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ASSESSMENT OF PHENOTYPIC VARIATION AND DIVERGENCE AMONG FARMER-MAINTAINED COLLECTIONS OF THE BYADGI DABBI CHILLI (*Capsicum annuum* L.) CULTIVAR ACROSS GROWING LOCATIONS

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ABSTRACT

Chilli (*Capsicum annuum* L.) is an economically important spice-cum-vegetable crop and the leading commodity in India's spice export basket, contributing nearly 28% of the total export value. Byadgi chilli, a major dried chilli cultivars of Karnataka accorded 'Geographical Indication' status in the year 2011 and recognized as Karnataka's flagship export-oriented dried chilli group. Byadgi Dabbi, a major byadgi chilli cultivar prized for its low pungency, high colour value, and sweet flavour. However, major concern in this cultivar is declining genetic purity due to pollen mediated gene exchange facilitated by natural outcrossing with nearby improved varieties and hybrids under farmer field conditions, resulting in dilution of its original characteristics and export quality. Therefore, the present investigation was undertaken to assess the extent of phenotypic variation among collections of the Byadgi Dabbi cultivar from farmer's fields across its traditional growing regions. Consistently higher PCV than GCV for majority of the traits indicated that environmental factors contributed significantly to the phenotypic expression. However, relatively narrow differences between the two estimates for most traits suggested that the observed variability was largely genetic in nature. Further, principal component analysis demonstrated that dry fruit yield per plant (DFY), fruit length (FL), fruit diameter (FD), fruit weight (FW), number of seeds per fruit (NSPP), number of fruits per plant (NFPP) and stalk length (SL) are the major contributors to the total variability. PCA biplot identified the collections BD-23, BD-13, BD-15 and BD-11 as the most phenotypically divergent. Overall, the farmer maintained open pollinated collections represent a genetically heterogeneous population exhibiting phenotypic variation distributed across several quantitative traits. The findings of the present study provide a scientific basis signifying the need for systematic genetic purification through conventional approaches such as selfing or rapid genetic purification approaches such as doubled haploid development.

Key words : Chilli, Byadgi dabbi, farmer-maintained collections and natural cross pollination

Introduction

Chilli (*Capsicum annuum* L.) (2n = 24) is a crop of immense economic importance, valued for its culinary versatility, nutritional richness, and wide range of industrial applications. It is known by different names, including *capsicum*, paprika, pimento, hot pepper, red pepper, bird pepper, and chilli pepper, in different parts of the world. The genus *Capsicum* is believed to have originated in

Mexico, with its centre of diversity in South America (Gonzalez and Bosland, 1991). Although, the genus comprises 38 recognized species (USDA-ARS, 2011), cultivation is largely confined to five domesticated species, namely *C. annuum*, *C. frutescens*, *C. pubescens*, *C. chinense* and *C. baccatum*, which originated through multiple domestication events (Moscone *et al.*, 2007). Among these, *C. annuum* is the most widely cultivated

species worldwide, including India (Tong and Bosland, 2003).

Globally, chilli is cultivated both as a spice and as a vegetable, ranking next only to tomato among solanaceous vegetable crops (Bosland, 1995). India is the world's leading producer of dried chilli, cultivating the crop over an area of 7.89 lakh hectares with an annual production of 26.94 lakh tonnes (Indiastat, 2025). Chilli is also the leading commodity in India's spice export basket, contributing approximately 28% of the total spice export value (Spice Board of India, 2025). Among the major chilli-producing states, Andhra Pradesh contributes the highest production, while Karnataka ranks fourth. In Karnataka, dried chilli is cultivated over 1.03 lakh hectares, producing approximately 2.04 lakh tonnes (Indiastat, 2025).

Among the indigenous chilli cultivars grown in the state, the Byadgi group is recognized as Karnataka's flagship export-oriented chilli, contributing significantly to the state's spice export economy. Byadgi Dabbi, predominant cultivar in this group, valued for its deep red fruit colour, high oleoresin content, colour value of 180–200 ASTA units, low pungency and characteristic sweet flavour. Owing to its distinct quality attributes and geographical uniqueness, Byadagi chilli was granted Geographical Indication (GI) status (Geographical Indications Registry, 2011) in 2011 (GI Application No. 129; Certificate No. 147). These attributes have established Byadgi chilli as a premium raw material for the oleoresin, food processing and natural colour industries, resulting in strong demand in both domestic and international markets.

Despite its greater commercial importance, *Capsicum annuum* L. is recognized as a facultative cross-pollinated crop (Franceschetti, 1972). Natural cross-pollination ranging from 6.8% to more than 66.4% has been reported in chilli (Murthy and Murthy, 1962; Singh *et al.*, 1973; Kim *et al.*, 2009; Justino *et al.*, 2018), depending on factors such as genotype, degree of stigma exertion, timing of anther dehiscence, prevailing wind direction, and pollinator activity (Ritonga *et al.*, 2018). Consequently, maintaining genetic purity under open-field conditions remains a major challenge, particularly in traditional farmer-saved seed systems. Kanwar (1995) reported that, in the absence of adequate isolation distance, genetic purity in chilli can decline by as much as 41% within four years. The occurrence of gene flow further complicates the maintenance of varietal purity. Pérez-Martínez *et al.* (2022) demonstrated clear evidence of gene flow between wild populations and cultivated landraces of *Capsicum annuum*. They further reported

that traditional farming systems, including backyard cultivation, mixed cropping, and the close proximity of wild and cultivated populations, facilitate continuous pollen-mediated gene exchange, thereby contributing to loss of genetic purity.

The superior quality and distinct identity of the Byadgi Dabbi cultivar have traditionally been maintained through continuous farmer selection for desirable fruit characteristics over successive generations. However, under farmers' field conditions, repeated natural outcrossing with neighbouring improved varieties and hybrids, coupled with the recurrent use of farm-saved seed, has progressively altered the genetic constitution of the cultivar. Consequently, the characteristic features of Byadgi Dabbi have been diluted through the introgression of alleles from adjacent cultivars, resulting in the deterioration of genetic purity and varietal uniformity. This genetic deterioration has adversely affected important economic traits, including fruit size, fruit shape, colour intensity, yield potential, and biochemical composition, thereby limiting the commercial value of this premium chilli cultivar.

Despite the increasing phenotypic variability observed in farmers' fields across the traditional growing regions of Byadgi Dabbi, systematic studies quantifying the extent of variation within this cultivar remain limited. Therefore, the present investigation was undertaken to evaluate the extent of phenotypic variation among collections of the Byadgi Dabbi cultivar collected from farmers' fields across its traditional growing regions.

Materials and Methods

The experimental material consisted of twenty-five collections of Byadgi Dabbi chilli cultivar from farmers' fields across the traditional Byadgi chilli growing districts such as Haveri, Hubli, Gadag and Ballary in Karnataka. Details of collections are mentioned in the Table 1. The field experiment was conducted during *Kharif-2025* at the Main Agricultural Research Station (MARS), University of Agricultural Sciences, Dharwad, Karnataka, India. The experimental site is located at 15°26' N latitude and 75°07' E longitude, at an altitude of 678 meters above mean sea level. The location falls under Agro-climatic Zone VIII (Northern Transitional Zone) of Karnataka.

The genotypes were evaluated in a Randomized Complete Block Design (RCBD) with two replications. Uniform agronomic and plant protection measures were adopted throughout the crop growth period to minimize environmental variation among treatments. For recording of observations, five healthy plants were randomly selected and tagged in each plot. Data were recorded on

Table 1 : Details of Byadgi Dabbi chilli cultivar collections from farmer's fields across the traditional growing locations.

S. no.	Districts of growing location	No. of collections	Name of the collections
01	Hubli	11	BD-02, BD-03, BD-04, BD-05, BD-06, BD-09, BD-11, BD-12, BD-14, BD-23 and BD-25
02	Bellary	7	BD-05, BD-07, BD-13, BD-15, BD-17, BD-19 and BD-21
03	Haveri	04	BD-08, BD-16, BD-20 and BD-22
04	Gadag	03	BD-01, BD-18 and BD-24

twelve quantitative traits comprising both growth and yield attributes. The mean value of the five sampled plants in each replication was computed and used for statistical analysis.

Analysis of variance (ANOVA) was performed to determine the significance of genotypic differences among the collections. Genetic variability parameters, including phenotypic and genotypic coefficients of variation (Sivasubramanian and Menon, 1973), broad-sense heritability (Robinson *et al.*, 1949), and genetic advance as percent of mean (Johnson *et al.*, 1955), were estimated following standard biometrical procedures. In addition, Principal Component Analysis (PCA) was carried out to identify the major traits contributing to the total variation. Principal component analysis (PCA) biplot was performed to identify phenotypically diverse collections. All statistical analysis were performed using R software version 4.3.3.

Results and Discussion

The analysis of variance (Table 2) revealed significant differences among the Byadgi Dabbi collections for all the studied growth, yield, and yield-attributing traits, indicating the existence of considerable phenotypic variation within the farmer-maintained populations. Highly significant ($P \leq 0.01$) variation was observed for days to 50% flowering, plant height, fruit diameter, stalk length, number of fruits per plant, fruit weight, dry fruit yield per plant, number of seeds per fruit, and test weight, while number of primary branches, number of secondary branches and fruit length exhibited significant ($P \leq 0.05$) variation.

Estimation of genetic variability parameters

The genetic variability parameters (Table 3) clearly demonstrated the existence of substantial variability among collections of the Byadgi Dabbi chilli cultivar from farmers' fields. Among the traits, dry fruit yield per plant recorded the highest GCV (32.00%) and PCV (35.92%), followed by number of fruits per plant (20.82 and 22.99%, respectively), dry fruit weight (17.10 and 20.94%), hundred seed weight (16.59 and 22.28%), and number of seeds per fruit (13.96 and 16.59%), indicating the

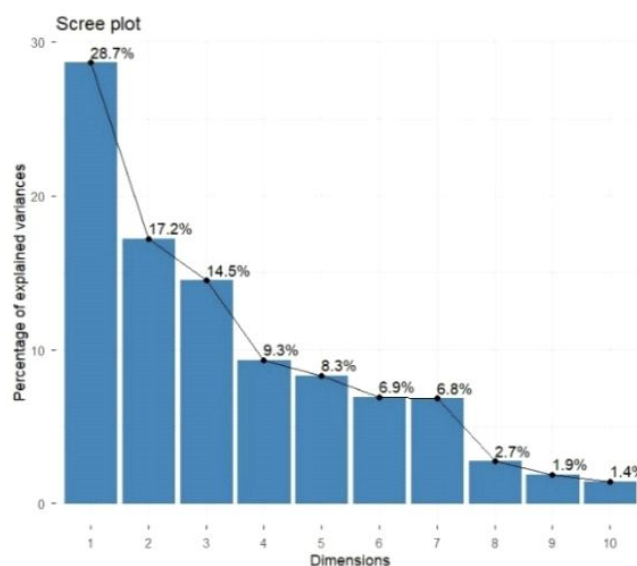


Fig. 1 : Scree plot depicting the distribution of eigenvalues and the proportion of total phenotypic variation explained by principal components for twelve quantitative traits.

presence of substantial genetic variability for these economically important traits. Moderate GCV and PCV were observed for stalk length (11.83 and 14.87%), fruit length (11.22 and 16.78%), fruit diameter (10.90 and 12.51%), and plant height (9.20 and 10.34%), suggesting the availability of moderate genetic variation. These observations are in close accordance with the results reported by Yogesh kumar *et al.* (2018) and Ahmad *et al.* (2022), who studied variability among Byadgi dabbi chilli collections. Estimates of genetic variability parameters are presented in the Table 3.

In contrast, days to 50% flowering exhibited the lowest GCV (5.17%) and PCV (6.00%), which is in parallel with results reported by Yogesh Kumar *et al.* (2018), while primary branches per plant (8.74 and 15.18%) and secondary branches per plant (8.42 and 13.51%) also recorded relatively lower GCV values, indicating comparatively limited genetic variability for these traits. Consistently higher PCV than GCV for majority of the traits indicated that environmental factors contributed to phenotypic expression; however, the

Table 2 : Analysis of variance for growth, yield, and yield-contributing traits in open-pollinated collections of the Byadgi Dabbi chilli cultivar.

Source of Variation	d.f.	DF	PH	NPBP	NSBP	FL	FD	SL	NFPP	FW	DFY	NSPP	HSW
Replication	1	20.48	7.738	0.0824	0.06771	0.4305	2.1259	0.1468	14.742	0.0994	27.93	238.97	0.0019
Treatments (Genotypes)	24	34.087**	110.836**	0.1516*	1.0699*	2.0014*	14.1499**	0.2912**	43.334**	0.6155**	475.15**	634.55**	0.0351**
Residual	24	5.063	16.122	0.0761	0.4711	0.7636	1.9302	0.06544	4.299	0.123	54.62	108.78	0.01

*Significance at 5% ** Significance at 1%

d.f. - Degrees of freedom, **DF** - Days to 50% flowering, **PH** - Plant height, **PB** - Number of primary branches per plant, **SB** - Number of secondary branches per plant, **FL** - Fruit length, **FD** - Fruit diameter, **SL** - Stalk length, **NFPP** - Number of fruits per plant, **FW** - Fruit weight, **DFY** - Dry fruit yield, **NSPP** - Number of seeds per fruit and **HSW** - Hundred Seed weight.

relatively narrow differences between the two estimates for most traits suggested that the observed variability was largely genetic in nature. These findings are consistent with the reports of Maga *et al.* (2013), Sushmitha *et al.* (2019) and Shivakumar *et al.* (2025), who also documented substantial genetic variability among Byadgi dabbi collections across locations for growth, yield, and yield-attributing traits. These results suggests that the variety under the traditional cultivation practices adopted by farmers across locations might have experienced natural cross pollination resulted in the accumulation and maintenance of considerable phenotypic variation for economically important yield traits.

Broad-sense heritability estimates ranged from 33.18% for primary branches per plant to 81.95% for number of fruits per plant. High heritability was observed for number of fruits per plant (81.95%), plant height (79.23%), dry fruit yield per plant (79.38%), fruit diameter (75.99%), days to 50% flowering (74.13%), and number of seeds per fruit (70.73%), indicating major proportion of the observed variation among the collections was heritable rather than environmentally induced. Moderate heritability was recorded for dry fruit weight (66.68%), stalk length (63.30%) and hundred seed weight (55.45%), whereas primary and secondary branches per plant exhibited relatively low heritability. Similar findings were reported by Jayasree *et al.* (2018) among byadgi dabbi collections. Results are also in parallel with the reports of Kadwey *et al.* (2016) and Pujar *et al.* (2017) within chilli collections.

Genetic advance expressed as per cent of mean (GAM) varied from 9.17% for days to 50% flowering to 58.73% for dry fruit yield per plant. High heritability coupled with high GAM was observed for dry fruit yield per plant (79.38% and 58.73%), number of fruits per plant (81.95% and 38.82%), dry fruit weight (66.68% and 28.76%), number of seeds per fruit (70.73% and 24.17%), hundred seed weight (55.45% and 25.45%), and fruit diameter (75.99% and 19.58%), indicating the predominance of additive gene action and the effectiveness of these traits for direct phenotypic selection in cultivar improvement. In contrast, days to 50% flowering, primary branches per plant and secondary branches per plant exhibited comparatively lower GAM despite moderate to high heritability, indicating comparatively limited genetic divergence and a possible influence of non-additive gene action. The results align with the reports made by Ahmad *et al.* (2022) and Shivakumar *et al.* (2025) where they reported high heritability along with high GAM for key yield parameters in byadgi dabbi collections.

While genetic diversity analysis provides an estimate of the extent of diversity among genotypes, a deeper understanding of the sources of variation can be achieved by identifying the traits that contribute most to the observed genetic divergence through multivariate analyses such as principal component analysis.

Principal Component analysis

Principal component analysis (PCA) was performed to determine the pattern and magnitude of variation among the open-pollinated collections of the Byadgi Dabbi chilli cultivar based on twelve quantitative traits. The analysis revealed that the first four principal components possessed eigenvalues greater than one (3.44, 2.07, 1.74 and 1.12, respectively), together accounting for 69.68% of the total phenotypic variation (Table 4.). Among these, PC1 explained the largest proportion of variation (28.65%), followed by PC2 (17.22%), PC3 (14.49%), and PC4 (9.31%). Similar results were reported by Babu *et al.* (2023) where first four principal components (PC1, PC2, PC3 and PC4) accounted for 70.60% of the total variation. High proportion of variation explained by the initial principal components indicates the existence of substantial phenotypic diversity among the farmer-maintained Byadgi Dabbi collections. Further, results are also in parallel with the reports made by Singh *et al.* (2020).

The scree plot (Fig. 1) showed a sharp decline in eigenvalues from PC1 to PC4, followed by a gradual flattening from PC5 onwards, indicating that most of the genetic variation was captured by the first few principal components. The first four components, having eigenvalues greater than unity according to the Kaiser criterion, were therefore considered the most informative for explaining the diversity present among the collections of Byadgi Dabbi cultivar.

Principal component-based characterization of trait relationships

The PCA variable correlation plot (Fig. 2) illustrated the distribution of the studied traits with respect of their association with the first two principal components, which together accounted for 45.90% of the total phenotypic variation (PC1 = 28.70%; PC2 = 17.20%). Traits including number of fruits per plant (NFPP), dry fruit yield per plant (DFY), fruit weight (FW), fruit diameter (FD), fruit length (FL) and hundred seed weight (TW) were represented by relatively longer vectors on the positive side of PC1, indicating that these traits contributed substantially to the variation explained by the first principal component. Among these, NFPP, DFY and FW were closely aligned, suggesting a similar pattern of variation

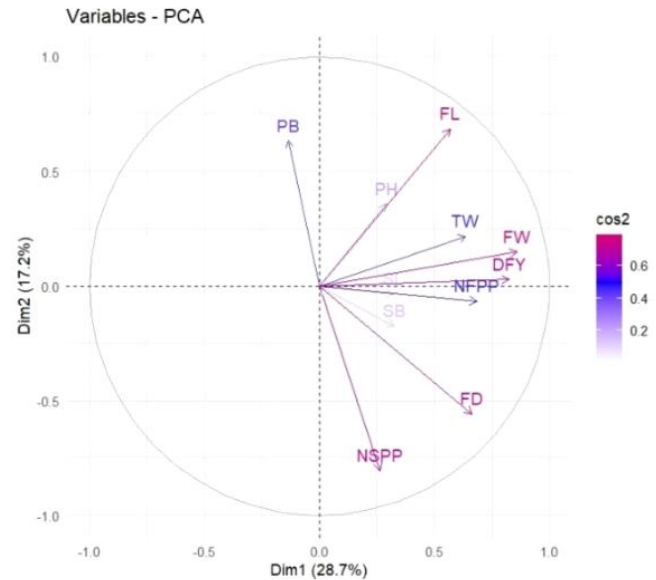


Fig. 2 : PCA variable correlation plot showing the contribution of growth, yield and yield-attributing traits to the first two principal components.

among the farmer-maintained collections.

In contrast, fruit length (FL), plant height (PH) and primary branches per plant (PB) were oriented towards the positive direction of PC2, whereas fruit diameter (FD) and number of seeds per fruit (NSPP) were positioned on the negative side of PC2, reflecting contrasting patterns of variation along the second principal component. The comparatively shorter vectors of secondary branches per plant (SB) and stalk length (SL) indicated a relatively smaller contribution to the variation explained by the first two principal components. The higher squared cosine (Cos²) values observed for FL, FD, FW, DFY, NFPP and NSPP indicated that these traits were better represented by the first two principal components than the remaining traits. Overall, the PCA variable correlation plot suggested that fruit morphology and yield-related traits were the principal contributors to phenotypic variation among the Byadgi Dabbi collections.

Genetic divergence among collections revealed by Principal Component analysis

The distribution of genotypes across the biplot (Fig. 3) demonstrated substantial genetic variability among the collections. With respect to PC1, genotype BD-1 exhibited the highest positive PC1 score (6.064) and was positioned in the direction of FW, DFY, and NFPP, indicating its superior association with major yield-contributing traits. Genotype BD-13 (4.289) and BD-15 (PC1 = 2.001) were also distinctly separated from the main cluster and closely aligned with fruit diameter (FD) and other fruit-related traits, suggesting greater

Table 3 : Estimates of genetic variability parameters for growth, yield, and yield-contributing traits in farmer-maintained collections of the Byadgi Dabbi chilli cultivar.

Trait	Mean $\pm$ SE	Range		σ^2_g	σ^2_e	σ^2_p	Coefficient of variation		h^2 (%)	GA	GAM (%)
		Min	Max				GCV(%)	PCV(%)			
DFE	73.72 $\pm$ 1.59	66.00	85.00	14.51	5.06	19.57	5.17	6.00	74.13	6.76	9.17
PH (cm)	78.07 $\pm$ 2.06	65.67	97.75	51.59	13.52	65.11	9.20	10.34	79.23	13.17	16.87
PB	2.22 $\pm$ 0.19	1.50	3.20	0.04	0.08	0.11	8.74	15.18	33.18	0.23	10.37
SB	6.50 $\pm$ 0.48	5.00	8.25	0.30	0.47	0.77	8.42	13.51	38.85	0.70	10.81
FL (cm)	7.01 $\pm$ 0.62	4.88	10.14	0.62	0.76	1.38	11.22	16.78	44.76	1.08	15.47
FD (mm)	22.67 $\pm$ 0.98	16.80	30.80	6.11	1.93	8.04	10.90	12.51	75.99	4.44	19.58
SL (cm)	2.84 $\pm$ 0.18	2.84	3.70	0.11	0.07	0.18	11.83	14.87	63.30	0.55	19.39
NFPP	21.22 $\pm$ 1.46	11.00	37.33	19.52	4.30	23.82	20.82	22.99	81.95	8.24	38.82
FW (g)	2.90 $\pm$ 0.24	1.98	4.96	0.25	0.12	0.37	17.10	20.94	66.68	0.83	28.76
DFY (g)	45.32 $\pm$ 5.23	21.25	58.73	210.27	54.62	264.90	32.00	35.92	79.38	26.61	58.73
NSPP	116.21 $\pm$ 7.37	78.67	164.67	262.88	108.78	371.66	13.96	16.59	70.73	28.09	24.17
HSW (g)	0.67 $\pm$ 0.07	0.42	1.06	0.01	0.01	0.02	16.59	22.28	55.45	0.17	25.45

DFE - Days to 50% flowering, **PH** - Plant height, **PB** - Number of primary branches per plant, **SB** - Number of secondary branches per plant, **FL** - Fruit length, **FD** - Fruit diameter, **SL** - Stalk length, **NFPP** - Number of fruits per plant, **FW** - Fruit weight, **DFY** - Dry fruit yield, **NSPP** - Number of seeds per fruit and **HSW** - Hundred Seed weight.

divergence. Conversely, genotypes BD-5 (-2.048), BD-10 (-1.826), BD-2 (-1.386), BD-6 (-1.293), and BD-1 (-0.908) were located on the negative side of PC1, indicating relatively lower expression of these yield attributes and representing genetically contrasting collections.

With respect to the second principal component, genotype BD-11 (3.862), followed by BD-24 (1.875) and BD-18 (1.823), occupied the upper quadrants and showed greater association with primary branches (PB) and plant height (PH), whereas genotype BD-15 (-2.307) was positioned towards the direction of fruit diameter (FD) and number of seeds per fruit (NSPP), reflecting a distinct trait combination. The majority of the remaining genotypes (BD-3, BD-7, BD-12, BD-14, BD-16, BD-17, BD-22, and BD-25) were clustered around the origin (Fig. 3), indicating relatively minimal phenotypic variation and a greater degree of similarity to the overall population mean. The wide separation of BD-23, BD-13, BD-15 and BD-11 from the central cluster reflects greater divergence among these farmer-maintained collections with three of them belonging to the Bellary region, indicating possible genetic contamination or segregation resulting in phenotypic variation among quantitative traits studied.

Trait-wise contribution to total variability explained by principal components

The contribution of individual traits to overall variability

Table 4 : Eigenvalues, percentage of total phenotypic variation, and cumulative variation explained by principal component analysis of twelve quantitative traits.

Principal Component	Eigenvalue	Percentage Variation	Cumulative Variation (%)
PC1	3.4383	28.65	28.65
PC2	2.0668	17.22	45.88
PC3	1.7393	14.49	60.37
PC4	1.1168	9.31	69.68
PC5	0.9981	8.32	77.99
PC6	0.8286	6.9	84.9
PC7	0.82	6.83	91.73
PC8	0.3295	2.75	94.48
PC9	0.2265	1.89	96.36
PC10	0.1726	1.44	97.8
PC11	0.14	1.17	98.97
PC12	0.1236	1.03	100

was assessed using the first three principal components since they capture largest proportion of the total variance and provide most comprehensive visualizations (Table 5). The loading values indicated that PC1, which explained the highest proportion of total variation (28.65%), was

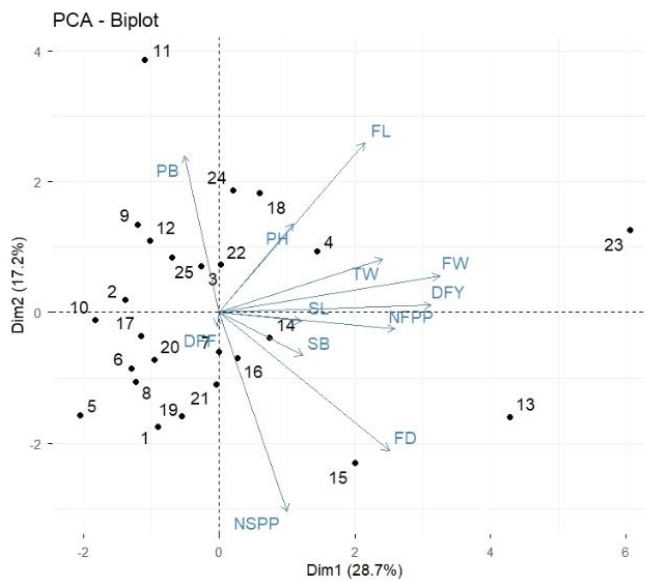


Fig. 3 : PCA biplot explaining genetic divergence among the collections of byadgi dabbi.

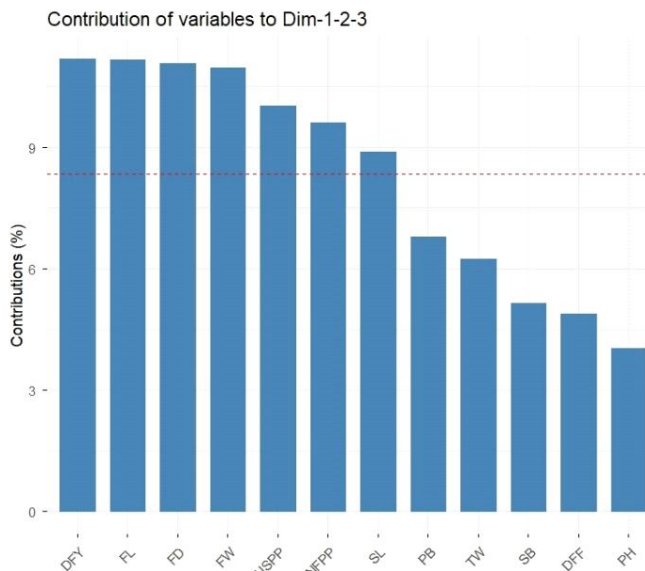


Fig. 4 : Variable contribution plot explaining the trait-wise contribution to the total phenotypic variation explained by the first three principal components.

predominantly influenced by fruit diameter (0.357), number of fruits per plant (0.335), fruit length (0.324), plant height (0.289), secondary branches per plant (0.232), fruit weight (0.173), hundred seed weight (0.163), stalk length (0.159), and dry fruit yield per plant (0.157), indicating that this component primarily represented variation associated with fruit and yield-related characters.

The second principal component (17.22%) was mainly characterized by higher positive loadings for primary branches per plant (0.632), fruit length (0.504), and plant height (0.462), while fruit diameter (-0.388) and number of seeds per fruit (-0.322) exhibited relatively higher

Table 5 : Trait wise contribution to total variability explained by significant principal components.

Trait	PC1	PC2	PC3	PC4
PH	0.289	0.462	-0.396	1.316
PB	-0.104	0.632	0.298	-0.059
SB	0.232	-0.16	0.486	0.844
FL	0.324	0.504	0.104	-0.161
FD	0.357	-0.388	0.172	-0.045
SL	0.159	-0.022	0.507	-0.123
NFPP	0.335	-0.042	-0.323	-0.026
NSPP	0.082	-0.322	-0.036	0.004
HSW	0.163	0.072	-0.012	-0.066
DFF	-0.002	-0.016	0.187	-0.017
FW	0.173	0.038	0.053	-0.021
DFY	0.157	0.007	-0.095	-0.045

DFF - Days to 50% flowering, **PH** - Plant height, **PB** - Number of primary branches per plant, **SB** - Number of secondary branches per plant, **FL** - Fruit length, **FD** - Fruit diameter, **SL** - Stalk length, **NFPP** - Number of fruits per plant, **FW** - Fruit weight, **DFY** - Dry fruit yield, **NSPP** - Number of seeds per fruit and **HSW** - Hundred Seed weight.

negative loadings. PC3 (14.49%) was primarily associated with stalk length (0.507), secondary branches per plant (0.486), and primary branches per plant (0.298), whereas PC4 (9.31%) was largely governed by plant height (1.316) and secondary branches per plant (0.844).

The variable contribution plot (Fig. 4) further demonstrated that dry fruit yield per plant (DFY), fruit length (FL), fruit diameter (FD), fruit weight (FW), number of seeds per fruit (NSPP), number of fruits per plant (NFPP), and stalk length (SL) contributed more than the average expected contribution (8.33%) represented by the horizontal dotted line in the Fig. 4, indicating that these traits were the major determinants of phenotypic divergence among the farmer maintained open-pollinated Byadgi Dabbi collections. Conversely, primary branches per plant (PB), test weight (TW), secondary branches per plant (SB), days to 50% flowering (DFF) and plant height (PH) contributed relatively less to the overall variability. Similar published reports of farmer-maintained collections of a single chilli cultivar are very limited. Therefore, direct comparisons with the present study are limited. However, the pattern of trait contribution to overall phenotypic variability observed in the present investigation is in accordance with the reports by Lahbib *et al.* (2012), Hasan *et al.* (2014), and Singh *et al.* (2020), who also identified fruit and yield-related

traits as the major contributors to total phenotypic variation among diverse chilli germplasm.

The predominance of yield and fruit-related traits among the major contributors indicates that the variability observed among the farmer-maintained open-pollinated collections was primarily driven by differences in fruit morphology and productivity rather than phenological or vegetative characters. The greater contribution of dry fruit yield, fruit size attributes, number of fruits per plant, and seed number suggests that these traits are the principal sources of genetic divergence and would therefore be the most informative descriptors for differentiating Byadgi Dabbi collections. Overall, the farmer maintained open pollinated collections represent a genetically heterogeneous population exhibiting phenotypic divergence distributed across several quantitative traits. While gene flow helps to maintain genetic diversity, cultivated landraces require conservation and purification to preserve their genetic identity (Pérez-Martínez *et al.*, 2022).

Conclusion

The present investigation identified moderate to high phenotypic variation among open pollinated farmer-maintained collections of the Byadgi Dabbi cultivar, indicating that the cultivar has become considerably heterogeneous under prolonged cultivation and farmer-led seed maintenance. The observed variation for economically important yield and fruit quality traits suggests that natural cross pollination with nearby improved cultivars, lack of scientific selection and repeated use of farm saved seed in the subsequent season might have progressively altered the original genetic constitution of the cultivar. Principal component analysis identified collections BD-11, BD-13, BD-15 and BD-23 as the most phenotypically divergent collections. Therefore, the findings of the present study provide a scientific basis for initiating genetic purification programmes aimed at restoring varietal identity, enhancing uniformity and ensuring the long-term productivity and market value of the Byadgi Dabbi cultivar. This can be achieved through conventional approaches such as successive selfing followed by selection or through doubled haploid development, which enables rapid development of completely homozygous lines in a single generation.

References

- Ahmad, S., Allolli B., Ganiger V., Jawadagi R., Sathish D., Gopali B. and Jhalegar J. (2022). Studies on genetic variability characteristics in Byadgi Dabbi derivatives of chilli (*Capsicum annuum* L.) under Northern Dry Zone of Karnataka. *The Pharma Innov. J.*, **11**(10), 701-704.
- Babu, U., Tembhurne B.V., Honnappa M. and Kisan B. (2023). The genetic dissection of economically important traits in chilli genotypes (*Capsicum annuum* L.) through multivariate analysis. *Int. J. Plant Soil Sci.*, **35**(22), 117-144.
- Bosland, P.W. (1995). *Capsicum*: history, cultivation and uses. In: Janick, J. (Ed.), *Horticultural Reviews: Species, Herbs and Edible Fungi*. Elsevier, New York, 347-366.
- Franceschetti, U. (1972). Natural cross-pollination in pepper (*Capsicum annuum* L.). In: Belletti, P., Nassi M.O. and Quagliotti L. (Eds.), *Proceedings of the Eucarpia Meeting on Genetics and Breeding of Capsicum*. Turin, Italy, 346-353.
- Geographical Indications Registry (2011). *Byadagi Chilli* (GI Application No. 129; Certificate No. 147). Office of the Controller General of Patents, Designs and Trade Marks, Department for Promotion of Industry and Internal Trade, Government of India, Chennai.
- Gonzalez, M. and Bosland P.W. (1991). Strategies for stemming genetic erosion of *Capsicum* germplasm in the Americas. *Diversity*, **7**, 52-53.
- Hasan, M.J., Kulsum M.U., Ullah M.Z., Hossain M.M. and Mahmud M.E. (2014). Genetic diversity of some chili (*Capsicum annuum* L.) genotypes. *Int. J. Agricult. Res., Innov. Technol.*, **4**(1), 32-35.
- Indiastat (2025). *Area, Production and Productivity of Dry Chillies in India (2024-2025)*. Indiastat, New Delhi.
- Jayasree, V., Allolli T.B., Evoor S., Ganiger V.M., Gopali J.B. and Jagadeesh R.C. (2018). Genetic variability in chilli (Byadgi Kaddi) genotypes. *Int. J. Curr. Microbiol. Appl. Sci.*, **7**(10), 3532-3536.
- Johnson, H.W., Robinson H.F. and Comstock R.E. (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J.*, **47**, 314-318.
- Justino, E., Fonseca M.E.N., Ferreira M.E., Boiteux L.S., Silva P.P., Medeiros W.N. and Nascimento N. (2018). Estimate of natural cross-pollination rate of *Capsicum annuum* using a codominant molecular marker associated with fruit pungency. *Gen. Mole. Res.*, **17**, gmr16039887.
- Kadwey, S., Dadiga A. and Prajapati S. (2016). Genotypes performance and genetic variability studies in hot chilli (*Capsicum annuum* L.). *Indian J. Agricult. Res.*, **50**(1), 56-60.
- Kanwar, J.S. (1995). Natural cross-pollination and its effect in chilli (*Capsicum annuum*). *Indian J. Agricult. Sci.*, **65**(6), 448-450.
- Kim, C.G., Kim D.I., Kim H.J., Park J.I., Lee B., Park K.W., Jeong S.C., Choi K.H., An J.H., Cho K.H., Kim Y.S. and Kim H.M. (2009). Assessment of gene flow from genetically modified anthracnose-resistant chili pepper (*Capsicum annuum* L.) to a conventional crop. *J. Plant Biol.*, **52**, 251-258.
- Lahbib, K., Bnejdi F. and El-Gazzah M. (2012). Genetic diversity evaluation of pepper (*Capsicum annuum* L.) in Tunisia

- based on morphologic characters. *Afr. J. Agricult. Res.*, **7(23)**, 3413-3417.
- Maga, T.J., Uguru M.I. and Ogbonna P.E. (2013). Variability and association studies on yield and yield characters in aromatic Nsukka yellow pepper (*Capsicum annuum* L.). *Int. J. Plant Breed.*, **7(2)**, 90-95.
- Moscone, E.A., Scaldaferrero M.A., Grabile M., Cecchini N.M., Sanchez Garcia Y., Jarret R., Davina J.R., Ducasse D.A., Barboza G.E. and Ehrendorfer F. (2007). The evolution of chili pepper (*Capsicum*-Solanaceae): a cytogenetic perspective. *Acta Horticulturae*, **745**, 137-169.
- Murthy, N.S.R. and Murthy B.S. (1962). Natural cross-pollination in pepper (*Capsicum frutescens* L.). *Andhra Agricult. J.*, **9**, 161-165.
- Pérez-Martínez, A.L., Eguiarte L.E., Mercer K.L., Martínez-Ainsworth N.E., McHale L., Van der Knaap E. and Jardón-Barbolla L. (2022). Genetic diversity, gene flow and differentiation among wild, semiwild and landrace chili pepper (*Capsicum annuum*) populations in Oaxaca, Mexico. *Amer. J. Bot.*, **109(7)**, 1157-1176.
- Pujar, U.U., Tirakannanavar S., Jagadeesha R.C., Gasti V.D. and Sandhyarani N. (2017). Genetic variability, heritability, correlation and path analysis in chilli (*Capsicum annuum* L.). *Int. J. Pure Appl. Biosci.*, **5(5)**, 579-586.
- Ritonga, A.W., Syukur M., Yunianti R. and Sobir (2018). Assessment of natural cross-pollination levels in chili pepper (*Capsicum annuum* L.). *IOP Conf. Ser.: Earth Environ. Sci.*, **196(1)**, 012008.
- Robinson, H.F., Comstock R.E. and Harvey P.H. (1949). Estimates of heritability and the degree of dominance in corn. *Agron. J.*, **41**, 353-359.
- Shivakumar, M.P., Biradar K., Naidu G.K. and Prabhu S.T. (2025). Genetic variability in local collections of Byadgi chilli (*Capsicum annuum* L.) for qualitative and quantitative traits. *J. Farm Sci.*, **38(1)**, 10-14.
- Singh, M., Nandpuri K.S. and Singh S. (1973). Natural cross-pollination in chilli as affected by direction and distance of planting between the varieties. *J. Res., Punjab Agricult. Univ.*, **10**, 419-422.
- Singh, P., Jain P.K. and Tiwari A. (2020). Principal component analysis approach for yield attributing traits in chilli (*Capsicum annuum* L.) genotypes. *Chem. Sci. Rev. Lett.*, **9(33)**, 87-91.
- Sivasubramanyam, M.S. and Menon M.P. (1973). Path analysis of yield components in rice. *Madras Agricult. J.*, **60(9-12)**, 1217-1221.
- Spices Board of India (2025). *Annual Report 2024-25*. Ministry of Commerce and Industry, Government of India, Kochi, Kerala.
- Sushmitha, A., Allolli T.B., Ganiger V.M., Ajjappalavar P.S., Evoor S., Gopali J.B. and Kareem A. (2019). Assessment of genetic variability, heritability and genetic advance for growth, yield and quality traits of Byadgi Dabbi genotypes of chilli (*Capsicum annuum* L.). *J. Pharmacog. Phytochem.*, **8(5)**, 944-947.
- Tong, N. and Bosland P.W. (2003). *Capsicum tovarii*, a new member of the *Capsicum* complex. *Euphytica*, **109**, 71-72.
- USDA-ARS (2011). *GRIN Species Records of Capsicum*. National Germplasm Resources Laboratory, Beltsville, Maryland.
- Yogeshkumar, H.J., Ajjappalavara P.S., Megharaj K.C., Patil H.B., Revanappa M.S. and Gollag S.G. (2018). Genetic variability, heritability and genetic advance for growth, yield and quality components of Byadgi Dabbi ecotypes of chilli (*Capsicum annuum* L.). *Int. J. Chem. Stud.*, **6(3)**, 879-881.