Original Research Article

The genetic dissection of economically important traits in chilli genotypes (*Capsicum annuum* L.) through multivariate analysis

Abstract:

Chilli (*Capsicum annuum* L.) cultivar share a variety of different and intriguing growth and yield characteristics, for a plant breeder studies on genotypic and phenotypic relationship for horticulture cum vegetable spicy crop and its traits are useful to design, evaluate and to develop selection criteria for desired traits. With this background information the present study focused on identification of crucial characteristics required for boosting yield and to determine the parameters for the selection of superior genotypes. A total of 30 chilli genotypes were subjected to variability, divergence and mutual correlation studies for yield and yield component traits by using multivariate analysis. Results from the ANOVA and variability revealed highly significant differences at ($p \leq 0.01$) and ($p \leq 0.05$) for all the studied traits. The highest GCV and PCV were observed for FL fallowed by FYP, NFP, IFW, WPDM, FD, PH and NSF respectively, except for MC has revealed low GCV and PCV. All the traits were shown the presence of high heritability (h^2h^2) in broad sense (>60%) coupled with high GAM (>20%), except for MC, indicating the presence of positive additive gene action and effective transmission of characters to the next generation with selection. Highly significant and positive strong correlation was observed for IFW ($r = 0.68^{**}$), WPDM ($r = 0.54^{**}$), TW ($r = 0.40^{*}$) and FD ($r = 0.37^{*}$) with FYP, while the path analysis revealed highest direct effect for the traits such as FPT, FL and NFP. Principle component analysis revealed a 70.60% total variation accounted with first four PCAs with Eigen vector values more than one. Further cluster analysis grouped the 30 chilli genotypes into four major cluster (Cluster I, II, III and IV) and combined cluster analysis identified genotypes contributing to the maximum variability, *viz*., cultivars such as LIPSTICK, B.KADDI, B.DABBI, BHOOT JALOKIA, SUM- 17, BCH- 42, PBC- 80, LCA- 310, M- 262, KA2- L, S. SELECTION 1, JCH- 42 and 9608- U, so these genotypes serves as a donor for further breeding programme to develop superior cultivars.

Key words: Chilli (*Capsicum annuum* L.), Analysis of variance, Genetic divergence, Principle component analysis.

Introduction:

Chilli (*Capsicum annuum* L.) a diploid species (2n = 24), with genus *Capsicum* belongs to the family Solanaceae (Tilahun *et al*., 2022), The 31 species of the genus *Capsicum* vary greatly in terms of morphology, particularly in terms of fruit color, size, shape, and levels of pungency (Cardoso *et al*., 2018), among these only five - *C. annuum* (hot chilli), *C. baccatum* (pungent chilli), *C. chinense* (West Indies chilli), *C. frutescens* (bird chilli), and *C. pubescens* (sweet pepper) have been domesticated and cultivated. The fruits are botanically known as berries, unlike most berries, chilli seeds are not embedded in the fleshy pericarp but are located in the placenta which is a surface of the carpel where the potential ovules are attached. In India chilli is one of the cutting edge vegetable cum spice crops valued for its aroma, taste, flavor, pungency and an important dietary component for Indians, that food is tasteless without chillies and their by- products. Considering that it is used in mature dried fruit as a spice and fresh green fruit as a vegetable with other foods. In addition it's a richest source of vitamin 'C' and anti- oxidant (Azlan *et al*., 2022; Paul *et al*., 2013), so it is appreciated as a medicinal and a decorative, and it is utilized in the culinary industry for flavour and coloring (Mongkolporn *et al*., 2011).The world's largest producer, user, and exporter of chillies is India, which also has the largest land area (7.33 lakh ha, or 42.81% of the global area).According to the Chilli Outlook 2021, India produces the most chillies in the world with 17.64 lakh tonnes, followed by China, Ethiopia, Thailand and Pakistan.

The origin of chilli is believed to be in Mexico with secondary centres in Guatemala and Bulgaria. It was introduced to Europe by Columbus in the 15th century and spread to the rest of the globe along the spice trading routes to Africa, India, China, and Japan (Kadwey *et al*. 2016). As a highly commercialised crop for extraction of oleoresin, in India it is grown under diverse ecosystems with major producing states as Andhra Pradesh, Telangana, Madhya Pradesh, Karnataka and West Bengal respectively (FAO, 2021), it ispopularly known as *mirchi* in Karnataka, the average yield of chilli in North Karnataka is higher side than in South, primly due to the difference in the soil and agro- climatic conditions (Ashoka *et al.*, 2022). The genetic variability and characteristic associations were previously studied by various workers, especially for *annuum spp* as it is the most eco- friendly species in the Indian subcontinent with great export potential (Choudhary and Samadia 2004). The Indian germplasm is mainly represented by two species, *C. annuum* and *C. frutescens* with autogamous *spp* however the most number of current cultivars are open pollinated varieties with 7- 90% cross pollination (Choudhary and Samadia, 2004; Paul *et al*., 2013; Tilahun *et al*., 2022).

Large genetic variety is present throughout India and beyond in the majority of its farmed areas as a result of the crop's long history of cultivation, outcrossing nature, bearing habit and crop duration and popularity (Kannan *et al*., 2016; Yatung *et al*., 2014).The population's genetic diversity aids in the identification of appropriate parents for use in chilli crop breeding programmes (Patel *et al*., 2011).Given that fruit yield is a complex trait influenced by a multitude of contributing characters (polygenic traits and their interaction), it is imperative to understand the significance of inter- association of different component characters and their association with fruit yield before breeding through selection (Yumnam*et al*., 2012; Iqbal *et al*. 2015).The information on genetic variability and character association with yield and its components are most crucial as it is a cash crop, to initiate the breeding programme to evolve high yielding varieties. Very little research work has been done in understanding the genetic diversity and phenotypic variability for diverse morpho- economic traits. By considering above available background information, the present study was undertaken to estimate the extent of genetic variability, principal component analysis (PCA), direct and indirect effects, character association, and clustering analysis in the chilli genotypes were done to understand existing variability through the multivariate statistical parameters, which is a prelude to potential chilli crop improvement.

Material and Method

Experimental Material and site:

The experiment was carried out at College of Agriculture, University of Agricultural Sciences (UAS) Raichur (Karnataka) during *Kharif* - 2020. The experiment material comprised of 30 diverse chilli genotypes including two checks like Byadgi Kaddi and Byadgi Dabbi, the details were given in Table 1. Byadgi chilli is a famous variety of chilli belongs to the species (*Capsicum annum* L.) grown in Karnataka state and it is named after the town, Byadgi, which is Taluk headquarter in the Haveri district of Karnataka. Byadgi chillies were designated as a Geographical Indication (GI application No. 129) product. Byadagi Kaddi and Byadagi Dabbi are the two primary varieties of Byadgi chillies grown in Karnataka. The key feature of Byadagi Kaddi has long fruit length (10 to 15) cm with very little pungency and it is thin, linear, light green in color, maturing to a deep red colour at the stage of ripening, develops the distinctive wrinkles. Another Byadagi chilli variation that works well for dry and green chilli purposes is the Byadagi Dabbi. The fruits have a medium length (8 to 10 cm), a small apical curvature, and a slight bulge at the calyx base, this particular cultivar is more prone to disease and pests. However the Byadagi Dabbi Chilli meets the same standards of excellence as the Byadagi Kaddi.

Experimental layout and data record

The experiment materials were grown in a randomized complete block (RCBD) design with two replications. Each experimental unit was represented by single row accommodating 10 plants with 75x45 cm inter and intra row spacing. Normal crop was raised by following all recommended cultural practices and plant protection measures. Five competitive plants were selected at random from each single row plot in each replication and observations were recorded on 12 economically useful traits *viz*., plant height (PH: cm), number of primary branches per plant (NPBPP), number of fruits per plant (NFP), fruit diameter (FD: mm), fruit length (FL: cm), individual fruit weight (IFW: g), number of seeds per fruit (NSF), test weight (TW: g), whole plant dry matter (WPDM: g), moisture content (MC: %), fruit pericarp thickness (FPT: mm) and fruit yield per plant (FYP: g).

Statistical analysis:

The mean over replication of data for each character was subjected to statistical analysis. The estimates of genotypic and phenotypic coefficient of variation and ANOVA, correlation, principle component analysis (PCA) was carried out by using standard protocol package called (*ggplot, agricolae, corrplot*,) R software (*version 4.3.2*) (R Core Team 2020), while the path coefficient analysis was carried out as per method given by Dewey and Lu (1959). Cluster analysis were done by Ward’s method using Paleontological Statistics Software (PAST) *version 4.03* (Hammer *et al*., 2001) package for education and data analysis.

Results and discussion:

ANOVA: A source of variation in chilli genotypes

The results of ANOVA from mean sum of squares (MSS) for yield and yield attributing traits in 30 chilli genotypes were given in Table 2. The results revealed that MSS due to genotypes were highly significant ($p<0.01$ and $p<0.05$) for all the traits under study, *viz.*, PH:

521.93**;NPBPP: 0.34**; NFP: 724.70**; FD: 16.69**; FL: 16.53**; IFW: 0.09**; NSF: 583.05**; TW: 1.35**; WPDM: 202.66**; MC: 66.72**; FPT: 0.08**; FYP: 552.92**.The MSS due to replication has revealed presence of significant difference ($p<0.01$ and $p<0.05$) for only three traits among the twelve investigated features such as FD: 5.51*; FL: 8.22** and MC: 16.99* for yield and its related traits (Table 2).The size of the observed significant differences suggested that the genotypes under investigation exhibit a greater amount of genetic diversity. The coefficient of variation (CV %) was substantial heterogeneity for yield and yield related component, for instance, the CV were reasonably higher for FPT: 10.82%; NPBPP: 9.60% with the least CV obtained for NFP: 1.90% and MC: 2.14%. The overall result of ANOVA revealed that, MSS due to genotypes and replication contributing for the existence of significant difference and to the variability. In literature similar kind of results were obtained from Pradhan *et al*., 2016; Usman *et al*., 2014; Dhal *et al*., 2021; Khan *et al*., 2022 and Jyothi *et al*., 2011.

Evaluation of the average performance and genetic plasticity:

Selection criteria for breeder preference depends on the extent of variation in fruit yield and its contributing agronomic traits including growth and yield parameters such as plant height (PH), number of primary branches per plant (NPBPP), number of fruits per plant (NFP), fruits diameter (FD), fruit length (FL), individual fruit weight (IFW), number of seeds per fruits (NSF), test weight (TW), whole plant dry matter (WPDM), moisture content (MC), fruit pericarp thickness (FPT) and fruit yield per plant (FYP). These were examined, for the mean value ($\Sigma x \Sigma x$), range, genetic variance components such as genotypic and phenotypic coefficient of variation (GCV and PCV) ($\sigma^2 g \sigma^2 g$ and $\sigma^2 p)\sigma^2 p)$, broad sense heritability ($h^2 h^2$) and genetic advance percent mean (GAM) as shown in Table 3 along with box plot showing replication wise graphical representation of frequency distribution for each traits. The box indicating the existence of the 50% of our data within the box, the lower end of the box is 1st quartile (Q_1), the upper end of the box is 3rd quartile (Q_3) which shows the existence of the 25% of our data above the Q_3 and below the Q_1 we find remaining 25% of the data distribution, the range between Q_1 and Q_3 are called inter- quartile range with solid line indicating the median value of the data distribution, the points above the outlier are the maximum value for the traits as shown in Figure 1. Genetic variability revealed existence of wide spectrum of variability in the mean performance among the 30 chilli genotypes for all the traits indicating the presence of sufficient genetic variability, PH was varied from 50.00 to 111.00 cm with $\bar{X}\bar{X}$ = 72.71 cm, GCV and PCV for the traits was 22.16 and 22.26 with h^2h^2 of 99.04 and GAM of 45.43. NPBPP was varied from 2.00 to 3.00 with $\bar{X}\bar{X}$ = 2.31, GCV and PCV for the traits was 16.57 and 19.14 with h^2h^2 of 74.90 and GAM of 29.54. NFP was varied from 21.85 to 127.00 with $\bar{X}\bar{X}$ = 63.80, GCV and PCV for the traits was 29.80 and 29.86 with h^2h^2 of 99.60 and GAM of 61.27. In chilli the size of the fruit is maximum at shoulders so in the current work FD was varied from 5.45 mm to 20.80 mm with $\bar{X}\bar{X}$ = 11.89 mm, GCV and PCV for the traits was 23.97 and 24.58 with h^2h^2 of 95.09 and GAM of 48.15. FL was varied from 1.55 cm to 13.56 cm with $\bar{X}\bar{X}$ = 6.81 cm, GCV and PCV for the traits was 41.93 and 42.45 with h^2h^2 of 97.55 and GAM of 85.32. IFW was varied from 0.29 g to 1.34 g with $\bar{X}\bar{X}$ = 0.75 g, GCV and PCV for the traits was 27.72 and 28.93 with h^2h^2 of 91.81 and GAM of 54.72. NSF was varied from 41.00 to 119.50 with $\bar{X}\bar{X}$ = 78.23, GCV and PCV for the traits was 21.71 and 21.93 with h^2h^2 of 98.07 and GAM of 44.30. TW was varied from 3.70 g to 7.60 g with $\bar{X}\bar{X}$ = 4.81 g, GCV and PCV for the traits was 16.90 and 17.30 with h^2h^2 of 95.44 and GAM of 34.02. WPDM was varied from 13.48 g to 55.50 g with $\bar{X}\bar{X}$ = 39.59 g, GCV and PCV for the traits was 25.33 and 25.50 with h^2h^2 of 98.67 and GAM of 51.84. MC was varied from 50.32% to 78.04% with $\bar{X}\bar{X}$ = 66.35%, GCV and PCV for the traits was 8.57 and 8.83 with h^2h^2 of 94.13 and GAM of 17.13. FPT was varied from 0.69 mm to 1.65 mm with $\bar{X}\bar{X}$ = 1.15 mm, GCV and PCV for the traits was 15.91 and 19.24 with h^2h^2 of 68.36 and GAM of 27.10. FYP was varied from 30.70 g to 87.00 g with $\bar{X}\bar{X}$ = 51.45 g, GCV and PCV for the traits was 32.26 and 32.36 with h^2h^2 of 99.38 and GAM of 66.25.The maximum range of variability reported in the current study's analyses of all the traits was found in the number of fruits per plant, the number of seeds per fruit, plant height, fruit yield per plant, and whole plant dry matter, while the minimum range of variability was found in the thickness of the fruit pericarp and the number of primary branches per plant (Table 2), most of the traits exhibit a wide range of variance, which provides room for enhancement of desirable types. The traits TW, NPBPP, and FPT showed moderate genotypic and phenotypic coefficients of variation (GCV and PCV), while only MC revealed the presence of low GCV and PCV. The highest GCV and PCV were observed for FL fallowed by FYP, NFP, IFW, WPDM, FD, PH, and NSF, respectively. Except for MC, which showed high heritability with a moderate amount of GAM, all the characteristics (PH, NPBPP, NFP, FD, FL, IFW, NSF, TW, WPDM, FPT, and FYP) were demonstrated to have high heritability in a wide sense (>60%) paired with high GAM (>20%).Since heritability value alone does not have much significance because it does not take into account the magnitude of absolute variability, the genetic progress is still a more meaningful assessment. In order to determine the projected genetic gain through selection, it is consequently required to use heritability in conjunction with selection differential or genetic advance and the expected genetic advance in *per- cent* mean were shown in Table 2. In the current study, the gain ranged from 17.13 (MC) to 85.32 (FL) and could be reached by choosing the genotypes that make up the top 5% of all genotypes.

Since high heritability estimates for quantitative traits have been found to be helpful for selection based on phenotypic performance, the present study's h^2h^2 estimates were high for all the traits and ranged from 68.36 to 99.60%, indicating that a greater proportion of phenotypic variance was attributed to the genotypic variance and was less influenced by environmental effects, and the characters are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a character and thus selection based on phenotypic expression could be relied upon, hence, selection can bring worthwhile improvement in these traits (Table 3) and this variation indicated the possibility of obtaining very high selection response with respect to these traits. Results were in accordance with the Pandit and Adhikary, 2014; Maurya *et al*., 2015, Pandiyaraj, 2017; Markam and Sharma., 2022, high heritability values for these variables suggest that genetic factors dominated the variation observed and that environmental factors had a less role. The occurrence of significant GCV for the qualities mentioned above indicates that these characters might be improved and fixed through altering selection. High GCV for green fruit yield per plant and number of fruit per plant was also reported by Munshi and Behera, 2000; Gogoi and Gautam , 2002; Sreelathkumary and Manju, 2002; Sreelathakumary and Rajamony 2004; Samadia, 2007, high heritability for PH, NPBPP, NFP, FD, FL, TW and FPT corroborate the findings of Ukkund *et al*., 2007; Tembhurne *et al*., 2008; Gupta *et al*., 2009; Sharma *et al*., 2010 and Kumar *et al*., 2012, while Markam and Sharma., 2022 reported high GCV, PCV, $h^2 h^2$, and GAM for fruit length, fruit diameter, and fruit thickness.

Phenotypic correlation:

Phenotypic correlation *ie*., the nature of mutual association of twelve yield and yield related traits for the 30 chilli genotypes were presented in Figure 2. In the present study, correlation coefficients ranged from − 0.51 (NFP *vs*. FD) to 0.68 (IFW *vs*. FY), for all traits examined, with the exception of NPBPP, there was a positive phenotypic connection between FYP and other traits. IFW: r = 0.68**; WPDM: r = 0.54**; TW: r = 0.40*; and FD: r = 0.37* have all shown a high positive and significant connection with FYP. The strong positive and significant correlation of the traits (IFW, WPDM, TW, and FD with FYP represent these characters are the main determinants and effective traits of fruit yield in chilli, suggests that these characters are useful for improving fruit yield through selective breeding because they contribute in a way that increases FYP in productivity, seed weight, and dry matter production. The result is in line with the work of other scholars Usman *et al*. 2017; Pradhan *et al*., 2016; Patel *et al*., 2015; Farwah *et al*., 2020; Tilahun *et al*., 2022 who observed that fruit yield per plant revealed strong and highly significant associations with fruit length, fruit weight, number of fruits and plant height at harvest characters.According to Lakshmi *et al*., 2017, average fruit weight and number of fruits per plant had a strong positive correlation with fruit yield in two tomato F_2 segregating populations. Bader and Gendy during 2018 reported significant positive association among fruit diameter and number of fruits per plant interpreted as the significant positive association for any pair of characters indicates that the improvement predicted under selection for one of them, would automatically extended to the other. Similar results were confirmed the above mentioned conclusion by Luitel *et al*., 2013, when studying a segregate population of *Capsicum annuum* L., a positive and significant link between the fruit length, width, and number of fruits per plant with and its overall production was confirmed by observing the correlation for features associated to yield.

On the other hand the overall inter correlation among the important yield attributing traits contributed to fruit yield per plant through the influence of following independent traits as fallows. The results illustrated that, a significant agronomic growth characteristic with a measurable feature is PH was non significantly correlated with all other traits however we noticed that the trait had maximum positive insignificant association with MC (r = 0.34) and fallowed the decreasing order of NSF: r = 0.31; IFW: r = 0.20; FYP: r = 0.14; TW: r = 0.11; FD: r = 0.09; FPT: r = 0.07; WPDM: r = 0.04 and NPBPP: r = 0.01in the present study it revealed direct link with the number of seeds per fruit, fruit weight, fruit diameter, plant dry matter production, that directly influences plant architecture with fruit yield potentiality through cell elongation rate, a clear evidence provided by Pradhan *et al*., 2016; Tembhurne *et al*., 2017, were they have reported positive association of plant height with the number of secondary and primary branches per plant, number of fruits per plant. The positive association of PH with FYP could be justified by the increase in the number of fruits as results of more number of branches per plant leading to higher fruit yield per plant. However the trait also revealed negative non- significant association with FL and NFP might be due to various factors have been advocated in contributing to negative relationships among plants components including competition for ambient resources such as nutrient, moisture, light; genetic factors such as linkage and pleiotropy (Misangu *et al*., 2007, Usman *et al*., 2017).

The NPBPP had revealed negative correlation for most of the traits except NFP, FL and NSF and *vice versa* is true, the positive association of NPBPP along with PH may be justifiable as the taller the plant produce more number of primary branches and more number of leaves which is very critical requirement for photosynthesis in plant intern will lead to the development of fruit bearing branches, Pandit, and Adhikary, 2014 were revealed similar results while studying reproductive characters in chilli genotypes collected from the local farmers and several researchers identified moderate to strong positive association between the different quantitative traits. The NFP was positive correlation with only for WPDM and FYP among other traits studied and *vice versa* is true, Ajjapplavara, *et al*., 2005; Kumari *et al*., 2011 reported negative correlation between fruit yield and primary branch per plant. FD had given positive association with traits like IFW, TW, FYP, FPT, WPDM, FL and MC. Fruit length was measured as the distance from pedicel attachment to its apex it has recorded highest inter- correlation with NSF: r = 0.50** fallowed by IFW: r = 0.32; FPT: r = 0.28; FYP: r = 0.23; NPBP: r = 0.17; TW: r = 0.15 and FD: r = 0.07 and *vice versa* is true. Pujar *et al*., 2017 revealed while studying with chilli germplasm accessions and popular local cultivar of Byadagi Kaddi and Byadagi Dabbi as the selection for higher number of fruits and longer fruited plants/fruit size would simultaneously result in selection for higher total fruit yield. Most of the studied traits has recorded strong inter-correlation with individual fruit weight and it is in the order of FYP: r = 0.68** followed by FD: r = 0.64**; FPT: r = 0.54**; TW: r = 0.50; WPDM: r = 0.39*; FL: r = 0.32; PH: r = 0.20; NSF: r = 0.19 and MC: r = 0.19 except for NPBP and NFP and *vice versa* is true. Number of seeds per fruit has revealed positive correlation in the order FL: 0.5**; PH: 0.34*; TW: 0.33*; FYP: 0.19; test weight has recorded positive significant association with FYP: 0.40**; MC: 0.34 and FPT, whole WPD M recorded positive significant association FYP: 0.54**; FPT: 0.35* and MC: 0.16, MC and FPT has revealed positive significant association with FYP: 0.23 and 0.18 respectively and *vice versa* is true.

Path analysis of fruit yield with other contributing traits:

Simple correlation metrics may not accurately capture the characteristics contribution to fruit yield, sometimes mislead may not be true always, so use of path analysis leads to partitioning of the data and permitting a critical examination of the relative importance of each trait (Kumar *et al*., 2013). In reality, path coefficient analysis provides a different image than correlation coefficients when evaluating the cause and effect relationship since it allows the correlation coefficients to be divided into components of direct and indirect effects. In the present work the path coefficient analysis was carried out using phenotypic correlation values of different yield components traits on fruit yield as an artefact, by using statistical software packages called Window stat *version 9.* The residual factor which measures the extent to which the causal factors implicated in the path analysis have explained the 33.00% variability in dependent character *ie*., fruit yield per plant and leaving 67.00% (p = 0.67) was unexplained. The results obtained in phenotypic direct and indirect effects as the path of influence of other quantitative characters on fruit yield per plant were presented in Table 3 and graphically shown in Fig. 3.

Direct effect on fruit yield:

Phenotypic correlations of the different characters were partitioned to path coefficient with the view to identifying important fruit characters having direct effect on yield. The characters contributing towards the highest positive direct effect *via* fruit yield per plant showed that FPT (p = 0.894), FL (p = 0.356), NFP (p = 0.246), PH (p = 0.239), TW (p = 0.213), IFW (p = 0.079), FD (p = 0.051), NPBPP (p = 0.028) and MC (p = 0.000). Even though the traits such as individual fruit weight, fruit diameter, number of primary branches and moisture content reported very small direct effect on fruit yield however these traits have a cumulative effect through its indirect effect. A similar trend of classification for path coefficient like as very high >1; 0.3-1 for high; 0.2-0.29 for moderate; 0.1-0.19 for low; 0.00-0.09 for negligible was noted by Lenka and Mishra 1973, and in our study the characters with direct favourable effect were observed for FPT, FL, NFP, PH and TW (Table 3, Fig. 3), which contributes maximum towards the fruit yield per plant, thus selection on the basis of those traits would be a paying preposition for evolving high yielding genotypes, so these characters can be used to develop an optimally reliable selection index for realizing improvement in chilli fruit yield. The importance of fruit length or size, fruit numbers and fruit weight and test weight has been highlighted by Jabeen *et al*., 2009; Sabin and Singh, 2009; Maga *et al*., 2013; Abraham *et al*., 2017; Bijalwan and Mishra, 2013, also verified positive direct effect of the variables on fruit yield in green pepper fruits, further Soares *et al*., 2017, in *C. chinense* L. reported that highest direct effects of FL, PH and FPT on fruit yield indicating a large contribution of these characters to increase the yield of peppers. However it is noted that the negative direct effect has observed for NSF ($p = -0.126$) and WPDM ($p = -0.007$), having all the traits in addition positive association with fruit yield per pant has revealed for all the studied traits in the order of individual fruit weight, test weight, fruit diameter, fruit length, moisture content, fruit pericarp thickness, plant height and number of fruits per plant except for number of primary branches per plant (Table 3) which contributed negatively to the fruit yield per plant, which means increase in the primary branches might contributes more to the vegetative growth rather than the contributing to the economic outcome. The present findings are in accordance with Tilahun *et al*., 2022 worked on green fruit chilli and reported as higher the number of fruits per plant and fruit length lead to an increased in chilli fruit yield.

Indirect effect on fruit yield:

The PH ($p = 0.130$)exhibited highest positive indirect effect towards FYP fallowed by WPDM ($p = 0.09$), IFW ($p = 0.073$), FL ($p = 0.056$), NSF ($p = 0.033$), FD ($p = 0.029$) and TW ($p = 0.019$), meanwhile, NPBPP ($p = 0.043$) has revealed highest positive indirect effect to the FYP *via* MC ($p = 0.006$), TW ($p = 0.002$), IFW ($p = 0.001$), FPT ($p = 0.001$), FD ($p = 0.000$), FL ($p = 0.000$) and NSF ($p = 0.000$). NFP showed highest positive indirect effect for FYP *via* two important weighted economic traits such as FYP ($p = 0.049$) and IFW ($p = 0.001$).FD ($p = 0.284$) has revealed highest positive indirect effect on FYP *via* FL (p = 0.026), NSF (p = 0.018), MC (p = 0.017), TW (p = 0.008), WPDM (p = 0.007), PH (p = 0.006), FPT (p = 0.001) and NPBPP (p = 0.000). These results confirmed by Lahbib *et al*., 2012 and Kadwey *et al*., 2015, Zhani *et al*., 2015, Munshi *et al*., 2000, Hasan *et al*., 2014 reported that plant height, number of primary branches, fruits number per plant and fruit diameter had an indirect and positive effect on production/plant, through other traits in pepper. FL (p = 0.600) has shown highest positive indirect effect on FYP through FD (p = 0.187), NSF (p = 0.151), MC (p = 0.147), TW (p = 0.136), WPDM (p = 0.103), PH (p = 0.084), FPT (p = 0.084), IFW (p = 0.048) and finally with the NPBPP (p = 0.002) except for NFP which has exhibited negative indirect effect on fruit yield.

Regarding IFW (p = 0.166) revealed positive indirect effect to FYP fallowed by FPT (p = 0.038), NSF (p = 0.027), PH (p = 0.024), FL (p = 0.010), WPDM (p = 0.010), MC (p = 0.002), TW (p = 0.001), NFP (p = 0.000) except with FD where it has exhibited negative indirect effect on fruit yield. Interestingly only two traits, NSF (p = 0.322) and NFP has revealed positive indirect effect on fruit yield per plant, while remaining traits revealed negative indirect effect on fruit yield *via* NSF. TW (p = 0.496) has shown highest positive indirect effect on FYP among all the traits studied in the present study fallowed by *via* MC (p = 0.084), FL (p = 0.081), NSF (p = 0.045), NFP (p = 0.043), FD (p = 0.035), WPDM (p = 0.031), PH (p = 0.017), NPBPP (p = 0.016), IFW (p = 0.005) except with FPT where it exhibited negative indirect effect on fruit yield *via* TW, it indicates that selection of promising genotypes with elevated fruit yield might be useful by the indirect selection of test weight and its positively associated characters. The dry matter of plant consists of all its constituents excluding water and this accumulation is increased in growth period and reach maximum at physiological growth period, so in the present study whole plant dry matter (p = 0.226) has revealed positive indirect effect on fruit yield fallowed by *via* FPT (0.001), NPBPP (p = 0.000), NFP (p = 0.000), IFW (p = 0.000). Sreekumar *et al*., 2023 while studying thecF_3 populations of Munduchilli cross (PKM CA 20 x PKM CA 08) reported positive direct and indirect effect of plant dry matter with the other agronomic traits, while, the trait was shown negative indirect effect via moisture content as the dry matter consist of all the cellular material except water or moisture content. Moisture content has revealed positive indirect effect on fruit yield via the other traits such as plant height, number of primary branches per plant, fruit diameter, fruit length, individual fruit weight, number of seeds per fruit and test weight as the water content is one of the most vital constituents in plants required for all the plant cellular growth. Fruit pericarp thickness has shown positive indirect effect on fruit yield via the other contributed traits such as IFW (p = 0.428), MC (p = 0.220), FL (p = 0.211), NSF (p = 0.130), NPBPP (p = 0.048) and FD (p = 0.002). so from overall study revealed that indirect effect on fruit yield is in the decreasing order of the traits like fruit length, test weight, number of seeds per fruit, fruit diameter, whole plant diameter, fruit pericarp thickness, moisture content, individual fruit weight, plant height, number of fruits per plant and number of primary branches per plant (Table 3 and Fig. 3).

Clustering and Principal Components Analysis:

For selecting the desired parents, estimation of existing diversity among the genotypes through genetic diversity analysis plays crucial role. The compiled information on the kind and extent of genetic variability is important for selecting the best parent for specific crosses. Analysis was carried out for yield and yield attributing traits in chilli genotypes in order to describe and to gain the better understand the source of genetic variation among the studied genotypes. The screen plot of the PCA showed in Fig. 4a and 4b explained both *percent* explained variation and eigen values associated with each principle component obtained by drawing a graph. The first four component *viz*., PC_1, PC_2, PC_3 and PC_4 revealed 31.50%, 14.60%, 13.10% and 11.40% of variations among the studied parameters respectively (Table 5; Fig.4a). The first four main PCAs are extracted from the complicated twelve PCA components, the total cumulative variance of these first four principal components (PC_1, PC_2, PC_3 and PC_4) account for 70.60% of the total variation. In literature similar results were reported for PCA analysis from Singh *et al*., 2020,

The eigenvectors decreased significantly from PC_1 (3.77) to PC_5 (0.86), it indicates that decrease in the eigenvalues after PC_5, the remaining principal components did not described much variation, thus only the first four PCs were considered which explaining much of the variation for the studied population. Elbow type with semi curve line is obtained after PC_5 tended to straight with minute difference observed in each PC and from the graph, it is clear that maximum variation was observed in PC_1 in comparison to the other four PCs, therefore the selection of lines for characters under PC_1 may be desirable, further principal components having more than one eigen value that showed more variation which act as key factor for selection of diverse breeding lines. The principle component with <1 Eigen value should be eliminated due to their minimum contribution towards variability. In literature similar results obtained from the morphological trait evaluation of chilli genotypes as mentioned by Lahbib *et al*., 2012, Hasan *et al*., 2014, Farhad *et al*., 2010. Results from rotated component matrix showed that the PC_1 which accounts for the maximum variability (31.50%) and highly loaded with characters such as IFW (0.464), FD (0.371), TW (0.356), FYP (0.351), FPT (0.308), WPDM (0.26), MC (0.155), FL (0.129), NSF (0.123) and PH (0.120) contributed in positive direction whereas, only the NPF and NPBPP contributed in negative direction as shown in Table 5 and Fig. 5b in variable PCA plot, PC_1 confirmed the maximum variability in association with the following 13 genotypes in the positive direction (LIPSTICK, B.KADDI, B.DABBI, BHOOT JALOKIA, SUM- 17, BCH- 42, PBC- 80, LCA- 310, M- 262, KA2- L, S. SELECTION 1, JCH- 42 and 9608- U), while remaining genotypes contributed in negative association to PC_1 (Table 6; Fig.5a). It clearly indicated that genotypes belongs to the PC_1 with positive association may be related to the major traits like fruit weight, fruit diameter, seed weight, fruit thickness and finally with the fruit yield thus PC_1 allows for the simultaneous selection of major economic traits with promising genotypes, results were accordance with Singh *et al*., 2020. Similarly, PC_2 accounted 14.60% of the total variation with 46.06% of cumulative proportion and loaded with the characters such as NSF (0.614) fallowed by FL (0.450), NPBPP (0.379), NFP (0.283), PH (0.232), FYP (0.192), TW (0.133), MC (0.132), IFW (0.033), while WPDM, FPT and FD contributed in the negative direction. PC_2 confirmed the maximum variability in association with the following 11 genotypes in the positive direction (KBCH- 1, O7- L, HDC- 75- 1, ACB1 L, LIPSTICK, S. SELECTION 2, 5- B, S. SELECTION 1, ENT- 1, RAJPUT and SUM- 17), while remaining genotypes contributed in negative association to PC_2 (Table 6; Fig.5a). It clearly indicated that genotypes belongs to the PC_2 with positive association were governed with major traits such as NSF, FL, NPBPP, NFP, PH, FYP and TW so on, PC_3 revealed 13.10% of the total variation with 59.21% of cumulative proportion and 1.57 of eigen values, it is loaded with the characters such as MC (0.489) fallowed by WPDM (0.361), NFP (0.356), PH (0.322), FYP (0.204),IFW (0.107) and TW (0.063), while, NSF, NPBPP, FD, FPT and FL contributed in the negative direction to PC_3, it is confirmed the maximum variability from the 14 genotypes such as RAJPUT, KA2- L, SITARA, JCH- 42, BCH- 42, S. SELECTION 1, S. SELECTION 2, S. SELECTION 3, O7- L, LCA- 310, P3, LCA- 960 and M- 262 while remaining genotypes contributed in negative association to PC_3.PC_4 revealed 11.40% of the total variation with 72.61% of cumulative proportion and 1.37 of eigen values, it is loaded with the characters such as WPDM (0.52) fallowed by NFP (0.46), FYP (0.288), FPT (0.221), FL (0.141), IFW (0.013), while, TW, FD, NSF, MC, NPBPP and PH contributed in the negative direction to PC_4, it is confirmed the maximum variability from the 17 genotypes such as 5- B, S. SELECTION 2, LCA- 310, JABALPUR LOCAL, S. SELECTION 3, S. SELECTION 1, SITARA, LCA- 960, LIPSTICK, O7- S, O7- L, ACB1 L, BHOOT JALOKIA, JCH- 42, ENT- 1, HDC- 75- 1, ACB1- S while remaining genotypes contributed in negative association to PC_4. PC_5 revealed 7.20% of the total variation with 80.12% of cumulative proportion and 0.86 of eigen values, it is loaded with the characters such as PH (0.642), FPT (0.527), WPDM (0.173), IFW (0.059) and NSF (0.026) while, NFP, FD, FL, FYP, MC, NPBPP and TW contributed in the negative direction to PC_5, it is confirmed the maximum variability from the 14 genotypes such as S. SELECTION 2, KBCH-1, SUM- 17, LCA- 310, S. SELECTION 3, ENT- 1, S. SELECTION 1, JABALPUR LOCAL, LCA- 960, RAJPUT, LIPSTICK, M- 262, RAICHUR BULLET and PBC- 80 while remaining genotypes contributed in negative association to PC_5.

From the study of multiple PCA components resulted in the identification of the promising genotypes with favourable traits, in the Fig. 6 it clearly indicates that S. SELECTION 1 genotype were positive selection which is grouped from the combinations of five PCA components with favourable contribution of the trait individual fruit weight with maximum diversity, three genotypAltaf es were favoured (LIPSTICK, LCA- 310 and S. SELECTION 2) from the grouping of four out of five PCAs which contributed more to the diversity of fruit yield per plant, whole plant dry weight and plant height. Similarly eight promising genotypes were identified (SUM- 17, M- 262, JCH- 42, O7- L, ENT- 1, RAJPUT, S. SELECTION 3 and LCA- 960) from three PCAs out of five PCAs grouped for the trait such as test weight, fruit pericarp thickness, moisture content, fruit length, number of seeds per fruits and number of fruits per plant, hence, the traits falling in these PCs may be given due importance. Eleven genotypes were identified (BHOOT JALOKIA, BCH- 42, PBC- 80, KA2- L, KBCH- 1, HDC- 75- 1, ACB1 L, 5- B, SITARA, RAICHUR BULLET and JABALPUR LOCAL) from two PCAs out of five PCAs grouped which is fevered by number of primary branches per plant. Three genotypes including two check varities such as B.KADDI, B.DABBI and 9608- U were grouped from any one of the PCA from five PCAs which is contributed with maximum diversity of fruit diameter (Fig.

6).Thus the prominent traits combining *vs* genotypes together in different principal components and contributing towards the explaining the variability and have tendency to remain together, so these traits may be kept into consideration and can be utilized in breeding program for improving chilli genotypes.

Cluster analysis for yield and yield attributing traits in chilli genotypes were grouped into four major clusters. Analysis was carried out for chilli genotypes by using Ward's hierarchical algorithm based on K means clustering on UPGMA method, using software Pasta *4.0 version* and it is classified 30 chilli genotypes into 4 hierarchy (level) and with optimal number of cluster (Fig. 7b),based on the degree of similarity further the members in one group are more homogeneous than members outside the group genotypes in the same group have narrow genetic diversity, while genotypes in different groups have wide genetic diversity as shown in the Fig. 7A.The genotypes in cluster I consisted of three genotype (LIPSTICK, B. DABBI and B. KADDI), genotypes in cluster II consisted of 7 genotypes namely O7- S, HDC- 75- 1, ACB1L, RAJPUT, KBCH- 1, O7- L and SITARA. Similarly the genotypes in cluster III is grouped into 7 genotypes based on the homogeneity such as ENT- 1, S. SELECTION 3, LCA- 960, 5- B, S. SELECTION 1, LCA- 310 and S. SELECTION 2, in the present study cluster IV has revealed by grouping higher number of genotypes as compared to the remaining cluster (BHOOT JALOKIA, TIWARI, JABALPUR LOCAL, RAICHUR BULLET, P3, ACB1- S, SUM- 17, JCH- 42, KA2- L, M- 262, PBC- 80, BCH- 42 and 9608- U) (Fig.7a), results were in accordance with the Hasan*et al*., 2014, Farhad *et al*., 2010; Geleta *et al*., 2005 also conducted an experiment with twenty- nine diversified genotypes and clustered them based on morphological character. The average inter and intra cluster distance was also calculated for yield and yield attributing traits with four cluster as given in (Table 7). The inter cluster distances were larger than the intra cluster distances. The inter- cluster distance was maximum between clusters III and IV (1939.05) indicating wide genetic diversity between these two clusters followed by the distance between cluster II and V (1650.72), cluster III and cluster VII (1473.29) and cluster IV and cluster VII (1461.12). Genotypes from these four clusters if involve in hybridization may occur a wide spectrum of segregating population as genetic diversity is very distinct among the groups. The selection of diverge genotype from cluster would produce a broad spectrum of variability for morphological traits studied which may enable further selection and improvement (Table 7). The minimum inter- cluster distance was observed between cluster I and cluster II (461.880) followed by cluster I and cluster IV (491.080) and cluster II and cluster III (187.080) indicating that the genotypes of these clusters were genetically close.

Cluster mean value of 12 different characters shown in Table 8. Difference in cluster means existed for almost all the characters studied. Highest mean value for NSF (81.96) fallowed by PH (80.14), MC (68.17), NFP (63.58), FYP (53.00), WPDM (37.58), FD (11.20), FL (6.40) and the genotypes belongs to cluster I such as Lipstick, B. Dabbi and B. Kaddi revealed more diversity for the seed number, height, moisture content and number of fruits per plant, similarly for cluster II revealed higher diversity for NSF, MC, NFP and PH. Cluster III has shown higher diversity for PH (75.80), followed by MC (71.75), NSF (59.50), NFP (57.50) and FYP (31.15) and cluster IV has the more diversity for NFP (72.00) fallowed by MC (70.90), PH (64.60), NSF (51.00), WPDM (38.50) and FYP (34.95),Cluster IV possessed genotypes with maximum number of fruits coupled with dwarf plant stature indicating selection of genotypes from these cluster for future chilli breeding program have positive impact for short plant type, and number of fruits. Cluster I had the genotypes that showed lowest mean value for almost all the characters studied indicating selection of genotypes from these cluster for future chilli breeding program have no positive impact on yield attributing traits. In literature similar results were obtained from Mubarak Begum (2002) and Prabhudeva (2003).

Conclusions:

Variability among the base generation of parental lines creates more scope for selecting the targeted genotypes to develop the recombinant type and for heterosis breeding. In the present study, information was gathered for 30 chilli genotypes regarding morphological and yield-related traits. Among the studied characters fruit pericarp thickness, fruit length, number of fruits per plant, fruit diameter and fruit yield per plant are the most trustworthy yield components traits as a breeder one should be given more weightage for these traits, based on the existing variability with strong association and path, PCA and diversity analysis revealed as preposition selection criteria in chilli breeding programs as a horticultural traits. The present study revealed there is enough scope for future study involving multi- location trials for the promising cultivars like., LIPSTICK, B.KADDI, B.DABBI, BHOOT JALOKIA, SUM- 17, BCH- 42, PBC- 80, LCA- 310, M- 262, KA2- L, S. SELECTION 1, JCH- 42 and 9608- U so these genotypes serves as a donor for further breeding programme to develop superior cultivars.

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Table 1: List of chilli genotypes used in the present investigation

Sl. No.	Genotypes
1	ACB1- L
2	ACB1- S

3	BCH- 42
4	BHOOT JALOKIA
5	ENT- 1
6	HDC- 75- 1
7	JABALPUR LOCAL
8	JCH- 42
9	KA2- L
10	KBCH- 1
11	LCA- 310
12	LCA- 960
13	LIPSTICK
14	M- 262
15	PBC- 80
16	P3
17	RAJPUT
18	RAICHUR BULLET
19	SANKESHWAR SELECTION 1
20	SANKESHWAR SELECTION 2
21	SANKESHWAR SELECTION 3
22	SITARA
23	SUM- 17
24	TIWARI
25	5- B
26	07- L
27	07- S
28	9608- U
29	BYADGIKADDI (check)
30	BYADGIDABBI (check)

Table 2: Analysis of variance for yield and yield attributing traits in chilli genotypes

Source of variation	*df*	Mean sum of squares											
		PH	NPBPP	NFP	FD	FL	IFW	NSF	TW	WPDM	MC	FPT	FYP
Genotypes	29	521.93**	0.34**	724.70**	16.69**	16.53**	0.09**	583.05**	1.35**	202.66**	66.72**	0.08**	552.92**
Replication	1	0.00	0.06	2.09	5.51*	8.22**	0.01	8.74	0.00	0.02	16.99*	0.00	1.31
Error	29	2.52	0.04	1.47	0.42	0.20	0.00	5.69	0.03	1.36	2.01	0.01	1.72
CV (5%)		2.18	9.60	1.90	5.45	6.64	8.30	3.05	3.69	2.94	2.14	10.82	2.55
CD (5%)		3.24	0.45	2.47	1.32	0.92	0.12	4.87	0.36	2.38	2.90	0.25	2.68
Sem±		1.12	0.15	0.85	0.45	0.32	0.04	1.68	0.12	0.82	1.00	0.08	0.92

Note 1:
PH: Plant height (cm);
NPBPP: Number of primary branches per plant;
NFP: Number of fruits per plant;
FD: Fruit diameter (mm);
FL: Fruit length (cm);
IFW: Individual fruit weight (g);
NSF: Number of seeds per fruit;
TW: Test weight (g);
WPDM: Whole plant dry matter (g);
MC: Moisture content (%);
FPT: Fruit pericarp thickness (mm);
FYP: Fruit yield per plant (g);
CV (5%): Coefficient of variation;
CD: Critical difference;
Sem±: Standard error of mean

Note 2: *Indicate significance @ 5% level;**Indicate highly significance @ 1% level

Table 3: Genetic plasticity and mean performance of chilli genotypes for yield and yield attributing traits

Traits	Range		Mean $(\overline{X})$ $(\overline{X})$	Coefficient of variation (%)		$h^2 h^2$ BS	GAM
	Min	**Max**		**GCV**	**PCV**		
PH	50.00	111.00	72.71	22.16	22.26	99.04	45.43
NPBPP	2.00	3.00	2.31	16.57	19.14	74.90	29.54
NFP	21.85	127.00	63.80	29.80	29.86	99.60	61.27
FD	5.45	20.80	11.89	23.97	24.58	95.09	48.15
FL	1.55	13.56	6.81	41.93	42.45	97.55	85.32
IFW	0.29	1.34	0.75	27.72	28.93	91.81	54.72
NSF	41.00	119.50	78.23	21.71	21.93	98.07	44.30
TW	3.70	7.60	4.81	16.90	17.30	95.44	34.02
WPDM	13.48	55.50	39.59	25.33	25.50	98.67	51.84
MC	50.32	78.04	66.35	8.57	8.83	94.13	17.13
FPT	0.69	1.65	1.15	15.91	19.24	68.36	27.10
FYP	30.70	87.00	51.45	32.26	32.36	99.38	66.25

Note 1:

PH: Plant height (cm);
NPBPP: Number of primary branches per plant;
NFP: Number of fruits per plant;
FD: Fruit diameter (mm);
FL: Fruit length (cm);
IFW: Individual fruit weight (g);
NSF: Number of seeds per fruit;
TW: Test weight (g);
WPDM: whole plant dry matter (g);
MC: Moisture content (%);
FPT: Fruit pericarp thickness (mm);
FYP: Fruit yield per plant (g)

Note 2:
GCV: Genotypic coefficient of variance;
PCV: Phenotypic coefficient of variance;
h^2 h^2: Heritability (%);
GAM: genetic advance percent mean

Note 3	High	Moderate	Low	Proposed by
GCV & PCV	> 20%	10 to 20%	<10%	Sivasubramanian and Madhavamenon(1973)
GAM	> 20%	10 to 20	<10%	Johnson *et al.* (1955).
h^2	> 60%	30 to 60	0- 30%	

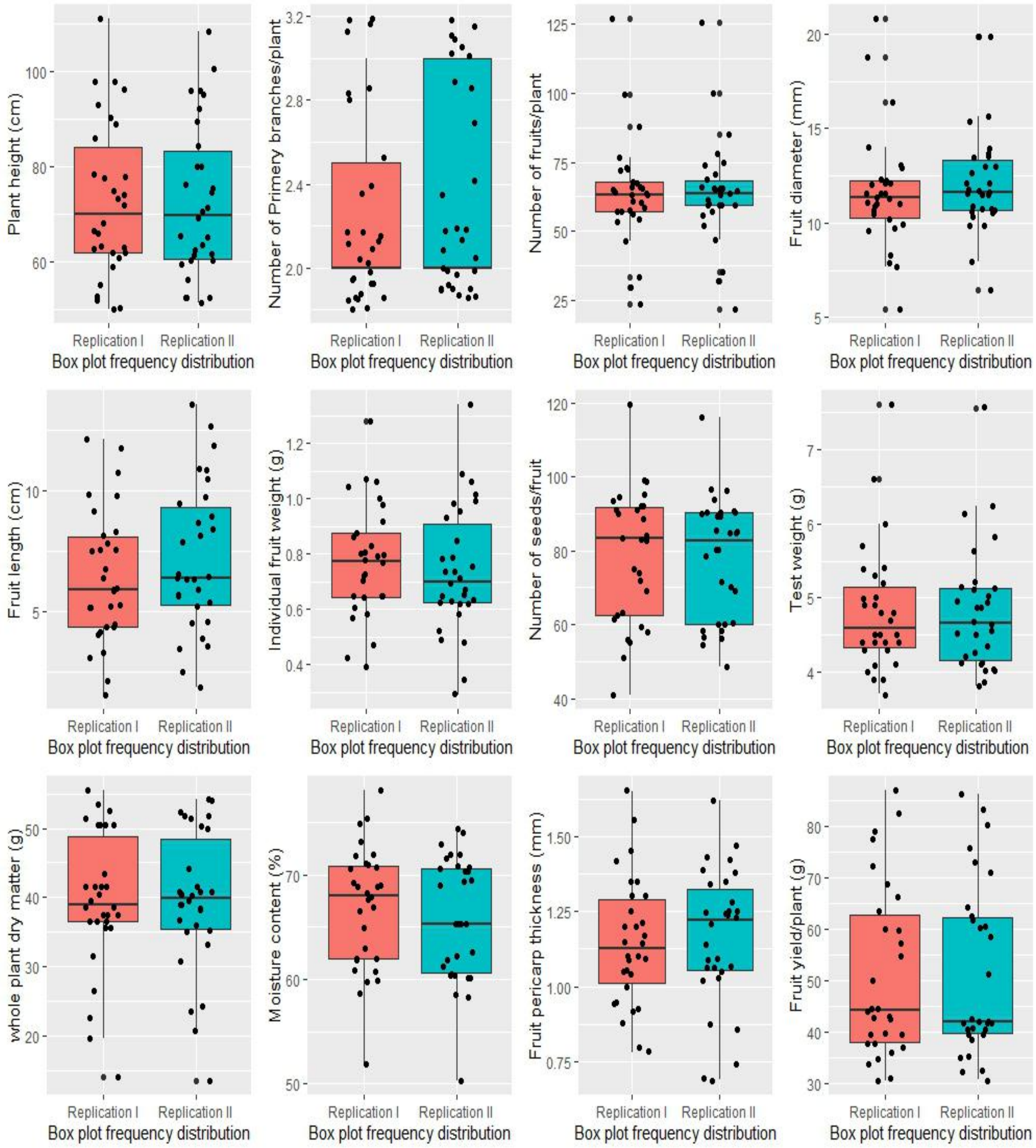


Figure 1: Box plots depicting the frequency distribution for yield and yield attributing traits in chilli genotypes

Note:

Red colour box showing the frequency distribution of genotypes for replication- I

Blue colour box showing the frequency distribution of genotypes for replication- II

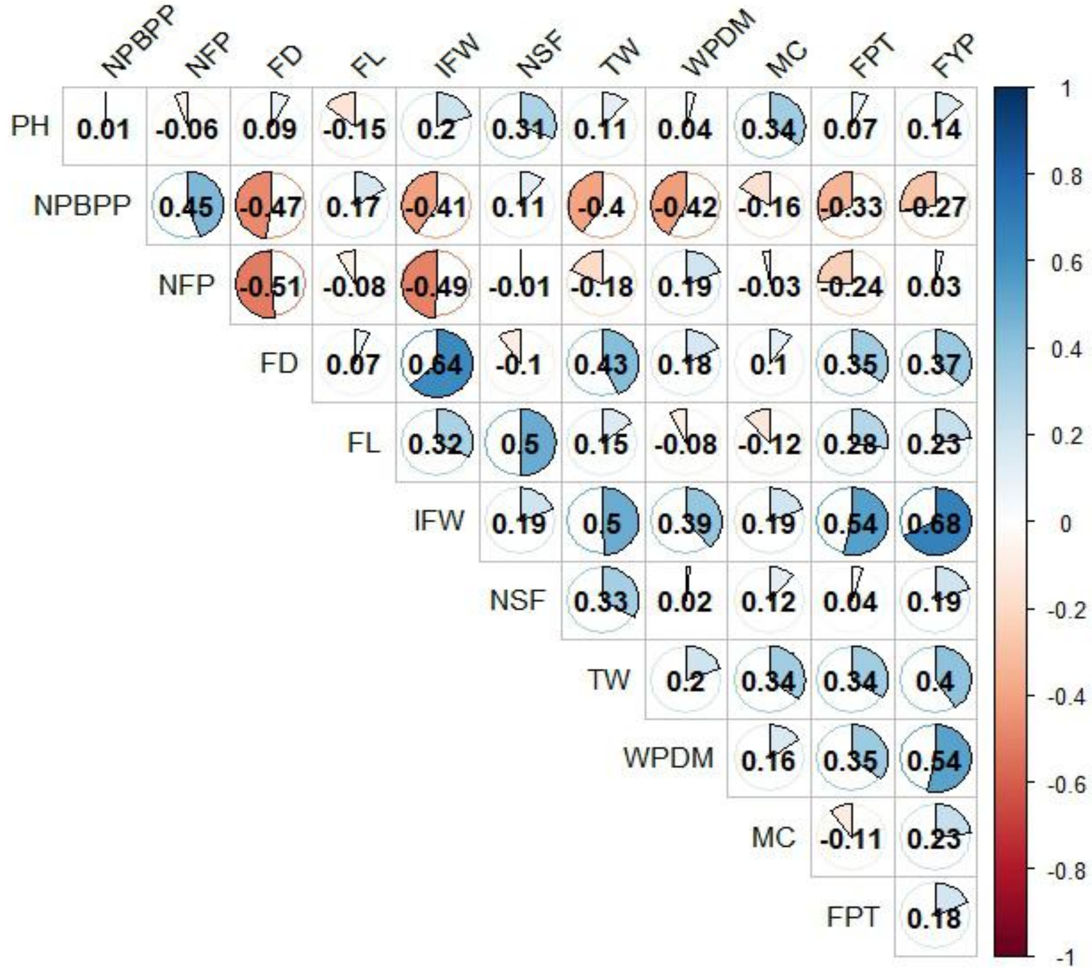


Figure 2: Phenotypic correlation coefficient among the 30chilli genotypes for yield and yield attributing traits

Note 1:

PH: Plant height (cm);
NPBPP: Number of primary branches per plant;
NFP: Number of fruits per plant;
FD: Fruit diameter (mm);
FL: Fruit length (cm);
IFW: Individual fruit weight (g);
NSF: Number of seeds per fruit;
TW: Test weight (g);
WPDM: whole plant dry matter (g);
MC: Moisture content (%);
FPT: Fruit pericarp thickness (mm);
FYP: Fruit yield per plant (g);
Significance level: 0.05 (*) = 0.355; 0.01 (**) = 0.455

Table 4: Path coefficient analysis showing direct and indirect effect for yield and yield attributing traits in chilli genotypes

Traits	PH	NPBPP	NFP	FD	FL	IFW	NSF	TW	WPDM	MC	FPT	FYP	DE	r^2 value with FYP
PH		− 0.0284	− 0.0134	0.0294	0.0566	0.0735	0.0334	0.0194	0.0901	− 0.0118	− 0.0303	0.1304	**0.2398**	**0.140**
NPBPP	− 0.0033		− 0.0011	0.0003	0.0002	0.0016	0.0008	0.0022	− 0.0013	0.0063	0.0015	0.0434	**0.028**	**− 0.270**
NFP	− 0.0138	− 0.0098		− 0.133	− 0.1192	0.0017	− 0.0339	0.0498	− 0.0135	− 0.0719	− 0.0144	0.0494	**0.2467**	**0.030**
FD	0.0063	0.0005	− 0.0275		0.0269	− 0.0072	0.0181	0.0085	0.0075	0.0172	0.0012	0.2846	**0.0511**	**0.370***
FL	0.084	0.0029	− 0.1721	0.1878		0.0489	0.151	0.1363	0.1031	0.1476	0.0842	0.6004	**0.3562**	**0.230**
IFW	0.0244	0.0047	0.0005	− 0.0112	0.0109		0.027	0.0019	0.0101	0.0026	0.0382	0.1668	**0.0798**	**0.680****
NSF	− 0.0176	− 0.0036	0.0174	− 0.0448	− 0.0536	− 0.0429		− 0.027	− 0.0397	− 0.0427	− 0.0184	0.3223	**− 0.1264**	**0.190**
TW	0.0173	0.0168	0.0431	0.0356	0.0817	0.0051	0.0457		0.0316	0.0846	− 0.011	0.4961	**0.2136**	**0.400****
WPDM	− 0.0028	0.0003	0.0004	− 0.0011	− 0.0021	− 0.0009	− 0.0023	− 0.0011		0.0003	0.001	0.226	**− 0.0074**	**0.540****
MC	0	0.0001	− 0.0002	0.0002	0.0002	0.00	0.0002	0.0002	0		0.0001	0.2006	**0.0006**	**0.230**
FPT	− 0.113	0.0489	− 0.052	0.0208	0.2115	0.4289	0.1301	− 0.0461	− 0.1266	0.2205		0.2066	**0.8946**	**0.180**
FYP	− 0.118	− 0.08	0.466	0.149	− 0.014	0.731	0.13	0.115	0.032	− 0.035	− 0.028		0.912	1.00

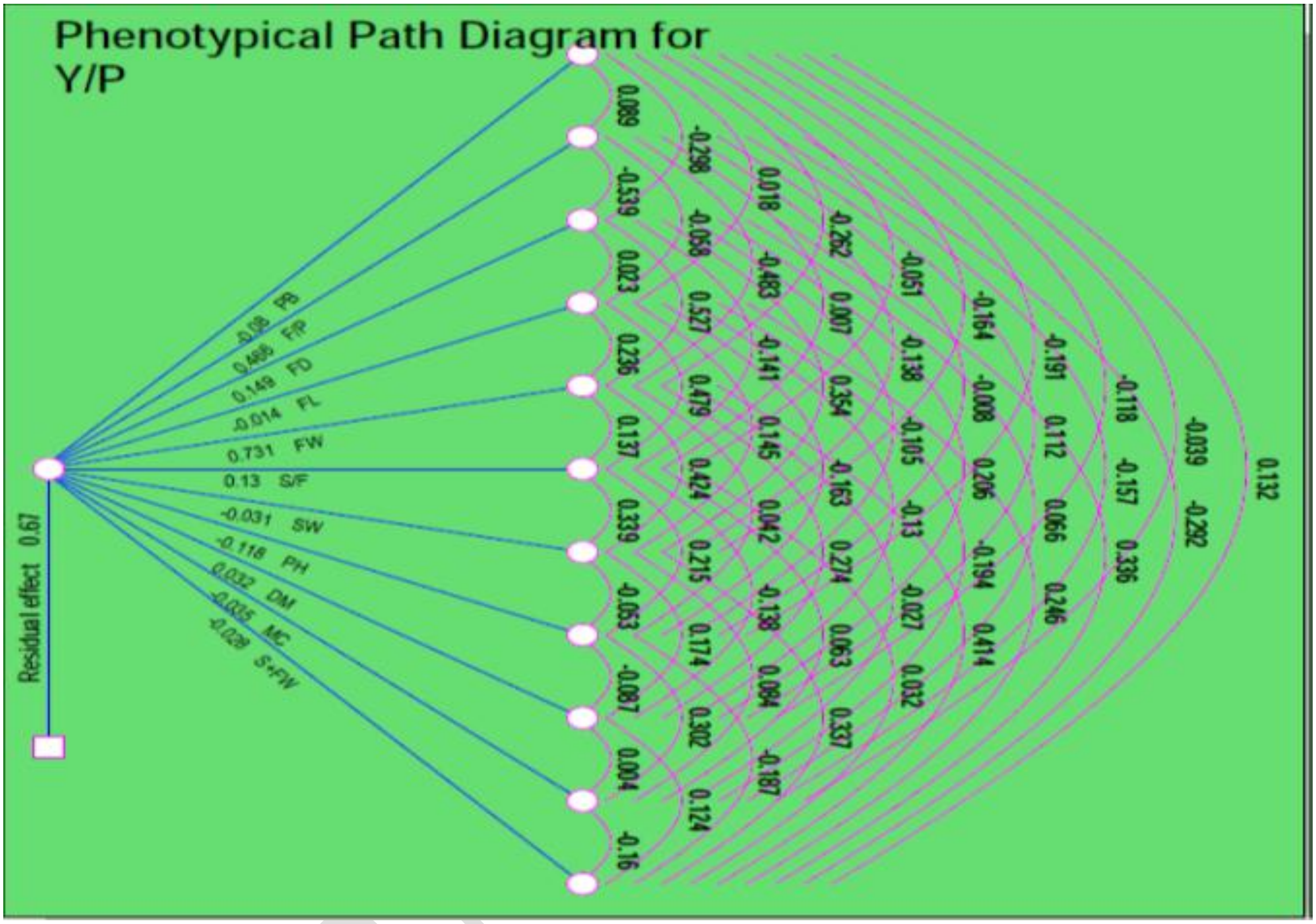


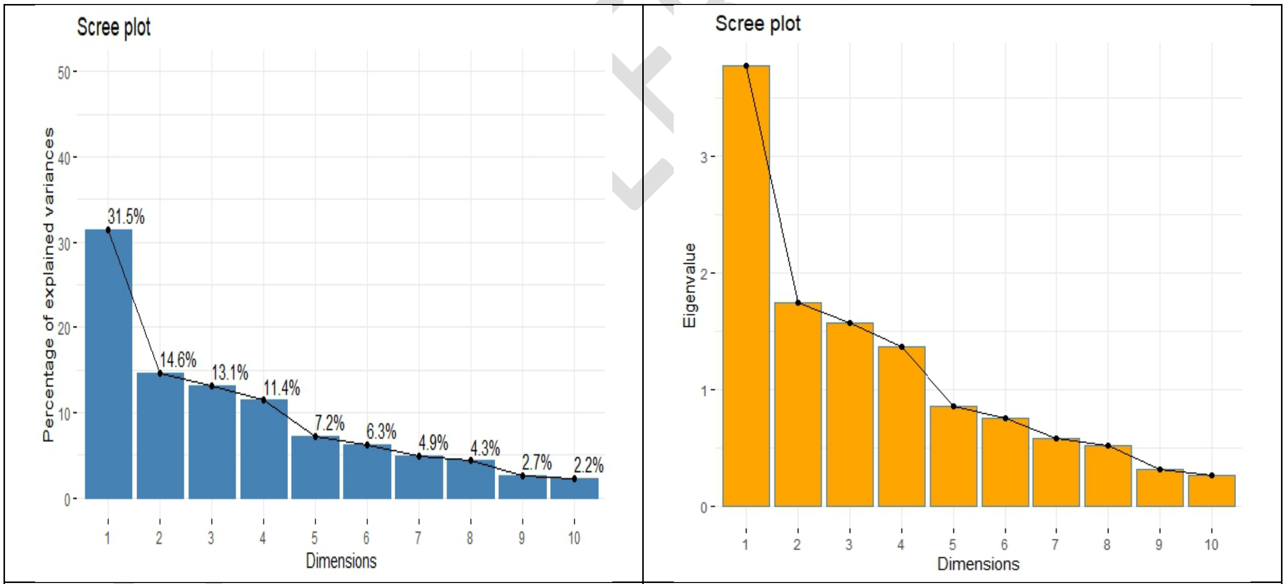
Figure 3: Path coefficient analysis showing direct and indirect effect foryield and yield attributing traits in chilli genotypes

Note 1:

PH: Plant height (cm); NPBPP: Number of primary branches per plant;
NFP: Number of fruits per plant; FD: Fruit diameter (mm);
FL: Fruit length (cm); IFW: Individual fruit weight (g);
NSF: Number of seeds per fruit; TW: Test weight (g);
WPDM: whole plant dry matter (g); MC: Moisture content (%);
FPT: Fruit pericarp thickness (mm); FYP: Fruit yield per plant (g);
Residual effect (RE) = 0.67; r^2 with FYP: Phenotypic correlation with fruit yield;
Significance level: 0.05 (*) = 0.355; 0.01 (**) = 0.455

Table 5: Eigen values, Per cent variance, cumulative proportion and component loading of yield and yield attributing traits in chilli genotypes

Traits	PC_1	PC_2	PC_3	PC_4	PC_5
PH	0.120	0.232	0.322	− 0.437	0.642
NPBPP	− 0.327	0.379	− 0.098	− 0.003	− 0.080
NFP	− 0.240	0.283	0.356	0.460	− 0.002
FD	0.371	− 0.259	− 0.128	− 0.136	− 0.101
FL	0.129	0.450	− 0.497	0.141	− 0.151
IFW	0.464	0.033	0.107	0.013	0.059
NSF	0.123	0.614	− 0.097	− 0.158	0.026
TW	0.356	0.133	0.063	− 0.115	− 0.324
WPDM	0.260	− 0.028	0.361	0.520	0.173
MC	0.155	0.132	0.489	− 0.346	− 0.305
FPT	0.308	− 0.054	− 0.246	0.221	0.527
FYP	0.351	0.192	0.204	0.288	− 0.198
Eigen value	3.77	1.75	1.57	1.37	0.86
Proportion of variance	31.50	14.60	13.10	11.40	7.20
Cumulative proportion	13.48	46.06	59.21	72.61	80.12



4a. Scree plot for PEV | **4b. Scree plot for Eigenvalue**

Figure 4: Scree plot showing percentage of explained variance (PEV) and Eigen values for number of components corresponding to the yield and yield attributing traits in chilli genotypes

Note: 1 to 10 number = component numbers

Table 6: Contribution of Genotypes to the Individual PCAs

Sl.NO.	**Genotypes**	**PC$_1$**	**PC$_2$**	**PC$_3$**	**PC$_4$**	**PC$_5$**
1	BHOOT JALOKIA	1.80562	−3.4157	−0.535	0.40707	−0.2438
2	TIWARI	−1.4712	−1.2346	−0.9006	−0.8273	−0.5223
3	BCH- 42	1.6664	−0.271	1.38934	−1.175	−0.827
4	M- 262	0.68183	−0.2923	0.22809	−1.148	0.12948
5	KBCH- 1	−0.7165	2.18606	−0.1102	−1.4501	1.49135
6	SUM- 17	1.70498	0.07499	−1.1621	−2.9575	1.42844
7	LIPSTICK	5.81074	0.58255	−0.5154	0.81318	0.42119
8	HDC- 75- 1	−2.4196	1.64369	−2.846	0.05156	−0.5492
9	ACB1 L	−1.8695	1.20415	−1.9886	0.47511	−0.4871
10	RAICHUR BULLET	−1.2187	−2.761	0.13185	−0.2883	0.04997
11	5- B	−0.4059	0.31971	−0.3614	2.08876	−0.7997
12	O7- S	−3.4722	−0.2402	−2.031	0.71923	−0.0334
13	P3	−0.1488	−1.0422	0.46686	−0.0689	−1.5106
14	O7- L	−2.164	1.74762	0.74585	0.53192	−0.7516
15	RAJPUT	−3.24	0.10394	2.18791	−2.7877	0.58236
16	ENT- 1	−0.185	0.18754	−0.3391	0.16898	1.04244
17	S. SELECTION 1	0.42898	0.22706	1.29732	0.88884	0.8485
18	LCA- 310	0.97511	−0.2574	0.54285	1.63307	1.37605
19	S. SELECTION 2	−0.0155	0.45421	1.07913	1.64034	1.71941
20	ACB1- S	−0.7056	−1.8932	−0.004	0.00884	−0.9421
21	S. SELECTION 3	−0.8994	−0.3569	0.82	0.9387	1.19544
22	PBC- 80	1.01187	−0.5868	−1.2566	−1.3127	0.01636
23	LCA- 960	−0.8962	−0.2732	0.41495	0.81902	0.73774
24	JABALPUR LOCAL	−0.5131	−1.6901	−1.0015	0.96302	0.82504
25	JCH- 42	0.41718	0.04361	1.47253	0.20717	−0.79
26	SITARA	−1.1498	1.88385	2.04834	0.82216	−0.7549
27	KA2- L	0.51317	0.24885	2.10527	−0.2879	−1.3575
28	9608- U	0.30037	0.45215	−0.1348	−0.4968	−0.6503
29	B.DABBI	3.05374	2.06129	−1.1032	−0.0659	−0.6268
30	B.KADDI	3.1211	0.89328	−0.6407	−0.3109	−1.0176

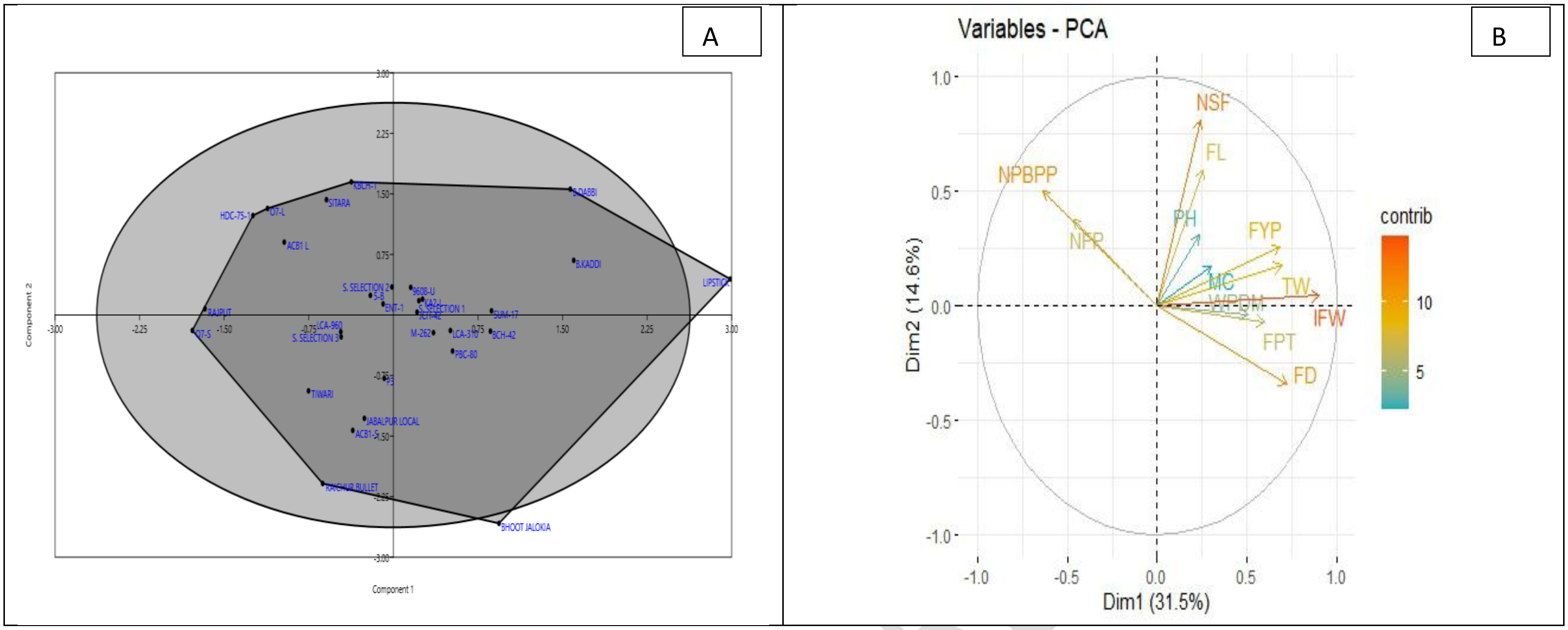


Figure 5: a and b showing the PCA Biplot for genotype clustering and PCA variable showing the contribution of the traits in PC_1 and PC_2 on the axes

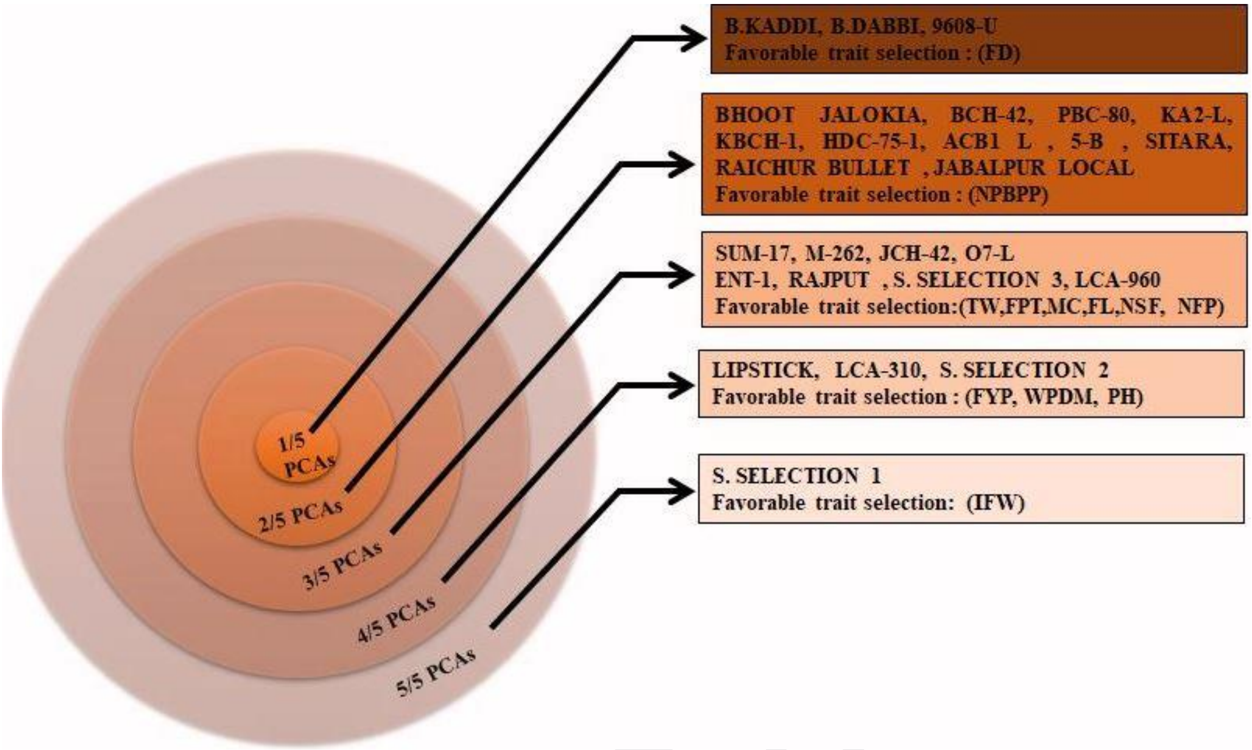


Figure 6: Selection of promising genotypes *VS* traits from multiple PCAs

Note:

1/5PCAs: Selection of favourable genotypes *Vs* Trait based on any one PCAs from five PCAs

2/5PCAs: Selection of favourable genotypes *Vs* Traits based on any two PCAs from five PCAs

3/5PCAs: Selection of favourable genotypes *Vs* Traits based on any three PCAs from five PCAs

4/5PCAs: Selection of favourable genotypes *Vs* Traits based on any four PCAs from five PCAs

5/5PCAs: Selection of favourable genotypes *Vs* Traits based on five out of five PCAs

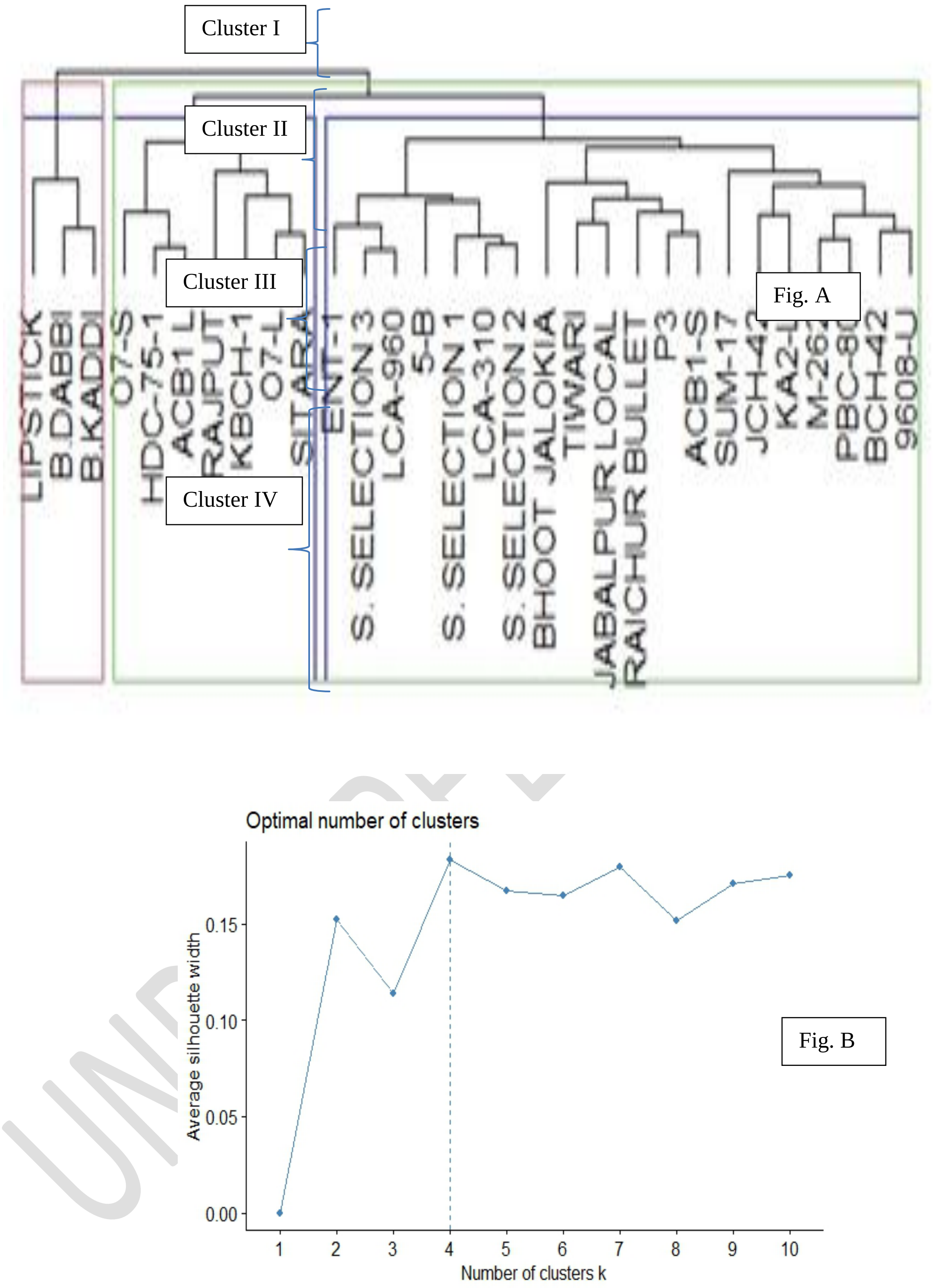


Figure 7: (a&b): Relationship among the 30 chilli genotypes based on yield and yield attributing traits and using K means clustering on UPGMA method.

Table 7: Average intra (Bold) and inter cluster (Un- bold) distance of chilli genotypes for yield and yield attributing traits.

Clusters	I	II	III	IV	V	VI	VII
I	**1.023**	461.880	587.740	491.980	781.080	687.700	906.570
II		**0.598**	187.080	1155.15	1650.72	1191.33	1018.27
III			**0.684**	1165.61	1939.05	1166.57	1473.29
IV				**0.450**	352.620	594.080	1461.12

Table 8: Cluster wise mean performance for yield and yield attributing revealed by 30 chilli genotypes

Cluster	No. of genotypes	Genotypes include in the cluster	PH (cm)	NPBPP	NFP	FD (mm)	FL (cm)	IFW (g)	NSF	TW (g)	WPDM (g)	MC (%)	FPT (mm)	FYP (g)
I	3	Lipstick, B. Dabbi and B. Kaddi	80.14	2.58	63.58	11.2	6.4	0.78	81.96	4.85	37.58	68.17	1.14	53
II	7	07- S, HDC-75- 1, ACB1L, Rajput, KBCH-1, 07- L and Sitara	58.55	2.5	63	9.95	12.15	0.57	98.5	3.7	22.5	63.6	1.05	30.7
III	7	Ent- 1, S. Selection- 3, LCA- 960, 5-B, S. Selection-1, LCA- 310 and S. Selection- 2	75.8	3	57.5	7.65	7.8	0.47	59.5	3.95	13.5	71.75	1	31.15
IV	13	Bhoot Jalokia, Tiwari, Jabalpur local, Raichur Bullet, P3, ACB1- 5, SUM- 17, JCH-42, KA2- L, M- 262, PBC-80, BCH- 42 and 9608- U	64.6	2.5	72	16.41	1.55	0.42	51	4.45	38.5	70.9	1.09	34.95

PH: Plant height (cm);
NFP: Number of fruits per plant;
FL: Fruit length (cm);
NSF: Number of seeds per fruit;
WPDM: whole plant dry matter (g);
FPT: Fruit pericarp thickness (mm);
NPBPP: Number of primary branches per plant;
FD: Fruit diameter (mm);
IFW: Individual fruit weight (g);
TW: Test weight (g);
MC: Moisture content (%);
FYP: Fruit yield per plant (g).