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Genetic variability studies for yield and yield-related traits in the F2 population derived from the cross, Fuzzy-linted (FL) x Fuzzy-lintless (Fl) isogenic lines of *G. herbaceum* in cotton

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Abstract
A total of 721 F2 plants derived from the cross, Fuzzy-linted (FL) x Fuzzy-lintless (Fl) isogenic lines of *G. herbaceum* were evaluated to study the variability parameters in yield and seven yield contributing traits. The phenotypic coefficient of variation (PCV) was slightly higher in magnitude than the genotypic coefficient of variation (GCV) for all characters studied indicating the meagre influence of environment over the expression of the traits studied. High phenotypic and genotypic coefficients of variation were obtained for number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant, ginning outturn and lint index. Medium PCV and low GCV values were observed for the trait, seed index. High heritability was observed in traits *viz.,* number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, seed index, ginning outturn and lint index. High heritability coupled with high genetic advance as percent over mean was observed for characters *viz.,* number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, ginning outturn and lint index indicating the role of the additive gene action in expressing these traits, suggesting better scope for improvement of these traits through direct selection or crossing followed by a pedigree method of selection.

Keywords: Cotton, genetic variability, genetic advance, heritability

Introduction
Cotton (*Gossypium* spp.) is a predominant source of natural textile fibre, which is known as the "king of fibre". With a share of over 50 percent of the global raw material market, cotton serves as a cornerstone of the global economy. It is cultivated in tropical and subtropical regions of more than 60 countries in the world (Jarwar *et al.,* 2018) [11]. There are 45 diploid and seven tetraploid species exist, and of which *Gossypium arboreum* and *Gossypium herbaceum* in diploid species (2n = 26), *Gossypium hirsutum* and *Gossypium barbadense* in tetraploid species (2n = 52) are cultivated ones (Wendel and Grover, 2015) [25]. Apart from its primary application as clothing, cotton linters (< 3.5 mm) along with other pulps are used in the paper industry to manufacture technical papers, art papers, *etc.* Coarse cotton is used in hospitals as cotton swabs. Cotton oil extracted from the seed is used in the cosmetics and paint industry; it can also be used for consumption if the gossypol content is low. Cotton seed meal is used as dairy feed.

Globally, cotton is cultivated in an area of 32.36 million hectares, yielding a total production of 142.70 million bales and achieving productivity of 749.67 kg ha^{-1}. Among these countries, India holds a significant position globally, boasting the largest cotton-growing area of 13.06 million hectares and the highest production of 34.34 million bales. However, India's productivity falls behind the world average, ranging from 30 to 50 percent lower, at 447 kg ha^{-1}. In India, cotton cultivation is divided into three zones, with the northern zone exhibiting the highest productivity at 570 kg ha^{-1} followed by the central zone at 473 kg ha^{-1} and the south zone at 464 kg ha^{-1}. The state of Maharashtra covers the largest cotton area with 42.29 lakh hectares, while Gujarat leads in production with 94.97 lakh bales and Rajasthan excels in productivity with 578.63 kg ha^{-1}. In Karnataka, cotton is cultivated across an area of 9.23 lakh hectares, producing 25.41 lakh bales and achieving a productivity of 468.01 kg ha^{-1} (INDIASTAT, 2022) [10].

Before breeding is taken up to accomplish the prime objective in cotton improvement, it is desirable to elicit information on the extent of genetic variability present in the material. The assessment of the extent of variation present in the genetic material becomes an essential step to know the magnitude of improvement that can be attained for various characters and deciding the ways to achieve it. The effectiveness of selection depends on the magnitude of genetic variability in a particular character. It is necessary to study variability in respect of quantitative characters with reference to genetic parameters such as genotypic variance, phenotypic variance, heritability and genetic advance as percent over mean (GAM). The coefficients of variation expressed in percent at phenotypic (PCV) and genotypic levels (GCV) have been used to compare the variability observed among the different characters. A wider spectrum of variability will enhance the chances of selecting a desired genotype.

Besides genetic variability, knowledge on heritability (h^2) and genetic advance measure the relative degree to which a character is transmitted to progeny, thereby helping the breeder to employ a suitable breeding strategy to achieve the objective quickly. GAM together with heritability estimates gives a relatively better picture of the amount of advance to be expected through selection (Johnson *et al.,* 1955) [12]. A relative comparison of heritability values and expected genetic advance expressed as the percent over mean gives an idea about the nature of gene action governing a particular character. Therefore, for the successful improvement of any crop, it is necessary to have a thorough knowledge on the variability present in the available breeding material. Several researchers worked out genetic variability parameters such as PCV and GCV, h^2 and GAM on various yield and fibre quality traits in cotton such as number of monopodia per plant, number of sympodia per plant, number of bolls, number of fruiting points per plant, seed index, lint index, micronaire value, and seed cotton yield per plant to know the extent of genetic variability present in the population and also to select promising lines based on their genotypic value without any mask of environment on the phenotype (Sakthi *et al.,* 2007; Dhamayanathi *et al.,* 2010; Choudki *et al.,* 2012; Raza *et al.,* 2016 and Meena *et al.,* 2022) [20, 4, 3, 18, 17]. With this background, the present investigation was carried out to assess the extent of genetic variability, heritability, and genetic advance for yield and seven yield-related traits in the F_2 segregating population derived from two isogenic lines *viz.,* Fuzzy-linted (FL) and Fuzzy-lintless (Fl) lines of *G. herbaceum.*

Materials and Methods
The present study was carried out in the Botanical Garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad. During *summer* 2021, the two isogenic lines *viz.,* Fuzzy-linted (FL) and Fuzzy-lintless (Fl) lines of *G. herbaceum* were crossed to get F_1 plants and generated F_2 population by selfing F_1 plants during *Kharif* 2021. In order to estimate the magnitude of genetic variability, heritability and genetic advance for yield and yield-related traits, in the present investigation a total of 721 F_2 individuals along with their parents and F_1 plants were raised during *Kharif* 2022. Before sowing, seeds were treated with imidacloprid to protect the crop from the incidence of sucking pests during the early growth stage. Seeds were hand-dibbled in rows of 4 m in

length with a spacing of 90 cm between rows and 20 cm between plants. Agronomic management was followed according to the recommended package of practices for irrigated conditions of the south zone.

The observation was recorded for eight traits *viz.,* number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), seed index (g), ginning outturn (GOT) (%) and lint index (g) on randomly selected five plants of each parent, F_1s and individual plant observations in F_2 population were recorded. The mean and variances were analyzed based on the formula given by Singh and Chaudhary (1977) [22]. The phenotypic and genotypic variability for each character was estimated by using the method given by Burton (1952), heritability (h^2) in the broad sense according to Lush (1940) and the genetic advance as percent over mean was worked out based on the method given by Johnson *et al*. (1955) [12]. All the variability parameters were calculated in Microsoft Excel.

Results and Discussion
Genetic variability is a prerequisite for any crop improvement programme. Selection can be done only when sufficient variation or variability is present in the base population which ultimately leads to an increase in the genetic gain in future generations. Selection is not effective when there is no variation and ultimately no improvement. The maximum variability released for a particular trait will be more in the F_2 generation when we cross genetically diverse parents. Therefore, we have crossed two isogeneic lines which are highly diverse with respect to fibre development *i.e.,* Fuzzy-linted (FL) and Fuzzy-lintless (Fl) lines of *G. herbaceum.* Variability parameters *viz.,* mean, range, phenotypic coefficients of variations (PCV), genotypic coefficients of variations (GCV), heritability and genetic advance as percent over mean for eight characters were calculated and presented in Table 1 and Fig 1. Statistical analysis revealed the presence of a considerable level of genetic variability for all the eight characters under study.

The minimum F_2 population size required for a trait governed by one locus is 4^n. However, yield and yield contributing traits like number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), seed index (g), ginning outturn (GOT) (%) and lint index (g) are quantitative in nature and are governed by several genes. Consequently, the minimum F_2 population required for these traits will be very high. Therefore, we evaluated 721 F_2 plants which are sufficient to identify positive transgressive segregants for yield as well. Statistically, the range is a difference between the highest to lowest value, which indicates the range of variation present for a particular trait. All eight traits showed a high range of variation which indicates the presence of continuous variation for all the traits. The number of monopodia per plant ranged from 0.00 to 4.00 with a mean value of 1.69. The number of sympodia per plant recorded the mean value of 25.03 and it ranged from 8.00 to 53.00. The trait expressed large variation in terms of number of bolls per plant with values ranging from 1.00 to 87.00 with a mean value of 16.89. Boll weight ranged from 0.32 to 3.58 g with a mean value of 1.67 g. The seed cotton yield per plant recorded a mean value of 40.52 g and it ranged from 0.70 to 207.10 g. The seed index ranged from 2.41 to 9.94 g with a mean value of 5.88 g. The range of variation for ginning outturn was 0.00 to 50.15% with a mean

value of 30.07%. The lint index ranged from 0.00 to 5.11 g with a mean of 2.76 g.

All eight traits studied were quantitative in nature; therefore, there was a high environmental influence on these traits, making selection ineffective. The phenotypic variation of a particular trait is the sum of its genotypic variation and environmental variation, so estimating PCV and GCV is highly necessary to determine whether the variation observed in the F_2 population is due to genotypic value or if there is any masking effect of the environment on the phenotype of yield and yield contributing traits. The higher PCV and GCV values indicate the presence of wider genetic variability in the F_2 population. The narrow difference between the genotypic coefficient of variation and the phenotypic coefficient of variation indicates that the characters were less affected by the environment and the variation was mainly due to the genetic component. The higher PCV and GCV values were observed for the traits *viz.*, number of monopodia per plant (59.21% and 39.36%), number of sympodia per plant (32.77% and 29.99%), number of bolls per plant (71.01% and 61.25%), boll weight (27.56% and 20.95%), seed cotton yield per plant (81.90% and 70.97%), ginning outturn (43.17% and 43.01%) and lint index (46.03% and 45.85%) respectively (Fig. 1), which indicated the presence of a large amount of variation in the F_2 population and since GCV and PCV were higher for these traits, indicating less influence of environment. So variation existing in this population is reliable and also gives confidence for selecting the positive transgressive segregants for seed cotton yield per plant as well. Similar findings were observed by Dhivya *et al.* (2014) [5], Manonmani *et al.* (2019) [16], Shruti *et al.* (2019) [21], Sahar *et al.* (2021) [19], Gowda *et al.* (2022) [8] and Meena *et al.* (2022) [17]. Medium PCV and low GCV were observed for the seed index (10.77% and 9.27% respectively). Similar results for seed index were obtained by Vinodhana *et al.* (2013) [24], Amanu *et al.* (2018) [1] and Hampannavar *et al.* (2020) [9].

Although GCV indicates a high degree of genetic variation, heritability estimates, and genetic gain are the parameters determining the amount of heritable portion in each trait (Falconer, 1981) [7]. The higher heritability values generally are the reflection of closed values of respective phenotypic and genotypic variances and also indicate that the selection of a character is useful in improving plant type. Cotton is often cross-pollinated crop with an outcrossing percentage of around six percent, which is highly negligible; it is as good as a self-pollinated crop. Therefore, there is less gap between genotypic variation (V_g) and additive genetic variation (V_A). Hence, we can rely on broad sense heritability estimate (V_g/V_p). High heritability was observed in traits *viz.,* number of sympodia per plant (83.72%), number of bolls per plant (74.40%), seed cotton yield per plant (75.09%), seed index (74.05%), ginning outturn (99.24%) and lint index (99.21%) whereas, moderate heritability was exhibited by the traits, number of monopodia per plant (44.20%) and boll weight (57.81%). Meena *et al.,* 2022 [17] also reported high heritability for most of the traits studied. Moderate heritability for number of monopodia per plant and boll weight was also observed by Eswari *et al.* (2017) [6] and Amanu *et al.* (2018) [1].

Heritability by itself does not provide an indication of the amount of genetic progress that would result from selecting the best individuals, rather it depends on the amount of genetic variance, especially additive genetic variance. Therefore, genetic advance and genetic advance over mean gain importance in providing an idea of the amount of progress that can be achieved by selection. Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. High genetic advance as percent over mean (GAM) was recorded for the traits, number of monopodia per plant (53.91%), number of sympodia per plant (56.52%), number of bolls per plant (108.83%), boll weight (32.82%), seed cotton yield per plant (126.68%), ginning outturn (88.26%) and lint index (94.07%) whereas, moderate GAM was exhibited by seed index (16.43%).

According to Johnson *et al.* (1955) [12], heritability estimates along with genetic gain are usually more useful. The traits *viz.,* number of monopodia and boll weight exhibited medium heritability and high GAM. High heritability and medium genetic advance were observed for the trait, seed index. These results are in agreement with the reports made by Tuteja *et al.,* (2006) [23], Choudki *et al.,* (2012) [3] and Lokeshkumar and Patil (2018) [14]. High heritability coupled with high genetic advance as percent over mean was observed in number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, ginning outturn and lint index indicating the role of the additive gene action in expressing these traits, suggesting better scope for improvement of these traits through direct selection. Tuteja *et al.* (2006) [23], Choudki *et al.* (2012) [3], Komala *et al.* (2018), Lokeshkumar and Patil (2018) [14] and Hampannavar *et al.* (2020) [9] also reported similar results in cotton.

Table 1: Genetic parameters of eight yield and yield-related traits in the F_2 population

Characters	Mean	Range	PCV (%)	GCV (%)	h² (%)	GAM
Number of monopodia per plant	1.69	0.00-4.00	59.21	39.36	44.20	53.91
Number of sympodia per plant	25.03	8.00-53.00	32.77	29.99	83.72	56.52
Number of bolls per plant	16.89	1.00-87.00	71.01	61.25	74.40	108.83
Boll weight (g)	1.67	0.32-3.58	27.56	20.95	57.81	32.82
Seed cotton yield per plant (g)	40.52	0.70-207.10	81.90	70.97	75.09	126.68
Seed index (g)	5.88	2.41-9.94	10.77	9.27	74.05	16.43
Ginning outturn (%)	30.07	0.00-50.15	43.17	43.01	99.24	88.26
Lint index (g)	2.76	0.00-5.11	46.03	45.85	99.21	94.07

*PCV- Phenotypic coefficient of variation; GCV- Genotypic coefficient of variation; h²- heritability and GAM- genetic advance as percent of mean
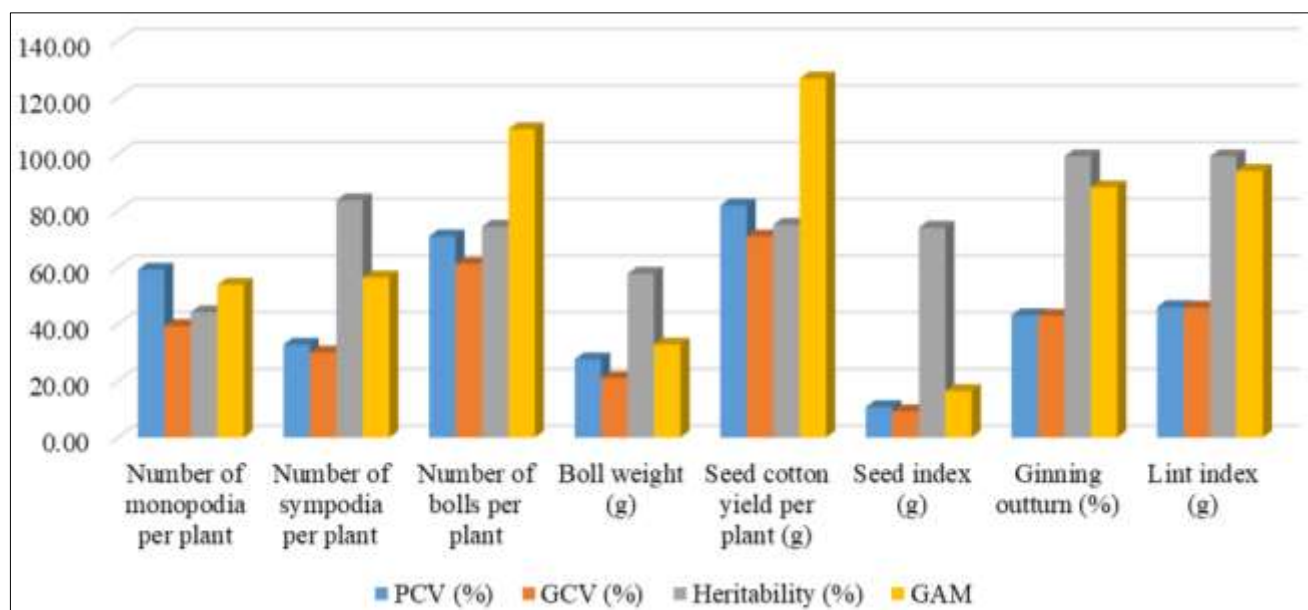
Fig 1: Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability (h^2) and Genetic advance as percent of mean (GAM) for eight characters in F_2 population.

Conclusion

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the effect of environment. The range of GCV and PCV were recorded higher for number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant, ginning outturn and lint index implying that variation existed in this population is reliable and gives confidence for selection while improvement. The traits *viz.,* number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, seed index, ginning outturn and lint index showed high heritability values indicating variation due to genotypic value is higher and environmental influence is lesser for these traits. High heritability coupled with high genetic advance as percent over mean was noted in number of sympodia per plant, number of bolls per plant, seed cotton yield per plant, ginning outturn and lint index. This observation underscores the role of the additive gene action in expressing these traits, suggesting a better scope for improvement of these traits through direct selection.

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