*Pak. J. Bot.*, 54(6): 2157-2166, 2022. DOI: http://dx.doi.org/10.30848/PJB2022-6(10)

# GENETIC DIVERSITY FOR PRODUCTION TRAITS IN HOT CHILLI (*CAPSICUM ANNUUM* L.)

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**Abstract**

Genetic diversity is the basis of generating new innovations. Nowadays there is great tendency towards the usage of hybrid technology especially in vegetable crops. In hot chillies, only a few commercial hybrids are known which are being marketed at high prices. The indigenous and high yielding hybrid development in hot pepper is a novel approach to boost the national yield along with its fair availability to the masses at low prices. The study reported herein regarding the genetic variability in chillies has triggered the hybrid vigour model. The performance of twenty two different hot chilli (*Capsicum annuum* L.) genotypes including the indigenously developed hybrids along with elite lines and commercial hybrids were studied to find out genetic diversity for the production traits. Noteworthy, significant statistical differences were found for all the parameters showed existence of adequate variation. The fresh fruit yield of the locally developed chilli hybrid CH-15140 remained on the top (141.4 t/ha) and was found significantly higher than the other local and international hybrids and varieties. However, the international hybrids such as Bonanza and Atlas Imp also performed well with the fruit yields of 119.5 t/ha and 102.2 t/ha respectively. Not only high (GCV) and (PCV) were estimated for traits viz; single fruit weight (81.3 and 83.2%), yield per plant (31.8 and 32%), fresh fruit yield per hectare (31.8 and 32%) and fruit length (29 and 29.1%) but also high heritability (≥95%) along with high genetic advance (≥40%) denoted actuality of considerable variability, with minimum engrossment of the environmental factors which may be exploited through selection for better advancement. Highest fresh fruit yield was mostly achieved by the early maturing genotypes as evident from their significant but negative values of correlation coefficients both at the genotypic (-0.38) and phenotypic (-0.33 levels). Seeds per fruit and pericarp thickness significantly but positively contributed towards fresh fruit yield. Cluster analysis identified two main clusters viz., Cluster I with only one genotype (CH-15140) while Cluster II with two sub- clusters; II-A and II-B. Diversity analysis, showed distinctiveness of eight genotypes from all other twenty-two genotypes which can be further improved through breeding for the development of high quality and high yielding chilli genotypes.

**Key words:** *Capsicum annuum* L., GCV, PCV, Heritability, GAM and Cluster analysis.

## Introduction

Chilli (*Capsicum annuum* L.) is a member of *Solanaceae* family which has 20 to 30 species that has a wide spread over the tropical and sub-tropical regions around the globe. It has a great economic value among vegetables for a flavour and a taste. Basically, chilli is considered a hot weather crop and mostly found in tropical regions of the world (Erickson & Markhart, 2002). South America and Mexico are known as pioneers of its origins. Portugues brought chilli to Indo-Subcontinent and Brazil (Rego *et al.*, 2011).

Chilli plays significant role in commercial sector by sharing 0.15% in total GDP of the country. It is crucial in human diet as compared to other vegetables because it is consumed both as fresh and dried to enhance the flavour of food. *C. annuum* L. and *C. frutescens* L. are the two commonly cultivated chilli species in Pakistan. Chilli occupies 20% of total area under vegetable cultivation in Sindh and Punjab. The target areas for hot pepper cultivation are Layyah, Hyderabad, Kunri and Tharparker (Anon., 2014-15). In Pakistan total area used for chilli cultivation is 47.35 thousand hectares, with total amount of 127 thousand tonnes (Anon., 2018-19). Kunri is the area of Sindh that is recognized as home of red pepper (Anon., 2015). Globally, the share of South Asia in the overall world chilli production is about 55.5%; however, production of chilli in India ranks first followed by China, Thailand, Ethiopia and Pakistan. Meanwhile, remaining contribution comes from American and African countries (Anon., 2020).

Chilli growers have been facing diverse problems such as less production, constraints in export, improper storage and fungal disease infestation. Lower Sindh areas have been recognized as the biggest chilli market of Asia. Currently, Loungi, Sanam, Gothki and Talhar varieties are popular in Pakistan. Nowadays, there's an extraordinary competition have been seen among the farmers in chilli hybrids cultivation. The main focus is on the yield and hybrids are considered better in yield than that of the local varieties. But a very few hybrids are available in the market (Noor *et al*., 2020). Fresh fruit yield has got a complex hereditary nature being influenced by various other plant traits (Datta & Jana, 2004). For an organized breeding strategy, availability of genetic variation in chilli crop should be present (Parkash, 2012). Characterization and evaluation is the pre-requisite in order to utilize the available variation for better improvement (Thul *et al.*, 2009). Genetic variability and its maintenance in chilli are imperative to break out the genetic loss. The authenticity of selection and progress of development of new and

improved cultivars is highly dependent upon the extent of the variability expressed by the yield contributing traits in germplasm (Peter & Rai, 1978).

Considering the importance of chilli crop and lower yield potential that has confined the masses to utilize the traditional open pollinated varieties; heterosis breeding was tested to improve the yield potential. Genetic analysis for diversity was applied in order to verify the existence of variability in the locally developed chilli hybrids, international hybrids and open pollinated varieties. The study evaluated twenty chilli genotypes and is a step forward towards local hybrid development in chillies in order to identify the distinctness of the locally developed hybrids with OPVs and international hybrids in respect of yield and its related components.

## Materials and Methods

**Plant material:** Thirteen locally developed chilli hybrids (CH-15103, CH-15111, CH-15116, CH-15123, CH-15130, CH-15133, CH-15138, CH-15140, CH-15144, CH-15148, Hybrid-1, Hybrid-2 and Hybrid-3) along with two advance lines (NARC15/4, NARC 16/5) and seven international hybrids (P6, Atlas#3, Atlas Imp, Bonanza, Appolo, KHHP-81 and KHHP-82) were evaluated in the present study.

**Nursery raising and experimental design:** Seed sowing for raising of nursery was done by mid of November 2016. The plant nurseries were grown on nursery beds under the protected structure of tunnel. The day and night temperatures of tunnel were retained at 30 ± 3°C and 23 ± 3°C respectively. Transplanting was followed in the first week of March 2016 in duplicate Randomized Complete Block Design at NARC during 2016-2017. Each entry was planted on both sides of a bed of 3 meters length, with P × P and R × R distances of 0.75 m and 0.45 m respectively. Farm yard manure @ 30 t $ha^{-1}$ along with a combination of NPK @ 120, 75 and 50% kg $ha^{-1}$ was also applied. All K and P while half dose of N was applied during nursery bed preparation. However, the remainder dose of nitrogen was pragmatic in two; one was applied and at flowering and the other after 3-4 green fruit pickings. Irrigation was applied to the crop according to the field requirements.

**Data recording and analysis:** The data on days to 50% flowering, plant height, fruit length, seeds $fruit^{-1}$, pericarp thickness, single fruit weight, yield $plant^{-1}$ and fresh fruit yield $ha^{-1}$ were collected from 10 plants, selected at random from each plot. Obtained data for all parameters were analyzed statistically (ANOVA) using Microsoft Excel following the method of. Steel & Torrie (1980) outlined for RCBD (Nawab *et al*., 2019). The coefficients variation (genotypic and phenotypic) were calculated and categorized as low, medium and high by Shivasubramanian & Menon (1973). Genetic advance and heritability in broad sense were premeditated by Burton (1952), Johnson *et al*., (1955) and Allard (1960). The heritability (%) was computed and categorized as low, moderate and high as suggested by Robinson *et al*., (1949). The GA as per cent of mean was characterised as low, moderate and high by Johnson *et al*., (1955). Genotypic ($r_{g.}$) and phenotypic ($r_{p.}$) correlations among the traits were estimated using the method as outlined by Singh & Chaudhary. (1985).

## Results and Discussion

**Genetic variability:** Variability analysis for eight traits revealed maximum difference among the chilli genotypes exhibited existence of sufficient variation (Table 1) and this variability can be utilized for establishing novel cross combinations for the recreation of genetic diversity in hot chilli genotypes. The existence of such type of variability was also noticed by Bhagwati & Changkija (2009), Patel *et al*., (2010), Usman *et al*., (2014), Janaki *et al*., (2015), Elahi *et al*., (2017) and Elahi *et al*., (2019).

The mean performances of different chilli genotypes for traits studied (Table 2) showed a comprehensive array of diversity among the hot chilli genotypes. Highest assortment of variability was observed for fresh fruit yield per hectare (28 $t.ha^{-1}$ to 141 $t.ha^{-1}$) followed by plant height (83.7 cm to 147.9 cm), seeds per fruit (34 to 78), single fruit weight (3.6g to 35.5g), fruit length (5.2 cm to 17.9 cm), fruit yield per plant (0.52 kg to 2.65 kg) and pericarp thickness (1 mm to 2.1 mm). Similar observations were also recorded by Ukkund *et al*., (2007), Sood & Kumar (2010) and Janaki *et al*., (2015) for plant height and seeds per fruit, Patel *et al*., (2010), Shrestha *et al*., (2011) and Rego *et al*., (2011) for single fruit weight, pericarp thickness and yield per plant and Kadwey *et al*., (2016) for yield per hectare. Yield is the sole aim of any breeding mission. The yield of the locally developed chilli hybrid CH-15140 remained on the top (141.4 t/ha) and was found significantly higher than the other local and international hybrids and varieties. However, the international hybrids such as Bonanza and Atlas Imp also performed well with the fruit yields of 119.5 t/ha and 102.2 t/ha respectively. Yield all alone cannot exert an impact on yield until and unless it is supported by its related traits. In this case the fresh fruit yield is also supported by yield per plant and average single fruit weight. Yield per plant (2.65 kg) and single fruit weight (8.4 g) of the CH-15140 was also significantly higher than Bonanza (2.24 kg; 7.5 g) and Atlas Imp (1.91; 6.5 g). Average single fruit weight and yield per plant had an impact on the overall fresh fruit yield. It is however, interesting that the locally developed chilli hybrid CH-15140 was not only high yielding but also earliest in flowering by taking only 34 days to 50% flower as compared to the international hybrids (Bonanza and Atlas Imp) which took 39 and 40 days to 50% flowering respectively. However, the local hybrid CH-15133 was proved to be the late in 50% flowering and took 62 days to 50% flower. The plant height of the local chilli hybrid CH-15140 (147.9 cm) was observed significantly higher among all the genotypes. The pericarp thickness (2.1 mm) of KHHP-81 was found significantly higher than all the genotypes statistically. Significantly maximum seed per fruit (72 seeds) were recorded for KHHP-81 followed by a local chilli hybrid CH-15133 with 67 seeds. Maximum fruit length of 17.9 cm was recorded for KHHP-81 followed by the international hybrid Atlas#3 (15.2 cm) but these two international hybrids did not manage to attain high yield potential because of their less yield per plant (1.71 kg; 1.0 kg) as compared to the local hybrid CH-15140 and the international hybrid (Bonanza) as shown in table 2.

**Table 1. Mean squares value for various production traits in hot chilli.**

| SOV | df | DFF | PH | FL | SPF | PT | SFWt | YPP | FFY |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 1 | 0.36 | 9.54 | 0.04 | 9.92 | 2.27 | 0.35 | 0.002 | 4.37 |
| Genotypes | 21 | 101.52** | 452.14** | 15.57** | 215.61** | 0.14** | 84.02** | 0.43** | 1213.54** |
| Error | 21 | 2.03 | 12.41 | 0.056 | 12.23 | 0.002 | 0.182 | 0.003 | 7.533 |

DFF = Days to 50% flowering; PH = Plant height (cm); FL = Fruit length (cm); SPF = Seeds fruit$^{-1}$; PT = Pericarp thickness (mm); SFWt. = Single fruit weight (g); YPP = Yield plant$^{-1}$; FFY = Fresh fruit yield (t/ha)
**Highly significant at p<0.01 levels; *Significant at p<0.05 level

**Table 2. Mean values for various traits in hot chilli genotypes.**

| Genotypes | DFF | PH | FL | SPF | PT | SFWt | YPP | FFY |
|---|---|---|---|---|---|---|---|---|
| CH-15140 | 34 | 147.9 | 9.5 | 62 | 1.4 | 8.4 | 2.65 | 141.4 |
| Bonanza | 39 | 123.1 | 8.5 | 61 | 1.5 | 7.5 | 2.24 | 119.5 |
| Atlas Imp | 40 | 108.3 | 12.7 | 62 | 1.2 | 6.5 | 1.91 | 102.2 |
| CH-15116 | 45 | 117.7 | 8.72 | 72 | 1.4 | 6.0 | 1.89 | 101.0 |
| CH-15123 | 50 | 108 | 8.16 | 51 | 1.3 | 6.0 | 1.88 | 100.5 |
| Atlas#3 | 41 | 115.5 | 15.2 | 53 | 1.3 | 6.6 | 1.71 | 91.2 |
| Hybrid-2 | 50 | 106.5 | 8.6 | 69 | 1.3 | 5.2 | 1.61 | 86.4 |
| P6 | 45 | 136.7 | 7.8 | 56 | 1.4 | 7.1 | 1.57 | 84.2 |
| NARC15/4 | 41 | 115.8 | 8.9 | 53 | 1.4 | 5.9 | 1.47 | 78.4 |
| Hybrid-3 | 37 | 105.7 | 10.1 | 51 | 1.2 | 5.5 | 1.44 | 76.9 |
| CH-15130 | 50 | 108.3 | 10.2 | 63 | 1.5 | 7.1 | 1.42 | 76.1 |
| CH-15138 | 47 | 110.3 | 9.8 | 46 | 1.6 | 6.4 | 1.41 | 75.3 |
| NARC 16/5 | 40 | 103.6 | 6.9 | 58 | 1.4 | 6.1 | 1.27 | 67.9 |
| **KHHP-82** | **35** | **94** | **11.1** | **78** | **1.9** | **13.4** | **1.25** | **66.9** |
| CH-15148 | 51 | 105 | 6.6 | 57 | 1.2 | 5.4 | 1.22 | 65.5 |
| CH-15144 | 48 | 102.3 | 9.4 | 60 | 1.2 | 5.7 | 1.19 | 63.9 |
| Hybrid-1 | 49 | 93.5 | 7.8 | 50 | 1.3 | 5.7 | 1.13 | 60.6 |
| CH-15111 | 51 | 94.3 | 9.29 | 38 | 1.3 | 7.5 | 1.11 | 59.4 |
| CH-15103 | **62** | 84.5 | 6.8 | 62 | **1.0** | 3.8 | 1.07 | 57.1 |
| **KHHP-81** | **37** | **83.7** | **17.9** | **72** | **2.1** | **35.5** | **1.0** | **53.7** |
| Appolo | 43 | 122.7 | 9.4 | **34** | 1.2 | 5.0 | 0.99 | 52.8 |
| CH-15133 | 48 | 120.1 | **5.2** | 67 | 1.2 | **3.6** | **0.52** | **28.2** |
| **Mean** | **44.64** | **109.43** | **9.48** | **57.95** | **1.38** | **7.72** | **1.45** | **77.69** |
| **LSD (0.05)** | **2.9** | **7.3** | **0.5** | **7.2** | **0.9** | **0.88** | **0.10** | **5.70** |

DFF = Days to 50% flowering; PH = Plant height (cm); FL = Fruit length (cm); SPF = Seeds fruit$^{-1}$; PT = Pericarp thickness (mm); SFWt. = Single fruit weight (g); YPP = Yield plant$^{-1}$; FFY = Fresh fruit yield (t/ha)

Genotypic (Vg) and phenotypic variance (Vp) for different traits showed wide ranges (Table 3). Phenotypic variance (Vp) was higher than relative genotypic variance (Vg) indicated the effect of external environment on the manifestation of the traits. Highest Vg and Vp were calculated for fresh fruit yield per hectare (603 and 610) chased by plant height (219.8 and 232.3), seeds per fruit (101.7 and 113.9), days to 50% flowering (43.5 and 49.6), single fruit weight (41.9 and 42.1), fruit length (7.7 and 7.8), yield per plant (0.21 and 0.22) and pericarp thickness (0.06 and 0.07). However, for the traits like days to 50% flowering, fruit length, pericarp thickness, single fruit weight, yield per plant and fresh fruit yield; only minor difference between the Vg and Vp was recorded which indicated the minor contribution of the environmental factor in the expressions of these traits which in other words explained that these were genetic traits. The acquired results corroborates to early findings of Sharma *et al*., (2010), Amit *et al*., (2014), Bijalwan & Madhvi (2016) and Meena *et al*., (2016). Values of phenotypic coefficient of variation (PCV) were found higher than genotypic coefficient of variation (GCV) for all the characters under study (Smitha & Basavaraja, 2006; Tembhurne *et al*., 2008 and Chattopadhyay *et al*., 2011) as shown in Table 3. Narrow differences were observed between GCV and PCV which indicated minimum influences of environment on phenotypic effect of these traits. Similar findings were also described by Sood & Kumar (2010), Butchera *et al*., (2013) and Bijalwan & Madhvi (2016). Maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation were estimated for traits viz. single fruit weight (81.3 and 83.2%), yield per plant (31.8 and 32% ) fresh fruit yield per hectare (31.8 and 32%) and fruit length (29 and 29.1%) while, moderate GCV and PCV were observed for characters like pericarp thickness (19.2 and 19.4%), seeds per fruit (17.6 and 18.6%), days to 50% flowering (16.2 and 16.3%) and plant height (13.5 and 13.9%). This categorization of GCV and PCV % values was made by Shivasubramanian & Menon (1973). High GCV and PCV indicated existence of wide genetic variation for these traits among genotypes and selection could be effective for improvement of these traits. Current findings were at par with observations of Chattopadhyay *et al*., (2011), Nehru *et al*., (2003), Sreelathakumary & Rajamony (2004), Singh *et al*., (2009), Butchera *et al*., (2013), Bijalwan & Madhvi (2016) and Rosmaina *et al*., (2016).

**Table 3. Components of variability for various traits of hot chilli genotypes.**

| Traits | Mean | $V_G$ | $V_P$ | GCV% | PCV% | $h^2_{bs}$ % | GAM % |
|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 43.5 | 49.6 | 51.6 | 16.2 | 16.3 | 96 | 28.73 |
| Plant height | 109.2 | 219.8 | 232.3 | 13.5 | 13.9 | 94 | 23.07 |
| Fruit length | 9.6 | 7.7 | 7.8 | 29.0 | 29.1 | 99 | 42.70 |
| Seeds fruit$^{-1}$ | 57.4 | 101.7 | 113.9 | 17.6 | 18.6 | 89 | 29.09 |
| Pericarp thickness | 1.4 | 0.06 | 0.07 | 19.2 | 19.4 | 97 | 32.14 |
| Single fruit weight | 7.7 | 41.9 | 42.1 | 83.1 | 83.2 | 99 | 146.75 |
| Yield plant$^{-1}$ | 1.5 | 0.21 | 0.22 | 31.8 | 32.0 | 98 | 52.00 |
| Fresh fruit yield ha$^{-1}$ | 77.2 | 603.0 | 610.5 | 31.8 | 32.0 | 98 | 55.18 |

$V_G$ = Genetic variance; $V_P$ = Phenotypic variance; GCV = Genotypic coefficient of variation (%); PCV = Phenotypic coefficient of variation (%); $h^2_{bs}$ % = Heritibility broad sense (%); GAM = Genetic advance (% over mean)

**Table 4. Genotypic correlation coefficient ($r_g$) above and phenotypic correlation coefficient ($r_p$) below the diagonal for various traits in hot chilli genotypes.**

| | DDF | PH | FL | SPF | PT | SFWt. | YPP | FFY |
|---|---|---|---|---|---|---|---|---|
| DDF | **1.00** | -0.34* | -0.48* | 0.25* | -0.50* | -0.37* | -0.38* | -0.38* |
| PH | -0.33* | **1.00** | -0.26* | 0.02 | -0.16 | -0.36* | 0.57* | 0.57* |
| FL | -0.48** | -0.26 | **1.00** | -0.05 | 0.56* | 0.73* | -0.13 | -0.13 |
| SPF | 0.24 | 0.01 | -0.05 | **1.00** | 0.24* | 0.10 | 0.17* | 0.17* |
| PT | -0.49** | -0.15 | 0.55** | 0.21 | **1.00** | 0.81* | 0.24* | 0.24* |
| SFWt. | -0.36* | -0.35* | 0.72** | 0.09 | 0.79** | **1.00** | 0.22 | 0. 22 |
| YPP | -0.37* | 0.56* | -0.12 | 0.16 | 0.22 | 0.21 | **1.00** | **0.98**** |
| FFY | -0.37* | 0.56** | -0.12 | 0.16 | 0.22 | 0.21 | **0.97**** | **1.00** |

DFF = Days to 50% flowering; PH = Plant height (cm); FL = Fruit length (cm); SPF = Seeds fruit$^{-1}$; PT = Pericarp thickness (mm); SFWt. = Single fruit weight (g); YPP = Yield plant$^{-1}$; FFY = Fresh fruit yield (t/ha)

**Table 5. Principal component analysis.**

| PC | 1 | 2 |
|---|---|---|
| Eigenvalue | 3.05 | 2.67 |
| % Variance | 38.15 | 33.35 |
| Cumulative variance | 38.15 | **71.5** |

**Genetic advances and heritability:** Broad sense heritability estimates provide knowledge about transmission for genetic variability to the offspring from parents. Heritability approximation for a specific trait is very important to assess its inheritance, if it is genetic or under environmental influence. Maximum heritability estimates were found for all plant attributes under observation viz., fruit length (99%), single fruit weight (99%), yield per plant (98%), fresh fruit yield per hectare (98%), pericarp thickness (97%), days to 50% flowering (96%), height of the plant (94%) and seeds per fruit (89%) indicated that variations were due to genotypic effect, transmittable to next generation and selection would be efficient at early generations. Early investigators like Singh *et al*., (2014); Chattopadhyay *et al*., (2011), Nehru *et al*., (2003), Basavaraja (2006), Ukkund *et al*., (2007), Datta & Das (2013); Sharma *et al*., (2014) and Bijalwan & Madhvi (2016) also reported high broad sense heritability for different plant attributes.

Consideration of heritability along with the genetic advance can have more precision for the selection of best genotypes rather than heritability alone. Maximum heritability along with maximum genetic advance is an essential predictor of expected genetic progress in next generation through simple selection**.** In this study high genetic advance (as percentage over the mean values) was calculated for all traits.

High genetic advance as percentage over the mean were estimated for days to 50% flowering (28.73%), height of plant (23.07%), fruit length (42.70%), seeds per fruit (29.09%), pericarp thickness (32.14%), single fruit weight (146.75%), yield per plant (52%) and fresh fruit yield per hectare (55.18%) which directed that these traits were under additive gene action and simple phenotypic selection will be helpful for enhancement of these traits in next generations. High genetic advance estimates for different traits were also confirmed by Manju & Sreelathakumary (2002), Krishna *et al*., (2007), Sharma *et al*., (2010), Pandit & Adhikary (2014), Amit *et al*., (2014) and Kadwey *et al*., (2016).

**Correlations**

Correlation coefficient is very useful in determining a relationship between two characters and infact, it is an indirect way of selecting one trait linked with other trait. Traits may have a positive or negative nature of association. A positive association indicates a simultaneous increase in the two associated characters. However, negative association of one trait inversely affects the other. Genotypic and phenotypic correlation coefficients are described in table 4. The magnitude of genotypic correlation was found higher than the phenotypic correlation specifying minor environmental

effects. These results also confirm the finding of Hasanuzzaman & Golam (2011) and Kumar *et al.*, 2012. A positive value gives the indication of uni-direction of the two variables and vice-versa (Nawab *et al*., 2011 and Elahi *et al*., 2017). Days to 50% flowering proved negative but significant association with plant height (rg = - 0.34* and rp = - 0.33*) at both levels indicated that immediate selection for these parameters is impossible and require improvement. Devi & Aramugam (1999) and Yadata *et al*., (2011) also reported similar associations. Fruit length represented negative relationship with days to 50% flowering and plant height (rg= -0.48* and rp = -0.48*) and (rg = -0.26* and rp = -0.26) which clearly showed that delayed flowering may cause reduction in the growth parameters. Similar correlations were also reported by Cankaya *et al*., (2010) and Lakshmi and Naidu (2010). Correlation between days to 50% flowering and seeds per fruit was found positive only at genotypic level (rg = 0.25*). This meant that early flowering has a positive effect on the development of seeds. Such observations were also observed by Vani *et al*., (2007). Pericarp thickness showed negatively significant correlation with days to 50% flowering at genotypic level and highly significant and negative correlation (rg = -0.50* and rp = -0.49**) at phenotypic level. There was a positive and significant correlation of pericarp thickness with fruit length at genotypic and highly significant at phenotypic level respectively (rg = 0.56* and rp = 0.55**) however, with seeds per fruit; pericarp thickness was positively but significantly associated at genotypic level (rg = 0.24*). These results depict that delayed flowering had an adverse effect of pericarp thickness while thickness of pericarp may increase with the increase in the fruit length and may also increase the number of seeds. The present results also match with the findings of Rao (2005), Sharma *et al*., (2010) and Luitel *et al*., (2013). Negative but significant correlation existed between single fruit weight and days to 50% flowering (rg = -0.37* and rp = -0.36*) and also with plant height (rg = -0.36* and rp = -0.35*), which indicated that delayed flowering might result in the depreciation of plant height and single fruit weight. The positive and significant association of fruit length with single fruit weight was indicated at genotypic level (rg = 0.73*) and highly significant at phenotypic level (rp = 0.72**) and the same trend was observed for pericarp thickness (rg = 0.81* and rp = 0.79**) which indicated that a simultaneous choice for these traits may result enhancement of both of the traits, in positively correlated traits and vice versa. These findings were same as found in results of Vikram *et al*., (2014) and Kadwey *et al*., (2016). Yield per plant and fresh fruit yield (per hectare) negatively associated with days to 50% flowering (rg = - 0.38* and rp = - 0.37*) which clearly pointed towards the reduction in yield due to delayed flowering and positively correlated with height of plant (rg = 0.57* and rp = 0.56**), pericarp thickness (rg = 0.24* and rp = 0.23*) both at phenotypic and genotypic level which showed that the genotypes tall stature with highest number of fruits, thick pericarp and heavy fruits apprehended higher yield and these traits could be useful selection criteria. Devi & Aramugam (1999); Rao (2005); Lakshmi & Naidu (2010); Lahbib *et al*., (2012); Amit *et al*., (2014) and Yatung *et al*., (2014) also found the similar associations.

**Cluster analysis:** In order to assess, utilize and retain germplasm successfully, it is important to find the amount of genetic variability existing. Morphological traits can be easily used for assessment of genetic diversity and thereafter for varietal development. Genetic differences in the germplasm may assist in cataloguing of genotypes and in the detection of possible utility of specific breeding principle (Nawab *et al*., 2013). The cluster analysis sequestrated genotypes into clusters/groups. There is a considerable level of uniformity within the clusters and high level of heterogeneity among the clusters (Jaynes *et al*., 2013).

The cluster analysis classified the chilli germplasm into two main clusters, sharing a common node at linkage distance of near about 85 (Fig. 1). Cluster I was comprised of only one genotype, CH-15140. This genotype was showing a larger extent of variation as it was outlier. Cluster II was partitioned into two sub-clusters such as groups II-A and II-B. Cluster II-A was also comprised of only one genotype as outlier, showing maximum variation from other members of the clusters; CH-15133. Cluster II-B was re-grouped into two sub-clusters II-$B_1$ and II-$B_2$. Sub cluster II-$B_1$ was again re-grouped into two sub-sub clusters, II-$B_1$a and II-$B_1$b. Sub-sub Cluster II-$B_1$a was comprised of 6 entries. Genotypes CH-15116 and Atlas-Imp, CH-15123 and Atlas#3 were significantly correlating each other at same linkage distance whereas; genotypes Bonanza and P6 were outliers, showing maximum diversity in this cluster. Sub-sub cluster II-$B_1$b was comprised of 12 genotypes. Genotype CH-151330 and Hybrid-2, CH-15138 and NARC-15/4, CH-15144 and CH-15148, CH-15111 and Hybrid-1 were correlating each other in term of studied traits at same linkage distance, while genotypes Hybrid-3, NARC-16/5, CH-15103 and Appolo were the most diverse genotypes in the said cluster for the studied traits. Sub-sub cluster II-$B_2$ was comprised of only two genotypes; KHHP-81 and KHHP-82, having similarity in term of studied traits. Out of 22 studied genotypes for diversity analysis, 8 genotypes were showing much distinctiveness from all other which can be further improved through breeding for the development of high quality and high yielding chilli genotypes.

The Fig. 2 showed the cluster formation based upon the average linkage distance among eight traits of chillies. The traits were classified into two clusters I and II linked at Euclidean distance near about 180.

Cluster first was consisted of two sub clusters i.e; I-A and I-B. Sub cluster I-A was comprised of four traits. Out of four traits, fruit length and fruit weight were at same linkage distance whereas pericarp thickness and yield per plant were at same linkage distance showing correlation among them, respectively. Sub cluster I-B was comprised of three traits, seed per fruit, days to 50% flowering and fresh fruit yield (per hectare). Days to 50% flowering and seeds per fruit were correlating with each other at the same distance while fresh fruit yield was outlier, showing variation as compared to other traits of same cluster.

Cluster II was comprised of only one trait as outlier that was plant height, showing maximum diversity from all other traits studied.

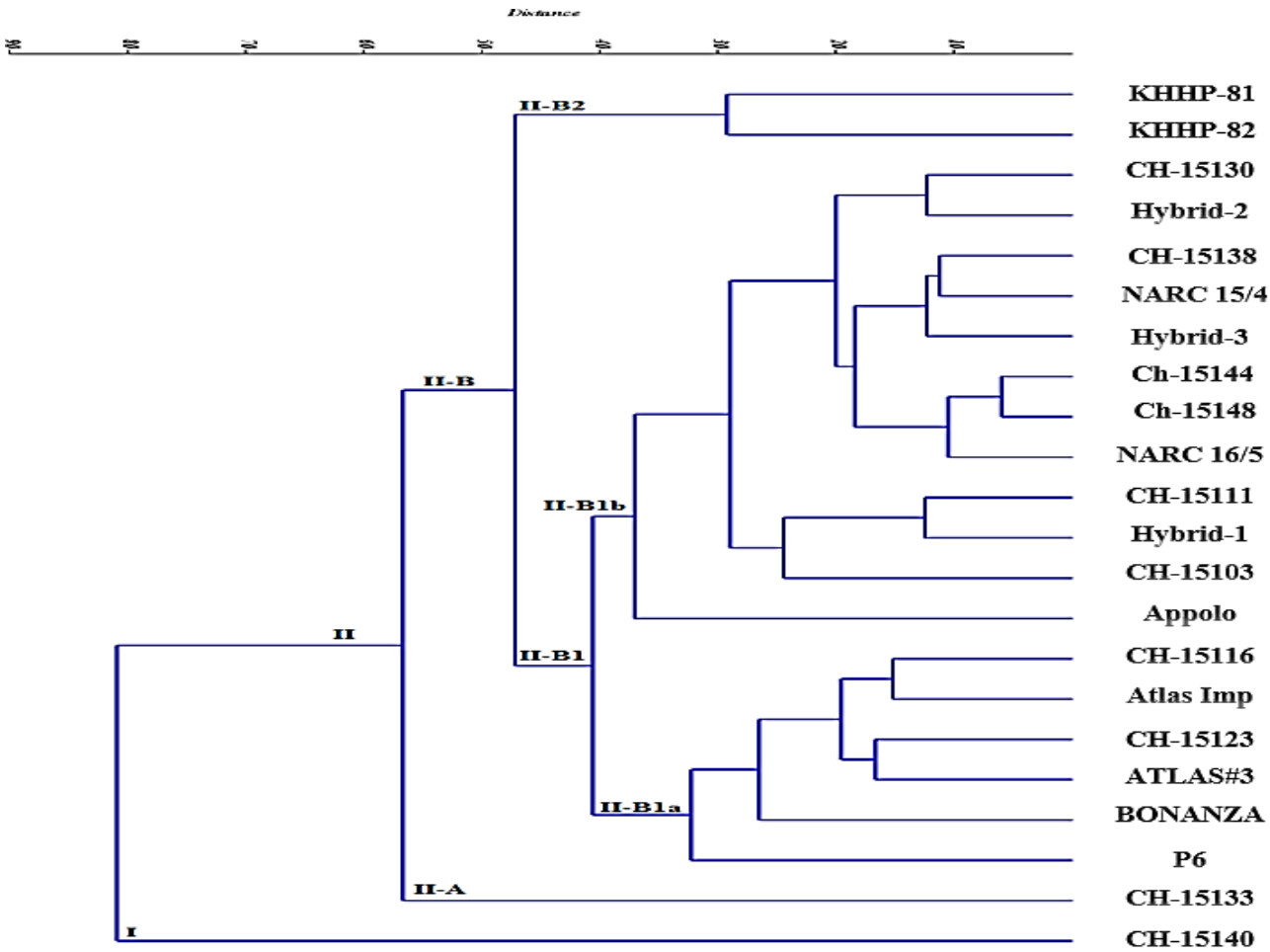


Fig. 1. Dendrogram constructed on the basis of average linkage distance among 22 chilli genotypes.

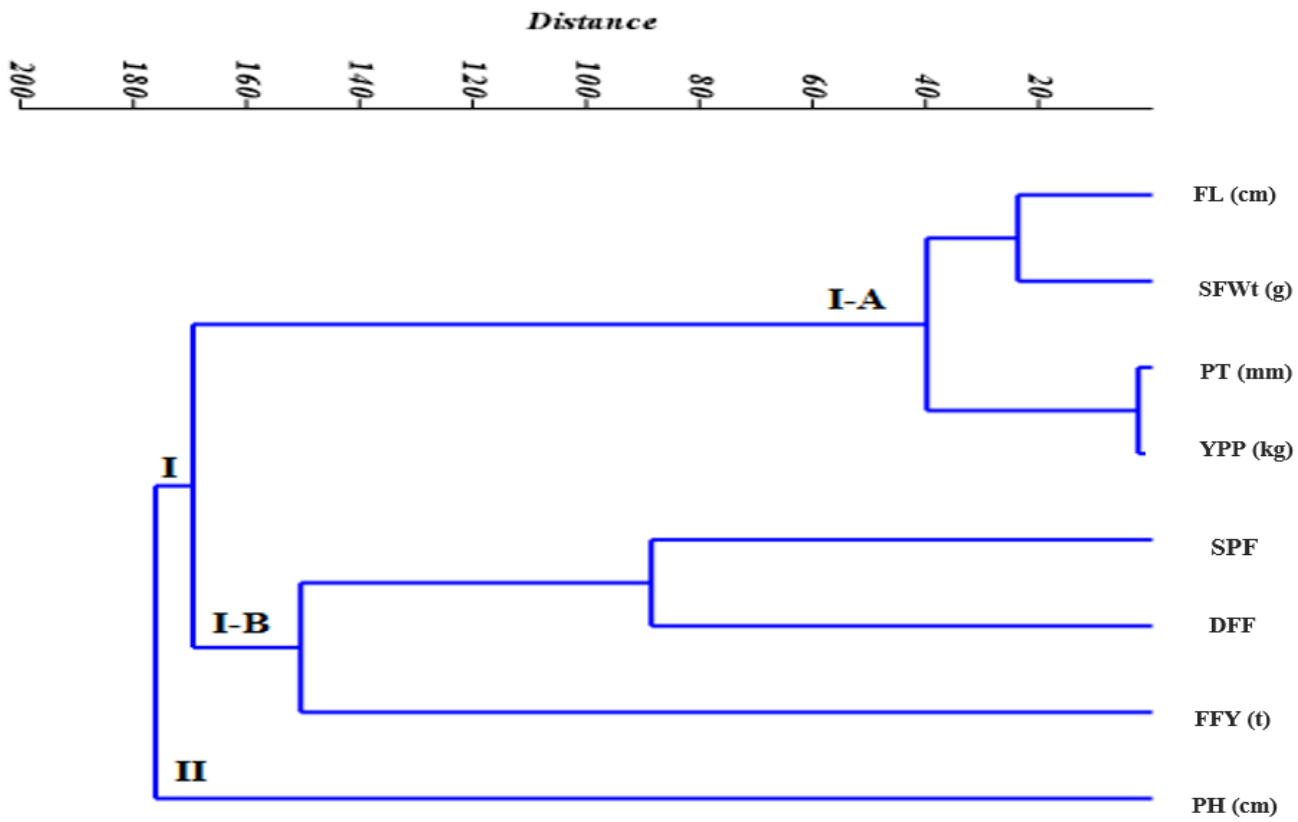


Fig. 2. Dendrogram constructed on the basis of average linkage distance among 8 traits of chillies.

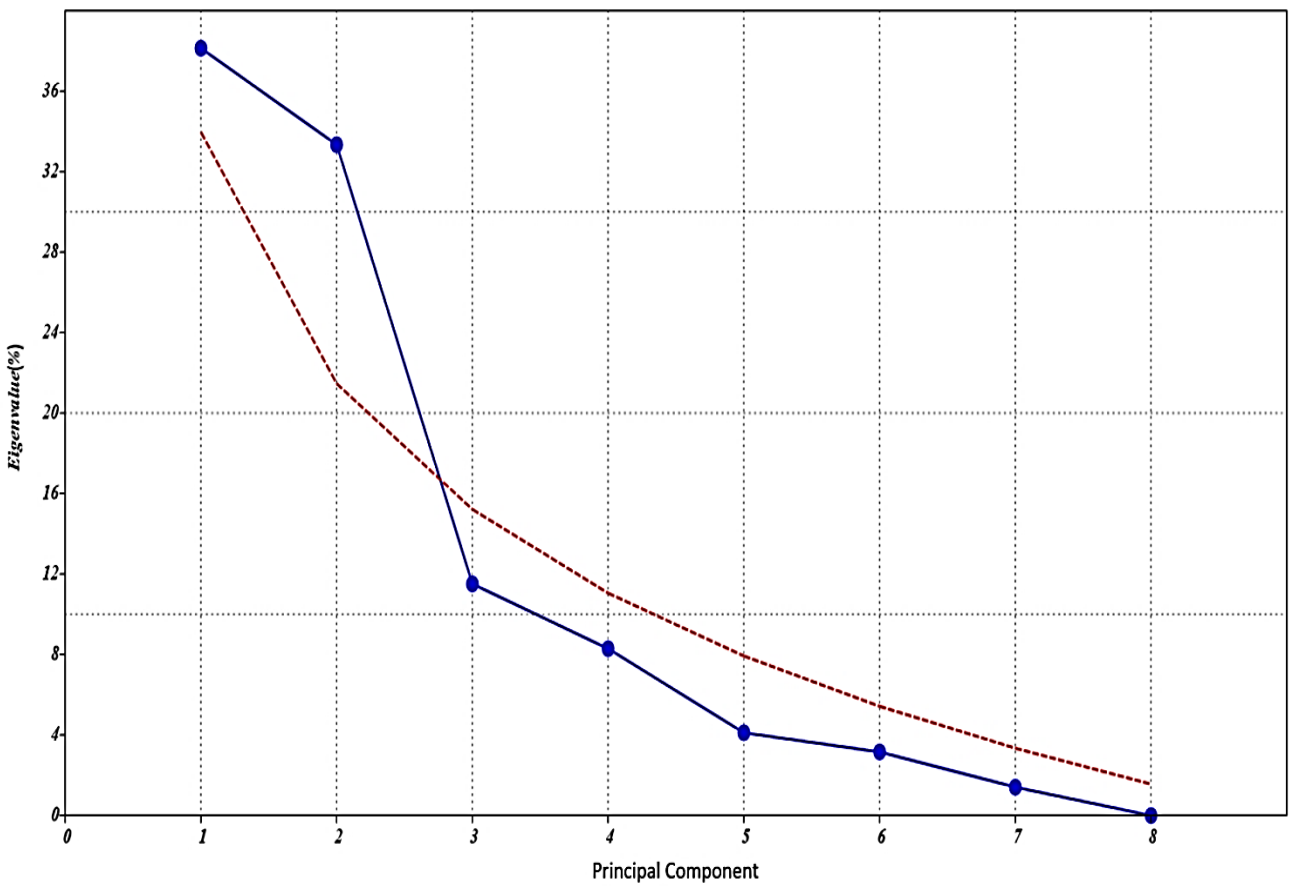


Fig. 3. Screen plot for principal component analysis.

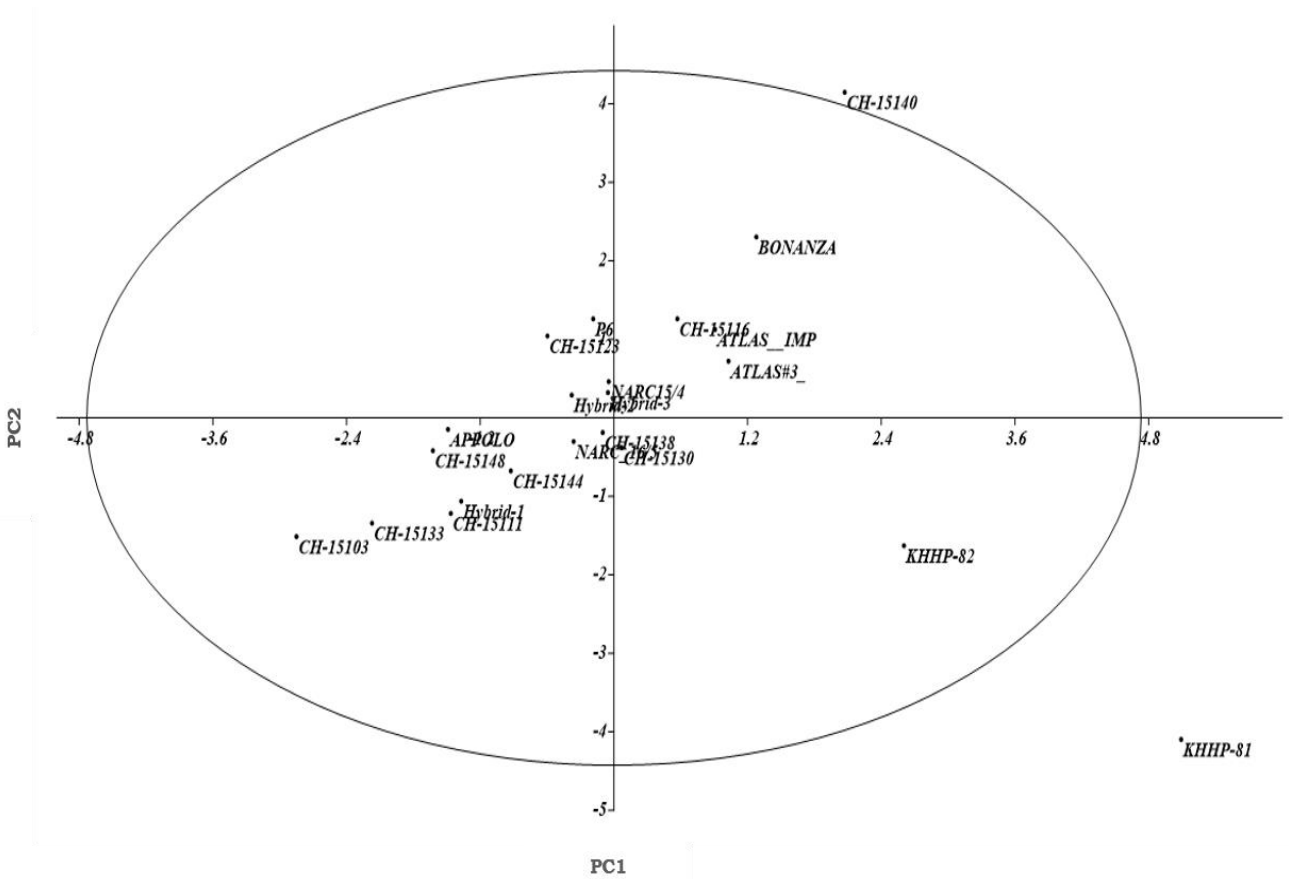


Fig. 4. Scatter plot diagram constructed for 22 chilli genotypes.

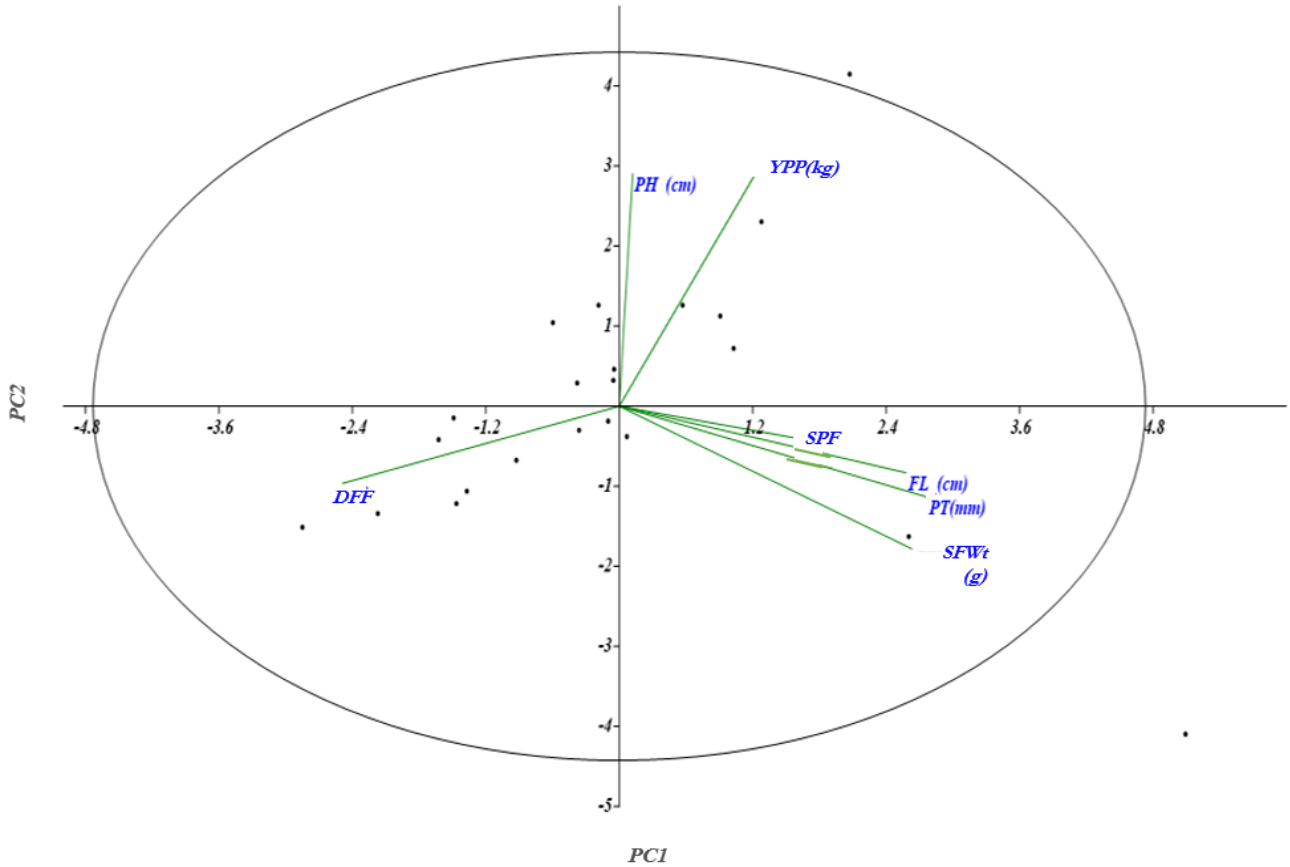


Fig. 5. Scatter plot diagram for various traits.

**Principal component analysis:** Principal component analysis distributed the variability into various components (Table. 5). Principal component analysis (PCA) was made from the first 2 axes because it expressed better total variability of the plant material (71.5%). The selection of principal components was highly dependent upon the Eigen values of principal components (Kovacic, 1994; Saba *et al*., 2017). The first PC contributed 38.15% while second PC contributed 33.35% variability. Screen plot diagram (Fig. 3) also revealed two main components, having Eigen value greater than 1.

**Scatter plot constructed for genotypes and traits:** First two PCs showed highest variance and were used to make a scatter plot based upon the morphological characteristics in various chilli genotypes. Scatter plot diagram (Fig. 4) constructed for 22 chilli genotypes described six cultivars i.e., Bonanza, CH-15140, P6, CH-15103, KHHP-81 and KHHP-82 as highly diverse, as they were spotted away from other genotypes.

Among eight traits (Fig. 5) studied, five traits plant height, single fruit weight, fresh fruit yield ($t.ha^{-1}$), pericarp thickness and fruit length showed maximum variation as these characteristics were found distant from the point of origin and lines representing these traits were longer in length. Days to 50% flowering showed negative interaction with all other traits studied as it was present on the negative axis.

**Acknowledgements**

This research work on chilli hybrid development is an endeavor of one of the students from the University of Peshawar, who worked with the team of scientists. The research work was done in "Indigenization of Hybrid Seed Production Technology (IHSPT-PSDP)" sponsored by the Government of Pakistan. Under which many students and internees from different universities of the country were trained in the hybrid technology. The field supervision staff members especially Mr. Shahbaz Gill is also acknowledged for providing a helping hand in data collection and other field operations. The authors also duly acknowledge the support of Dr. Muhammad Shafique Zahid Project Director (IHSPT).

**References**

Allard, R.W. 1960. *Principles of Plant Breeding*. John Wiley and Sons Inc., New York. p. 485.

Amit, K., I. Ahad, V. Kumar and S. Thakur. 2014. Genetic variability and correlation studies for growth and yield characters in chilli (*Capsicum annuum* L.). *J. Spp Aroma. Crops*, 23(2): 170-177.

Anonymous. 2014-15. Ministry of National Food Security and Research, Government of Pakistan.

Anonymous. 2015. Pakistan Bureau of Statistics, Government of Pakistan.

Anonymous. 2018. Fruit, vegetables and condiments statistics of Pakistan (2018-19). Ministry of National Food Security & Research, Islamabad.

Anonymous. 2020. Chillies and pepper dry. Food and Agriculture Organization of the United Nations.

Basavaraja, S. 2006. Variability and correlation studies in chilli (*Capsicum annuum* L.). *Karnataka J. Agri. Sci*. 19 (4): 888-891.

Bhagwati, R.R. and S. Changkija. 2009. Genetic variability and traditional practices in Naga king chilli landraces of Nagaland. *Asian Agri-History*, 13(3): 171-180.

Bijalwan, P and N. Madhvi. 2016. Genetic variability, heritability and genetic advance of growth and yield components of chilli (*Capsicum annuum* L.) genotypes. *Int. J. Sci. Res*., 7(5): 1305-1307.

Burton, G.W. and E.H. DeVane. 1952. Estimation of heritability in tall *Festuca* (*Festuca arundinacea*) from replicated clonal material. *Agron. J*., 45(4): 478-481.

Butchera, J.D., K.M. Crosbya, K.S. Yooa, B. Patil, J.L. Jifon and W.L. Rooneyc. 2013. Heterosis in different $F_1$ (*Capsicum annuum*) genotypes for fruit traits, ascorbic acid, capsaicin and flavonoids. *Sci. Hort*., 159(2): 72-79.

Cankaya, S., A. Balkaya and O. Karaagac. 2010. Canonical correlation analysis for the determination of relationships between plant characters and yield components in red pepper (*Capsicum annuum* L.) genotypes. *Spanish J. Agri. Res*., 8(1): 67-73.

Chattopadhyay, A., A.B. Sharangi, N. Dai and S. Dutta. 2011. Diversity of genetic resources and genetic association analyses of green and dry chillies of eastern India. *Chilean. J. Agric. Res*., 71(3): 350-356.

Datta, S. and J.C. Jana. 2004. Studies on the performance of chilli genotypes under Terai zone of west Bengal. *Ind. J. Hort*., 65(3): 353-355.

Datta, S. and L. Das. 2013. Characterization and genetic variability analysis in *Capsicum annuum* L. germplasm. *SAARC J. Agric*. 11(1): 91-103.

Devi, D.S. and R. Aramugam. 1999. Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.). *Crop Res.*, 17: 90-93.

Elahi, Z., N.N. Nawab, A. Ramzan, T. Noor, M. U. Qasim, T. N. Khan and N. Batool. 2017. Hybrid performance and analysis of genetic variability in green chillies (*Capsicum annum* L.). *Pak. J. Bot*., 49(6): 2221-2225.

Elahi, Z., N.N. Nawab, T. N. Khan, A. Ramzan, M. U. Qasim, T. Noor, M.S. Tariq and Muhammad Farooq. 2019. Assessment of genetic variability and association between yield and yield components in indigenously developed chilli hybirds (*Capsicum annum* L.). *The J. Anim. Plant Sci*., 29(5): 1318-1324.

Erickson, E.R. and A.F. Markhart. 2002. Flower developmental stage and organ sensitivity of bell pepper (*Capsicum annuum* L.) to elevated temperature. *Plant Cell & Environ.*, 25: 123-130.

Hasanuzzaman, M. and F. Golam. 2011. Selection of traits for yield improvement in chilli (*Capsicum annuum* L.). *J. Innov. Dev. Strategy*, 5: 78-87.

Janaki, M., L. Naram, N.C.V. Ramana and M.P. Rao. 2015. Assessment of genetic variability, heritability andgenetic advance for quantitative traits in chilli (*Capsicum annuum* L.). *Suppl. Gen. Plant Breed*., 10(2): 729-733.

Jaynes, D.B., T.C. Kaspar, T.S. Colvin and D.E. James. 2003. Cluster analysis of spatiotemporal corn yield pattern in an Iowa field. *Agron. J*., 95: 574-586.

Johnson, H.W., H.F. Robinson and R.E. Comstock. 1955. Estimates of genetic and environmental variability in soya bean. *Agron. J*. 47: 314-318.

Kadwey, S., A. Dadiga and S. Prajapati. 2016. Genotypes performance and genetic variability studies in hot chilli (*Capsicum annum* L.). *Ind. J. Agri. Res*., 50(1): 56-60.

Kovacic, Z. 1994. Multivarijaciona analiza. Univerzitet u Beogradu, Ekonomski fakultet, 282str.

Krishna, C.U., M.B. Madalageri, M.P. Patil, R. Mulage and Y.K. Kotlkal. 2007. Variability studies in green chilli (*Capsicum annuum* L.). *Karnataka J. Agri. Sci*., 20(1): 102-104.

Kumar, D., V. Bahadur, S.B. Rangare and D. Singh. 2012. Genetic variability, heritability and correlation studies in chilli (*Capsicum annuum* L.). *Hort. Flora Res. Spec*., 1: 248-252.

Lahbib, K., F. Bnejdi and M. Gazzah. 2012. Genetic diversity evaluation of pepper (*Capsicum annuum* L.) in Tunisia based on morphologic characters. *Afr. J. Agri. Res*., 23(7): 3413-3417.

Lakshmi, R.R. and M.V. Naidu. 2010. Evaluation of chilli (*Capsicum annun* L.) varieties in high altitude and tribal zone of Sarikulam district of Andhra Paradesh. *J. Res. Angrau*., 15(2): 15-19.

Luitel, B.P., C.S. Yoon, Surendra and W.H. Kang. 2013. Correlation and path coefficient analysis for fruit yield and quality characters in segregating population of mini-paprika (*Capsicum annuum* L.). *J. Agri. Life Env. Sci*., 25(1): 1-7.

Manju, P.R. and I. Sreelathakumary. 2002. Genetic variability, heritability and genetic advance in hot chilli (*Capsicum chinense* Jacq.). *J. Trop. Agri*., 40(1): 4-6.

Meena, M.L., N. Kumar, J.K. Meena and T. Rai. 2016. Genetic variability, heritability and genetic advances in chilli, (*Capsicum annuum* L.). *Biol. Biotech. J. Spp. Aroma. Crops*, 22(2): 154-164.

Nawab, N.N., G.M. Subhani and M.N. Ullah. 2013. Patterns of morphological diversity and character association in chickpea genotypes through multivariate approach. *J. Anim. Plant Sci*., 23(4): 1107-1114.

Nawab, N.N., Q. Shakil, S. Niaz, M.M. Iqbal, M.A. Asif and I.A. Khan. 2011. Genetics of trichomes and its association with fibre and agronomic traits in cotton. *Afr. J. Biotechnol*., 10(20): 3964-3972.

Nawab, N.N., S. Niaz and A. Rashid. 2019. Peas 2009: A high yielding pea variety for early, mid and late growing seasons in Punjab. *Int. J. Agri. Biol*., 22: 43-50.

Nehru, S.D., A. Manjunath and S. Rangaiah. 2003. Genetic variability and stability for fruit yield and other characters in chilli (*Capsicum annum* L.). *Karnataka J. Agri. Sci*., 16(1): 44-47.

Noor, T., A. Shahzad, N.N. Nawab, G.M. Ali and A. Ramzan. 2020. Authentication of indigenously developed chilli (*Capsicum annuum* L.) hybrids through ISSR markers. *Pak. J. Bot*., 52(6): 2157-2163.

Pandit, M.K. and S. Adhikary. 2014. Variability and heritability estimates in some reproductive characters and yield in chilli (*Capsicum annuum* L.). *Int. J. Plant Soil Sci*., 3(7): 845-853.

Parkash, C. 2012. Estimation of genetic variability and implications of direct effects of different traits on leaf yield in bathua (*Chenopodium album*). *Ind. J. Agri. Sci*., 82(4): 71-74.

Patel, M.P., A.R. Patel, J.B. Patel and J.A. Patel. 2010. Heterosis for green fruit yield and its components in chilli (*Capsicum annuum* L.) over environments. *Elect. J. Plant Breed*., 6(1): 1443-1453.

Peter, K.V. and B. Rai. 1978. Heterosis as a function of genetic distance in tomato. *Ind. J. Genet. Plant Breed*., 38 (2): 173-178.

Rao, N.S.B. 2005. Heterosis and combining ability in chilli (*Capsicum annuum* L.) M.Sc. Agri. Thesis, Acharya N. G. Ranga Agricultural University, Hyderabad.

Rego, E.R.M., M.D. Rego, C.D. Cruz, F.L. Finger and V.W.D.C. Genet. 2011. Phenotypic diversity, correlation and importance of variables for fruit quality and yield traits in Brazilian peppers (*Capsicum baccatum*). *Genet. Resour. Crop Evol*., 58: 909-918.

Robinson, H.F., R.E. Comstock and P.H. Harvey. 1949. Estimates of heritability and degree of dominance in corn. *Agron. J*. 41: 253-259.

Rosmaina, Syafrudin, Hasrol, F. Yanti, Juliyanti and Zulfahmi. 2016. Estimation of variability, heritability and genetic advance among local chili pepper genotypes cultivated in peat lands. *Bulgarian J. Agri. Sci*., 22: 431-436.

Saba, I., P.A. Sofi, N.Z. Zeerak, R.R. Mir and M. Gull. 2017. Using augumented design for evaluation of common bean (*Phaseolus vulgaris* L.) germplasm. *Int. J. Curr. Microbiol. Appl. Sci*., 6(7): 246-254.

Sharma, S., S. Barche, S. Sengupta, B.Verma and T. Jamkar. 2014. Genetic variability, heritability and genetic advance in chilli (*Capsicum annum* L.). *Int. J. Farm. Sci*., 4(4): 112-116.

Sharma, V.K., C.S. Semwal and S.P. Uniyal. 2010. Genetic variability and character association analysis in bell pepper (*Capsicum annuum* L.). *J. Hort. Forest*., 2(3): 58-65.

Shivasubramanian, S. and N. Menon. 1973. Heterosis and inbreeding depression in rice. *Madras Agri. J*., 60: 1139-1144.

Shrestha, S.L., B.P. Luitel and W.H. Kang 2011. Heterosis and heterobeltiosis studies in sweet pepper (*Capsicum annuum* L.). *Kang Hort. Environ Biotechnol*., 52(3): 278-283.

Singh, P.K., A. Kumar and I. Ahad. 2014. Correlation and path coefficient analysis in yield contributing characters in chilli (*Capsicum annum* L). *Int. J. Farm Sci*., 4(4): 104-111.

Singh, R.K. and B.D. Chaudary. 1985. *Biometrical methods in quantitative genetic analysis*. Kalyani Publ. New Delhi.

Singh, Y., M. Sharma and A. Sharma. 2009. Genetic variation, association of characters and their direct and indirect contributions for improvement in chilli peppers. *Int. J. Veg. Sci*., 15(4): 340-368.

Smitha, R.P. and N. Basavaraja. 2006. Variability and correlation studies in chili (*Capsicum annuum* L.). *Karnataka J. Agri. Sci*., 19(4): 888-891.

Sood., S. and N. Kumar. 2010. Heterotic expression for fruit yield and yield components in intervarietal hybrids of sweet pepper (*Capsicum annuum* L.). *SABRAO J. Breed. Gen.,* 42(2): 106-116.

Sreelathakumary and L. Rajamony. 2004. Variability, heritability and genetic advance in chilli (*Capsicum annuum* L.). *J. Trop. Agri*., 42(2): 35-37.

Steel, R.G.D. and J.H. Torrie. 1980. *Principles and procedures of statistics, a biological approach*, 2nd ed. McGraw Hill, Inc. New York, Toronto, London.

Tembhurne, B.V., Revanappa and P.H. Kuchanur. 2008. Varietal performance, genetic variability and correlation studies in chilli (*Capsicum annuum* L.). *Karnataka J. Agri. Sci*., 21(4): 541-543.

Thul, S.T., R.K. Lal, A.K. Shasany, M.P. Darokar, A.K. Gupta, M.M. Gupta, R.K. Vermaand and S.P.S. Khanuja. 2009. Estimation of phenotypic divergence in a collection of *Capsicum* species for yield related traits. *Euphytica*, 168(2): 189-196.

Ukkund, K.C., M.B. Madalageri, M.P. Patil, R. Mulage and Y.K. Kotlkal. 2007. Variability studies in green chilli (*Capsicum annuum* L.). *Karnataka J. Agri. Sci*., 20(1): 102-104.

Usman, M.I., M. Rafii, M.R. Ismail, M.A. Malek and M. Latif. 2014. Heritability and genetic advance among chilli pepper genotypes for heat tolerance and morpho-physiological characteristics. *Sci. World J*., 1-14.

Vani, S.K., O. Sridevi and P.M. Salimath. 2007. Genetic divergence in chilli (*Capsicum annuum* L.). *Ann. Biol*., 23(2): 123-128.

Vikram, A., I. Warshamana and M. Gupta. 2014. Genetic correlation and path coefficient studies on yield and biochemical traits in chilli (*Capsicum annuum* L.). *Int. J. Farm. Sci*., 16(2): 70-75.

Yadata, B., D. Belew, W. Gebreselasie and F. Marame. 2011. Variability, heritability and genetic advance in hot pepper (*Capsicum annum* L.) genotypes in West Ethiopia. *Amer. J. Agri. & Environ. Sci*., 587-592.

Yatung, T., R. K. Dubey, V. Singh and G. Upadhyay. 2014. Genetic diversity of chilli (*Capsicum annuum* L.) genotypes of India based on morpho-chemical traits. *Aust. J. Crop Sci*., 8(1): 97-102.

(Received for publication 26 April 2021)