1130 F_1, Adventa 509, 32350, 32385, 32326, AZRI-I-A-20B, 30880, Red Gaint F_1 and CKD 2204 genotypes.

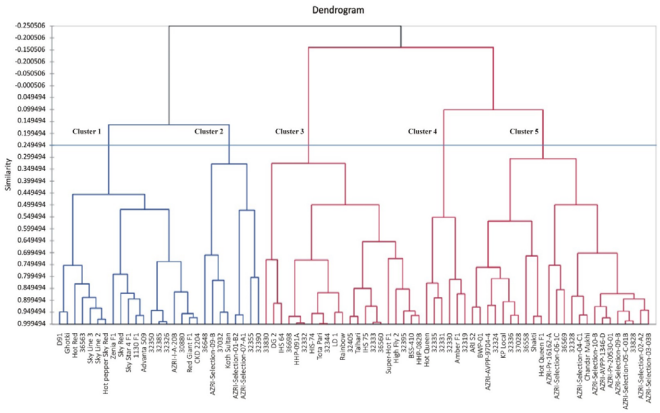

Figure 1: *Dendrogram showing relationship among 78 genotypes of Capsicum frutescens based on morphological attributes.*

Cluster 2 consisted of 08 genotypes 36648, AZRI-Selection-09, 37032, Kot Sultan, AZRI-Selection-01-B2, AZRI-Selection-07-A1, 32355 and 32390 which represented 10.25% of total genotypes. Genotypes AZRI-selection-01-B2 and AZRI-selection-07-A1 stood very close to each other; while the maximum similarity was shown among 08 genotypes of this Cluster 2. Based on similarity, Cluster 2 is divided into two subgroups i.e. group 1 contained 36648, AZRI-Selection-09, 37032 and Kot Sultan genotypes, while group 2 consisted of AZRI-Selection-01-B2, AZRI-Selection-07-A1, 32355 and 32390 genotypes.

Cluster 3 consisted of 21 genotypes 33830, DG 2, ISH-64, 36698, HHP-091A, 32332, IHS-74, Tota Pari, 32344, LD 1, Rainbow, 32405, Talhari, IHS 75, 32333, 36560, Super Hot F1, High Fly 2, 32395, BSS-410 and HPP-082B which comprised of about 26.92% of total genotypes. Within this cluster two genotypes Tota Pari and 32344 and also two genotypes HHP-091A and 32332 showed the maximum similarity with each other. Further, Cluster 3 was divided into three groups i.e. group 1 consisted 33830, DG 2 and IHS-64. Group 2 comprised of 36698, HHP-091A, 32332, IHS-74, Tota Pari, 32344, LD 1 and Rainbow, while group 3 consisted of 32405, Talhari, HIS-75, 32333, 36560, Super Hot F1, High Fly 2, 32395, BSS-410 and HPP-082B.

Cluster 4 comprised of 06 genotypes (Hot Queen, 32335, 32331, 32330, Amber F_1 and 32319). This cluster was the smallest cluster which shared 7.69% of total genotypes used in this study. Two genotypes 32335 and 32331 were closer to each other within Cluster 4 as the maximum similarity was observed among morphological characters of these two genotypes.

Cluster 5 was the largest cluster among five clusters as it comprised of 24 genotypes (ARI S2, BWP-01, AZRI-AVPP-9704-4, 32324, KP Local, 32336, 37028, 36558, Shakti, Hot Queen F1, AZRI-Pr-16162-A, AZRI-Selection-06-1C, 36569, 32328, AZRI-Selection-04-C1, Chandar Mukhi, AZRI-selection-10-B, AZRI-AVPP-1346-D, AZRI-Pr-20530-01, AZRI-Selection-09-B, AZRI-selcetion-05-C-01B, 33828, AZRI-Selection-02-A2 and AZRI-Selection-03-03B). Cluster 5 is most diversified cluster as it was divided into five groups i.e. group 1 comprised of seven genotypes i.e. ARI S2, BWP-01, AZRI-AVPP-9704-4, 32324, KP Local, 32336 and 37028, group 2 consisted of only three genotypes 36558, Shakti and Hot Queen F1, group 3 also contained three genotypes i.e. AZRI-Pr-16162-A, AZRI-Selection-06-1C and 36569, group 4 also comprised of three genotypes i.e. 32328, AZRI-Selection-04-C1 and Chandar Mukhi, while group 5 comprised of eight genotypes i.e. AZRI-Selection-10-B, AZRI-AVPP-1346-D, AZRI-Pr-20530-01, AZRI-Selection-09-B, AZRI-Selcetion-05-C-01B, 33828, AZRI-Selection-02-A2 and AZRI-Selection-03-03B. Two genotypes AZRI-Selcetion-05-C-01B and 33828 were closer to each other based on similarity among the morphological traits.

Diversity among 78 genotypes was observed as most of the genotypes were different as no duplication was recorded in principal component analysis (PCA). High magnitude of diversity was recorded among the genotypes based on morphological attributes but closely related genotypes were grouped in the same cluster. According to Cruz and Carneiro (2003), selection of genotypes for breeding program evaluated under different environment conditions, comparatively more significant however, adulteration during multiplication could influence selection process, as cross pollination in *Capsicum* ranges from 05 to 70%. The results of current study are in line with Karad *et al.* (2002) who evaluated 40 genotypes of chilli on morphological basis and grouped into eight clusters. Further, Manju and Sreelathakumary (2006) estimated genetic diversity among 32 genotypes and divided into six clusters. Similarly, Senapati *et al.* (2003) evaluated 20 genotypes of chilli and cluster analysis showed six clusters. Sudré *et al.* (2005) observed that 50 genotypes of chilli and sweet pepper were grouped in eight distinct groups based on diversity estimation in their morphological characters. Geleta *et al.* (2006) grouped 39 genotypes of pepper (*Capsicum annuum* L.) in various clusters based on their morphological characters, especially fruit size and shape. Hasan *et al.* (2015) evaluated 13 genotypes of pepper (*Capsicum annuum* L.) based on yield characters, genotypes were grouped in five different clusters, cluster-I had 5 genotypes and IV and V clusters had only one genotype in each. Andrade *et al.* (2020) assessed the diversity among 192 genotypes of chilli collected from 21 countries and found that 09 distinct groups were developed in cluster analysis due to significant diversity. García-González and Silvar (2020) organized 42 genotypes of *Capsicum* species

into groups by principal component analysis based on morphological characters. They found that genotypes were divided into two main clusters and five sub-clusters.

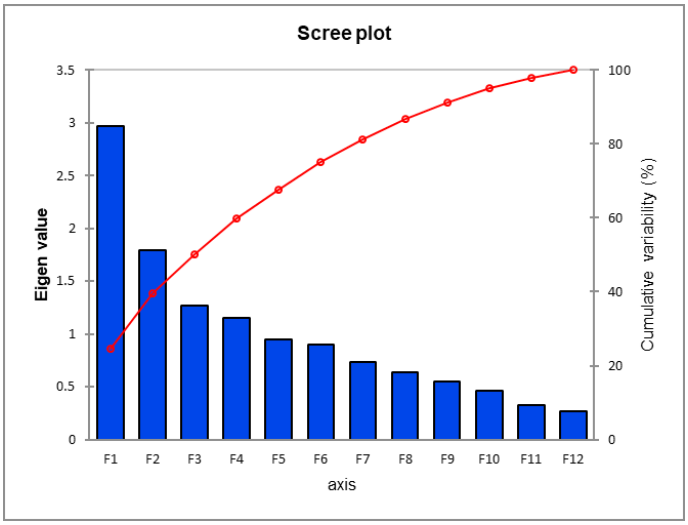

Figure 2: *The scree plot for morphological variables of Capsicum frutescens genotypes.*

Principal component analysis (PCA) for morphological variables of Capsicum frutescens genotypes (2019-2020)
Among the *Capsicum frutescens* genotypes, factor analysis was based on 12 morphological characters. Cumulative variability (%) and Eigen values are shown as scree plot (Figure 2). The Eigen values for first three components dropped sharply but these gradually decreased for next nine components. On the other hand, a sharp increase was observed in cumulative variability for first three components, while gradual increase in cumulative variability was observed for next nine components. About 67.679% variation was covered by first 05 components, so the results of first 05 components have considerable variation and sufficient to discuss variability (Table 3). Variability 24.71% was observed in first component which contained fruit weight, fruit length, fruit diameter, yield per plant, leaf area and time to fruit ripe among *Capsicum frutescens* genotypes. The second component pertained 14.90% variability which included leaf density, pedicel length, yield per plant, fruit diameter, fruit weight and time to fruit ripe. The third component showed 10.60% variability which consisted of fruit length, pedicel length, yield per plant and number of stomata. The fourth component described 9.59% variability pertained fruit length, fruit weight, fruit diameter, pedicel length, plant height, yield per plant, leaf density, leaf area and time to flower. The fifth component exhibited 7.86% variability which included plant height, fruit length, time to ripe fruit, number of stomata, relative chlorophyll content and fruit weight (Table 3).

Variables of first two factor accounted for 39.61% (Figure 3) of total variation through which a linkage map was developed. The two dimensional plot described that morphological parameters including time to ripe fruits, fruit length, fruit diameter, yield and fruit weight were present within the first quadrant and were correlated, but strong correlation was found between fruit length and fruit weight and similarly between fruit diameter and plant yield. Further, the variables were correlated with each other. The second quadrant pertained leaf density and pedicle length and both these factors were strongly correlated with each other. Third quadrant consisted of leaf density, plant height, number of stomata and relative leaf chlorophyll content (SPAD) that have negative correlation with each other, while the fourth quadrant comprised of only one variable i.e. leaf area that is divergent from other variables and showed some association with fruit length. PCA plot based on two principal components showed that all 78 genotypes of chilli were scattered in all four quadrants, while few genotypes were far away from center of axis indicating high diversity level for various morphological parameters. Most of the genotypes close to central axis were very close to each other thus showed less variability. However, AZRI-Selection-09-B, Hot Red, Kot Sultan, AZRI-Selection-06-1C, 30880, AZRI-Selection-10-B, Zenia F1, 30880, Hot Pepper Sky Red, Sky Line 2 and Sky Line 3 were highly divergent and varied from rest of genotypes. Biplot of genotypes (Figure 4) showed that genotypes were scattered in four quadrants. Genotypes scattered in right planes were positively correlated with fruit length, fruit weight, fruit diameter, yield per plant, time to ripe fruit and leaf area. Further, the genotypes Advanta 509, 1130 F1, 32326, AZRI-I-A-20B, Super Hot F1, AZRI-Selection-07-A1, 32385 showed a strong correlation with fruit diameter, time to ripe fruit and plant yield. Genotypes scattered in left plane showed a weak association with fruit diameter and pedicel length but strong correlation for days to flower, plant height, number of stomata and relative chlorophyll content. Genotypes KP Local and BWP-01 have good association with days to flower; however, genotypes AZRI-Selection-01-B, 36648 and 36569 have strong correlation with plant height. LD1 and 36698 showed good association with number of stomata and relative chlorophyll content, respectively.

Table 3: *Eigen values and cumulative variance for 12 components for morphological variables of Capsicum frutescens genotypes (2019-2020).*

	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12
Eigen value	2.96	1.78	1.27	1.15	0.94	0.899	0.736	0.637	0.549	0.458	0.328	0.272
Variability (%)	24.71	14.90	10.60	9.59	7.86	7.495	6.133	5.309	4.573	3.813	2.731	2.267
Cumulative %	24.71	39.61	50.21	59.81	67.67	75.17	81.30	86.61	91.18	95.00	97.73	100.00

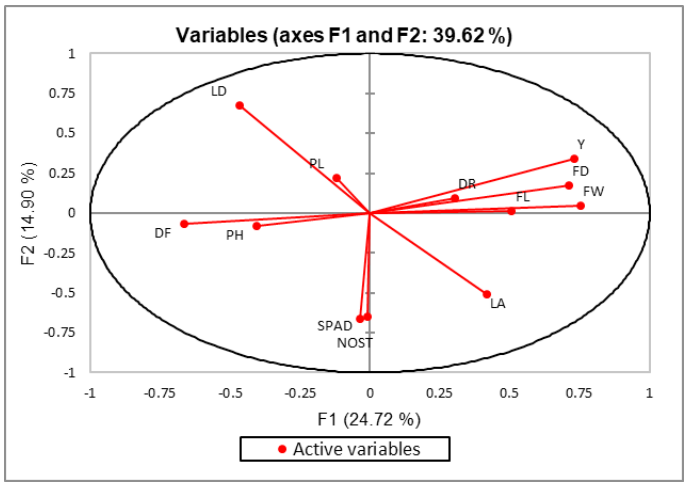

Figure 3: *PCA analysis based on first two components for morphological attributes of Capsicum frutescens genotypes. FW, Fruit weight, FL, Fruit length, FD, Fruit diameter, PL, Pedicel length, PH, Plant height, Y, Yield per plant, LD, Leaf density, LA, Leaf area, DF, Days to flower, DR, Days to ripe, SPAD, Relative chlorophyll content, NOST, Number of stomata.*

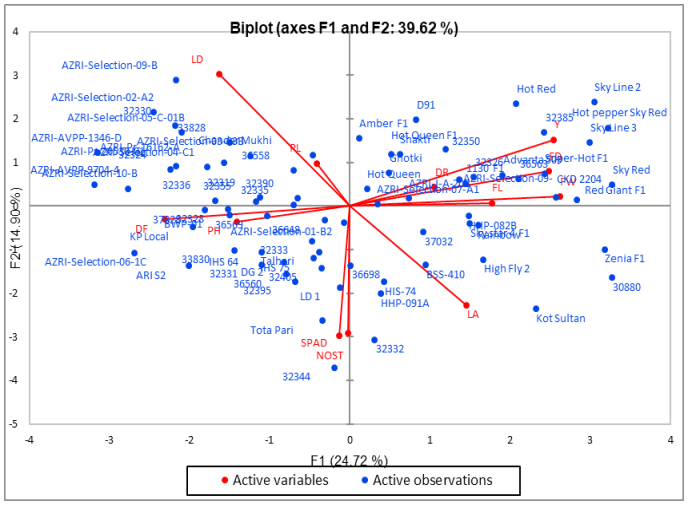

Figure 4: *PCA biplot based on first 2 components for morphological attributes of Capsicum frutescen genotypes.*

The results of current study are in line with Singh *et al.* (2020) who estimated genetic diversity based on morphological attributes of 18 genotypes and found 88.85% variability in five principal components out of ten with >0.5 Eigen value. The results of our study are also favored by Dutta *et al.* (2018) who compared 72 genotypes of *Capsicum frutescens* for qualitative and quantities attributes and found that cumulative variation was 69.88% for five components and all genotypes were grouped into five clusters. Further, Janaki *et al.* (2015) evaluated 63 genotypes for quantitative and qualitative attributes and first six components pertained 76.83% variation of total. Similarly, Peña-Yam *et al.* (2019) reported that first three components showed 94.02% variability of the total, among 11 genotypes of *Capsicum chinense* Jacq. Morphological characters such as fruit shape, leaf shape and flower color are helpful to differentiate genotypes of *Capsicum* species (Weerakoon and Somaratne, 2010). Morphological diversity was assessed among 48 genotypes of pepper (*Capsicum annuum* L.) collected from different areas of Turkey. Results indicated that 54.29% of variability was accounted for first six components (Bozokalf *et al.*, 2009).

Table 4: *Factor coordinates of the morphological attributes of (Capsicum frutescens) based on correlations.*

Morphological characters	F1	F2	F3	F4	F5
Fruit weight (g)	0.752	0.048	-0.223	0.310	0.072
Fruit length (cm)	0.507	0.016	0.533	0.020	0.472
Fruit diameter (mm)	0.712	0.176	-0.237	0.220	-0.103
Pedicle length (cm)	-0.119	0.218	0.769	0.218	-0.101
Plant height (cm)	-0.405	-0.081	-0.165	0.550	0.613
Yield per plant (g)	0.730	0.339	0.188	0.115	-0.001
Leaf density (number)	-0.467	0.673	-0.099	0.086	0.251
Leaf area (cm^2)	0.418	-0.506	-0.082	0.483	-0.144
Days to flower	-0.664	-0.068	-0.077	0.407	-0.120
Time to ripe fruit (days)	0.302	0.094	-0.327	-0.445	0.407
Relative chlorophyll content (SPAD)	-0.007	-0.653	-0.079	-0.053	0.106
Number of stomata	-0.037	-0.662	0.304	-0.190	0.212
Variability %	24.71	14.90	10.60	9.59	7.86

Fruit yield, fruit length, fruit diameter and fruit weight showed highest positive values as data were analyzed with principal component analysis (Rana *et al.*, 2014). Similar results were described by Sarmah *et al.* (2018) who estimated biodiversity among 37

genotypes of chilli based on morphological traits. They found that principal component analysis indicated 99.7% variability of total up to 22 components. They described that first six components accounted for 81.44% of the total variability, while greater variability was accounted for fist component i.e 34.93%. Further, Belay *et al.* (2019) assessed the genetic diversity among 64 genotypes of chilli, principal component analysis explained 79.45% variability of total in first five components.

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Novelty Statement

Focused on selection of potential genotypes for development of high yielding varieties suitable for local climate.

Author's Contribution

Ishtiaq Ahmad: Executed the field research and laboratory analyses.
Muhammad Akbar Anjum: Conceived the idea and supervised the work

Conflict of interest
The authors have declared no conflict of interest.

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