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## GENETIC VARIABILITY AND CORRELATION STUDIES IN THE F<sub>3</sub> POPULATION OF THE CROSS JNA-1 AND BYADGI DABBI IN CHILLI (*CAPSICUM ANNUUM* L.)

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### ABSTRACT

During the late *Kharif* season of 2023, a study was conducted at the Postgraduate Research Block, Main Agricultural Sciences Station (MARS), University of Agricultural Sciences (UAS), Raichur to determine the genetic variability and correlations for yield and its attributing traits in the F<sub>3</sub> population of chilli. Among the traits studied, a marked extent of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit yield/plant, indicating substantial variability in these traits. High heritability (h<sup>2</sup>) coupled with a high genetic advance as a percent of the mean (GAM) was observed for the count of primary branches, length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit yield/plant, suggesting these traits are primarily governed by additive gene action. Dry fruit yield/plant showed a positive and significant correlation with the number of fruits/plant, fruit width and fruit weight/plant, and a positive but non-significant correlation with length of the fruit. Therefore, the traits with high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values, along with high heritability (h<sup>2</sup>) and genetic advance as a percent of the mean (GAM) and positive correlations with dry fruit yield/plant are considered crucial for selection to effectively enhance dry fruit yield/plant in chilli.

**Keywords :** Chilli, JNA-1, Byadgi, Variability, Correlation.

### Introduction

Chilli (*Capsicum annuum* L.), a key culinary vegetable and spice crop from the Solanaceae family, is extensively cultivated in tropical and sub-tropical regions. Originating in South and Central America, it has a diploid chromosome complement of  $2n=2x=24$  and a natural outcrossing rate reaching 66.4 per cent (Pickersgill, 1991; Singh *et al.*, 1994). Chilli is an essential ingredient in Indian cuisine because of its pungency, color and aroma and additionally it is valued globally in condiments, medicines and as an ornamental. Its fruits are abundant in vitamins A and

C, antioxidants and capsaicin, with oleoresin used in the food, beverage and pharmaceutical industries (Bhutia *et al.*, 2015; Nehra, 2016).

India is a key player among nations in the production, export and consumption of chilli. In India, chilli is cultivated on approximately 8.9 million hectares, yielding about 29.13 million tonnes. Despite being the world's largest producer, India's chilli productivity remains relatively low at 3.3 tonnes per hectare, relative to modernized countries like the USA and South Korea, where yields reach 6.9 tonnes per hectare (Anon., 2023).

The Byadagi dabbi chilli, popular for fresh and dried use, measures 8-10 cm with a slight curve and bulge near the calyx. Renowned for its vivid color and gentle pungency, its thin, wrinkled skin makes it ideal for masala, oleoresin extraction and cosmetics, including nail polish and lipstick. Its high color, aroma and oleoresin recovery make it highly valued by chilli producers and the oleoresin industry. Nevertheless, despite its capacity for domestic and export markets, productivity remains low due to a lack of superior genotypes, highlighting the need to develop high-yielding cultivars to enhance production and productivity.

Improvements in chilli breeding have been achieved by harnessing existing genetic variability and tapping into the naturally high diversity found in yield-related traits (Rahman *et al.*, 2024). The exchange of chilli germplasm and extensive gene introgression among local cultivars have further expanded this variability, supporting the creation of new genetic combinations (Saisupriya *et al.*, 2020). With such a wide array of variability in chilli, there is substantial potential to enhance fruit yield through a systematic, well-organized selection program.

Burton (1952) emphasized the significance of considering both variability and heritability when assessing the potential impact of selection. Understanding the type and extent of genetic variability within a population is critical for designing an effective breeding program aimed at enhancing yield potential. Heritability, which refers to the part of phenotypic variation passed from parents to offspring, is an significant metric, as higher heritability increases the possibility of fixing desirable characters refined by selection. Heritability studies are thus essential for determining whether observed variations in specific traits are because of its genetic factors or environmental influences.

However, focusing solely on heritability estimates may limit the ability to fully predict breeding value. Genetic advance offers valuable insights into the expected gains from selecting superior plants (Lingaiah *et al.*, 2019) and the effectiveness of selection can be evaluated using genetic advance (Ashish *et al.*, 2017). Given that yield is a multifactorial trait influenced by numerous component traits, understanding the interrelationships between these traits is crucial for developing optimal selection indices to enhance yield. Phenotypic correlations, which examine the associations and interdependencies between observable traits, provide key insights into the strength and nature of these relationships. Thus, parameters such as genetic variability, heritability ( $h^2$ ), genetic advance as percent

of mean (GAM) and phenotypic correlations are instrumental in understanding both genetic and environmental effects on plant characteristics.

Keeping this in view, the current study was designed to evaluate the F<sub>3</sub> population of chilli for genetic variability, heritability ( $h^2$ ), genetic advance as percent of mean (GAM) and phenotypic correlations between yield and its attributing traits.

## Materials and Methods

The experimental study was conducted during the late *Kharif* season of 2023-24 at the Post Graduate Research Block, Main Agricultural Sciences Station (MARS), University of Agricultural Sciences (UAS), Raichur. This research location was located in the North-Eastern Dry Zone (Zone-II) of Karnataka, India, at 16° 12' N latitude and 77° 21' E longitude, having an elevation of 389 meters above the sea level. The area experiences an average yearly rainfall of around 608 mm and the mean maximum temperature exceeds 34°C throughout the calendar year. Data on weather conditions were obtained from the MARS observatory, University of Agricultural Sciences (UAS), Raichur.

An Augmented Block Design was employed in the experiment with six blocks, each containing ten F<sub>3</sub> lines and four checks. The checks were randomized to ensure a degree of freedom  $\geq 12$ . Seedlings, at thirty-five days of age, were transplanted into the research plot with spacing of 60 cm  $\times$  45 cm and the recommended dose of fertilizers (NPK) were applied according to the UAS, Raichur recommended cultivation of practices.

Five plants per F<sub>3</sub> line were chosen at random for recording observations for eleven yield and yield contributing traits: Height of the plant (cm), Count of primary branches, Days to 50 per cent flowering, Length of the fruit (cm), Fruit width (cm), Number of fruits/plant, Average fruit weight/plant (g), Average dry fruit yield/plant (g), Leaf area/plant (dm<sup>2</sup>/plant), Total chlorophyll content (mg/g) and 1000 seed weight (g). The calculation of genotypic and phenotypic coefficients of variation was performed as per Burton and Devane (1953), heritability in the broad sense ( $h^2$ ) was estimated following Lush (1945), expected genetic advance (Johnson *et al.*, 1955) and phenotypic correlation was analyzed according to Singh and Chaudhary (1979).

## Results and Discussion

The analysis of variance (ANOVA) (Table 1) showed a marked difference among the F<sub>3</sub> population for predominant characters studied, signalling the availability of substantial variability within the

population. The significant differences in traits like height of the plant, count of primary branches, number of fruits/plant, fruit weight/plant and dry fruit yield/plant, chlorophyll content, leaf area and test weight in both the treatment: check and treatment: test indicate strong genetic influence and substantial variability within the population. The check genotypes effectively captured this variability, making them valuable benchmarks for distinguishing superior plants. These results coincide with the findings of Vidyashree *et al.* (2018) for the count of primary branches and fruit width, Bekele *et al.* (2023) for height of the plant, Yatung *et al.* (2014) for chlorophyll content, Nahak *et al.* (2018) for leaf area, Usman *et al.* (2014) for days to 50 per cent flowering, and Patel *et al.* (2022) for length of the fruit, number of fruits/plant, fruit weight, test weight and dry fruit yield/plant.

Key measures of variability including the mean, range and major components such as phenotypic and genotypic coefficients of variation (PCV and GCV), heritability in the broad sense ( $h^2$ ) and genetic advance as a percent of the mean are summarized in Table 2. The results of the phenotypic correlation coefficient estimations for the 11 traits are showed in Table 3.

Across the characters studied, significant estimates of GCV and PCV were observed for length of the fruit (20.84% and 21.78%), fruit width (20.73% and 26.24%), number of fruits/plant (28.27% and 29.23%), fruit weight/plant (28.05% and 28.87%) and dry fruit yield/plant (28.08% and 28.96%). These values indicate a broad genetic variability within the population and recommended that these characters are primarily governed by additive gene effects, offering significant potential for improvement through simple selection methods. Conversely, moderate to low genetic and phenotypic coefficient of variation estimates were recorded for height of the plant (6.42% and 9.54%), days to 50 per cent flowering (3.35% and 4.70%), count of primary branches (16.80% and 20.63%), chlorophyll content (10.53% and 17.59%), leaf area (6.60% and 7.97%) and test weight (7.70% and 8.87%), suggesting reduced genetic variability for these traits.

For each of the characters observed, PCV values were steadily exceeding the associated GCV values, indicated that the observed variation is influenced not only by genetic factors but also by environmental conditions. Therefore, selection based solely on phenotype for these characters may not be impactful, as their expression is significantly influenced by environmental factors. Similar outcomes were reported in chilli by Hulagannavar *et al.* (2024). The PCV and GCV had only slight differences for all attributes, apart

from chlorophyll content, suggesting limited environmental impact on the expression of these characters. These results correspond to earlier studies of Tembhrne and Belabadevi (2015) and Hulagannavar *et al.* (2024). The substantial gap between PCV and GCV for chlorophyll content indicates a strong environmental effect on its expression. These outcome validate the findings from earlier work of Usman *et al.* (2014) regarding chlorophyll content.

Heritability provides an estimate of the proportion of phenotypic variation attributable to genetic variation, offering insight into the heritable component of variability. This information aids plant breeders in identifying elite plants within a population. A considerable amount of heritability was recorded for characters such as the count of primary branches, length of the fruit, fruit width, number of fruits/plant, leaf area, test weight, fruit weight/plant and dry fruit yield/plant. These results correspond to earlier studies of Tembhrne and Belabadevi (2015) for traits like the count of primary branches, length of the fruit, fruit width, number of fruits/plant, test weight and dry fruit yield/plant, as well as by Sai *et al.* (2023), who found high heritability for length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit yield/plant. In a broad sense, the high heritability of these traits suggests that a substantial portion of the phenotypic variance as a consequence of genotypic factors, with minimal environmental influence, thereby making selection a viable approach for advancing these characters.

Heritability, combined with genetic advance, sheds light on the magnitude of environmental influence on trait expression along with the chance for development through selection. High heritability, when paired with high genetic advance as a percent of the mean, suggests the involvement of additive gene action. This was observed for characters such as the count of primary branches, length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit yield/plant, suggesting that direct selection could be effective in achieving desirable genetic improvements for these traits. These outcomes validate the findings from earlier work of Tembhrne and Belabadevi (2015) for the count of primary branches, length of the fruit, fruit width, number of fruits/plant and dry fruit yield/plant. Additionally, the results for the number of fruits/plant, fruit weight/plant and dry fruit yield/plant align with the findings of Sai *et al.* (2023). The combination of high heritability and high genetic advance in these traits presents a promising

opportunity for further improvement in subsequent generations through selection.

Moderate genetic advance as a percent of the mean, combined with high or moderate heritability, suggests the involvement of both additive and non-additive gene action, with the environment playing a favourable role in trait expression. This pattern was observed in characters such as chlorophyll content, leaf area and test weight. Conversely, moderate to low heritability, coupled with low genetic advance as a percent of the mean indicates that non additive gene action predominates and environmental factors significantly influence trait expression, as seen in height of the plant and days to 50 per cent flowering. Therefore, breeders should adopt strategies that leverage both additive and non-additive gene effects to maximize genetic gains. This approach, encompassing both varietal and hybrid development, would be highly beneficial for long-term breeding programs.

The phenotypic correlation analysis of 11 yield and yield-attributing characters, as detailed in Table 3, revealed that dry fruit yield/plant was positively correlated with length of the fruit (0.01) and test weight (0.05) and showed highly significant and positive associations with fruit width (0.38), number of fruits/plant (0.97) and fruit weight/plant (0.96). These results concur with the research findings of Ajjappalavara *et al.* (2005) and Yadav *et al.* (2024). Similarly, fruit weight/plant displayed a positive correlation with test weight (0.03) and exhibited highly significant positive correlations with the number of fruits/plant (0.98), fruit width (0.37) and dry fruit yield/plant (0.96). These results coincide with the results of Patel and Chaurasiya (2023). Furthermore, fruit width was positively correlated with the count of primary branches (0.08), length of the fruit (0.03), chlorophyll content (0.14), leaf area (0.03) and test weight (0.14), along with highly significant positive correlations with the number of fruits/plant (0.36), fruit weight/plant (0.37) and dry fruit yield/plant (0.38), as reported by Ajjapanavar *et al.* (2005) and Belay and Tsehaye (2020). The correlation analysis also highlighted that length of the fruit was positively correlated with traits such as height of the plant (0.20), fruit width (0.03), number of fruits/plant (0.03), chlorophyll content (0.15), test weight (0.07) and dry fruit yield/plant (0.01). Notably, it showed a significant positive correlation with the count of primary branches (0.29), with similar results reported by Hasanuzzaman and Golam (2011), Pandit *et al.* (2014) and Bekele *et al.* (2022). The number of fruits/plant was positively correlated with length of the fruit (0.03), chlorophyll content (0.05) and test weight (0.10), while exhibiting

highly significant positive correlations with fruit width (0.36), fruit weight/plant (0.98) and dry fruit yield/plant (0.97). These results aligned with the observations of Pandit *et al.* (2014) and Bekele *et al.* (2022). The strong correlations of dry fruit yield/plant with fruit width, number of fruits/plant and fruit weight/plant underscored its dependence on these traits for yield enhancement. Thus, higher yields could be achieved by applying selection pressure to any of these traits. This may also suggest the occurrence of complementary gene actions among these traits, allowing for their simultaneous selection. As a result, length of the fruit, fruit width and fruit weight/plant have been identified as key traits for enhancing fruit yield in chilli, making them important targets in breeding programs focused on yield improvement.

### Conclusion

The research experimental was performed to examine genetic variability, heritability, genetic advance and phenotypic correlations for yield-related traits in the F<sub>3</sub> population derived from the cross between JNA-1 and Byadgi dabbi. The analysis of variance demonstrated significant variation across most traits. High heritability combined with substantial genetic advance as a percent of the mean suggests strong additive gene action, particularly in traits such as the count of primary branches, length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit yield/plant. These findings indicate that direct selection could be highly effective for genetic improvement of these traits. Traits exhibiting moderate genetic advance and high or moderate heritability such as chlorophyll content, leaf area and test weight suggest a balance of additive and non-additive gene action with environmental factors also influencing trait expression. In contrast, traits like height of the plant and days to 50 per cent flowering which exhibited moderate to low heritability and low genetic advance as percent of mean indicate a dominance of non-additive gene action with prominent environmental influence. For these characters breeders should consider strategies that harness both additive and non additive effects to maximise genetic gains. This dual approach incorporating both varietal and hybrid development is critical for the success of long term breeding programs. Furthermore, phenotypic correlation analysis demonstrated that characters such as fruit width, number of fruits/plant and fruit weight/plant show a highly significant positive correlation with dry fruit yield/plant. Additionally positive correlations were observed between dry fruit yield and length of the fruit and also test weight. These associations underscore the significance of selecting

these traits to effectively enhance yield related attributes in chilli breeding efforts.

Overall, the high variability, heritability and genetic advance as a percent of the mean (GAM) in key traits such as length of the fruit, fruit width, number of fruits/plant, fruit weight/plant and dry fruit

yield/plant along with the strong positive correlations of these traits with the main yield trait *i.e.*, dry fruit yield/plant, imply that selective breeding could be used effectively to enhance these characters in future generations.

**Table 1 :** Analysis of variance (ANOVA) for various quantitative traits considered in the study

Source	Df	Mean sum of squares (MSS)					
		HP	DFP	CPB	LF	FW	NFP
Treatment (ignoring Blocks)	63	44.24*	14.13**	0.19**	7.02**	0.13**	361.91**
Treatment: Check	3	208.70**	162.94**	0.07 <sup>ns</sup>	103.83**	1.82**	3173.04**
Treatment: Test	59	29.50 <sup>ns</sup>	6.79 <sup>ns</sup>	0.18*	2.13**	0.05*	168.36**
Treatment: Test vs. Check	1	420.61**	0.39 <sup>ns</sup>	1.06**	5.14**	0.02 <sup>ns</sup>	3348.01**
Block (eliminating Treatments)	5	24.13 <sup>ns</sup>	6.57 <sup>ns</sup>	0.16 <sup>ns</sup>	0.17 <sup>ns</sup>	0.00 <sup>ns</sup>	14.64 <sup>ns</sup>
Residuals	15	16.11	3.34	0.06	0.18	0.02	10.84

Source	Df	Mean sum of squares (MSS)				
		FWP	DFYP	CC	LA	TW
Treatment (ignoring Blocks)	63	6315.25**	5123.89**	118.69*	7.29**	4.82**
Treatment: Check	3	64709.71**	52031.69**	299.41**	16.75**	69.21**
Treatment: Test	59	2858.28**	2333.68**	63.07 <sup>ns</sup>	4.40**	0.38**
Treatment: Test vs. Check	1	35092.80**	29023.21**	2858.19**	149.57**	73.37**
Block (eliminating Treatments)	5	192.52 <sup>ns</sup>	225.55 <sup>ns</sup>	100.91 <sup>ns</sup>	4.24 <sup>ns</sup>	0.14 <sup>ns</sup>
Residuals	15	159.77	139.10	40.48	1.38	0.09

<sup>ns</sup> p > 0.05; \* p <= 0.05; \*\* p <= 0.01

HP – Height of the plant

DFP – Days to 50 per cent flowering

CPB – Count of primary branches

LF – Length of the fruit

FW – Fruit width

NFP – Number of fruits/plant

FWP – Fruit weight/plant

CC – Chlorophyll Content

LA – Leaf area

TW – 1000 seed test weight

DFYP – Dry fruit yield/plant

**Table 2 :** Estimates of genetic variability parameters for yield and its attributing traits in F<sub>3</sub> population of the JNA-1 × Byadgi dabbi in chilli

Sl. No	Trait	Range		Mean	GCV (%)	PCV (%)	h <sup>2</sup> (%)	GAM (%)
		Minimum	Maximum					
1	Height of the plant (cm)	46.98	71.23	56.96	6.42	9.54	45.36	8.92
2	Days to 50 per cent flowering	48.50	63.08	55.44	3.35	4.70	50.76	4.92
3	Count of primary branches	1.27	3.27	2.06	16.80	20.63	66.29	28.22
4	Length of the fruit (cm)	3.60	9.19	6.71	20.84	21.78	91.50	41.12
5	Fruit width (cm)	0.36	1.40	0.85	20.73	26.24	62.39	33.77
6	Number of fruits/plant	16.60	87.34	44.39	28.27	29.23	93.56	56.41
7	Chlorophyll content (mg/g)	26.46	63.53	45.14	10.53	17.59	35.82	13.00
8	Leaf area (dm <sup>2</sup> /plant)	20.24	31.58	26.33	6.60	7.97	68.68	11.29
9	Test weight (g)	5.56	8.27	6.97	7.70	8.87	75.20	13.77
10	Fruit weight/plant (g)	73.58	336.11	185.18	28.05	28.87	94.41	56.23
11	Dry fruit yield/plant (g)	64.35	301.02	166.83	28.08	28.96	94.04	56.18

GCV: Genotypic Coefficient of Variation

PCV: Phenotypic Coefficient of Variation

h<sup>2</sup>: Broad Sense Heritability

GAM: Genetic Advance as Percent of Mean

**Table 3 :** Estimation of phenotypic correlation coefficients for yield attributing traits in F<sub>3</sub> population of the JNA-1 × Byadgi dabbi in chilli

	HP	DFP	CPB	LF	FW	NFP	CC	LA	TW	FWP	DFYP
HP	1										
DFP	0.11	1									
CPB	0.05	-0.16	1								
LF	0.02	-0.03	0.29*	1							
FW	-0.02	-0.3*	0.08	0.03	1						
NFP	-0.11	-0.31*	-0.11	0.03	0.36**	1					
CC	-0.03	0.001	0.06	0.15	0.14	0.05	1				
LA	0.02	0.08	-0.11	-0.03	0.03	-0.04	0.73**	1			
TW	0.001	0.08	-0.1	0.07	0.14	0.1	0.89**	0.85**	1		
FWP	-0.1	-0.31*	-0.12	-0.01	0.37**	0.98**	-0.04	-0.1	0.03	1	
DFYP	-0.1	-0.32*	-0.12	0.01	0.38**	0.97**	-0.03	-0.09	0.05	0.96**	1

\* p &lt;= 0.05; \*\* p &lt;= 0.01

HP – Height of the plant

FW – Fruit width

LA – Leaf area

DFP – Days to 50 per cent flowering

NFP – Number of fruits/plant

TW – 1000 seed test weight

CPB – Count of primary branches

FWP – Fruit weight/plant

DFYP – Dry fruit yield/plant

LF – Length of the fruit

CC – Chlorophyll Content

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