Original Research Article

Unravelling the genetic divergence and trait association for seed yield and its components ~~traits~~ among germplasm lines in cotton (*Gossypium hirsutum* L.)

ABSTRACT

The current study was focused on unravelling the genetic basis for seed cotton yield and yield attributing traits with an emphasis on isolating most potential germplasm accessions. A set of 192 cotton germplasm accessions were evaluated for two cropping seasons and two environments. The results of correlation analysis indicated the presence of significant and positive correlation between seed cotton yield with number of sympodia per plant, number of bolls per plant, lint yield, boll weight and lint index, indicating selection for these traits indirectly enhance the seed cotton yield. While diversity analysis categorized germplasm accessions into eight different clusters. These results indicated the existence of adequate genetic diversity among the germplasm lines which can be exploited to manifest higher magnitude of heterosis through hybridization of genotypes belonging to different clusters.

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Keywords: Germplasm, Correlation, Genetic diversity, K means clustering and R software

INTRODUCTION

Cotton, the foremost non-food agricultural commodity globally, stands as one of the earliest plant fibers utilized for textiles. Even in contemporary times, cotton remains an undisputed natural textile fiber seamlessly integrated into our daily lives in diverse manners, esteemed above hundreds of other fiber-yielding plants known to humanity. The volume of cotton production surpasses that of all other fibers combined. Being the precious gift of nature to mankind contributed by genus *Gossypium* to the people all over the world, cotton remains the most miraculous fiber, even after 8000 years of its first use. No agricultural commodity in the world exercised such a profound influence on men and matter as cotton has done from time immemorial Anon [1]. India has been the traditional home for cotton and cotton textiles. A comprehensive knowledge of genetic basis of quantitative traits is of prime importance in understanding the genetic potential of germplasm accessions and its use in crop improvement. Most of the yield and fiber ~~fibre~~ traits known to be controlled by polygenes or quantitative trait loci (QTLs) Ulloa [2].

The correlation reveals the nature of relationship between yield and its components ~~traits~~. If the correlation between two traits is positive and significant, improvement in one trait will exert a significant impact on the other, which helps the breeder to exhibit his skills in designing selection strategies in plant breeding. Comprehending correlation enables the concurrent enhancement of multiple traits, aiming to achieve the desirable blend of various yield components. The appraisal of genetic diversity is important to understand the pattern and evolutionary relationship among germplasm or genotypes, which will aid in sampling the genetic resources in a more systematic manner for conservation and crop improvement. Hence, this study was conducted to get insights into the genetic divergence and traits association among germplasm lines for yield and its components ~~traits~~ in cotton Wakelyn and Chaudhry, [3].

Comment [r2]: Note the genetic differences of cotton in terms of seed yield?

MATERIAL AND METHODS

A set of 192 cotton germplasm accessions maintained at ~~All~~ all India Co-ordinated Research Project (AICRP) on Cotton in University of Agricultural Sciences (UAS) Raichur were used in the current investigation. The phenotyping was done by raising the germplasm lines in two locations *i.e.*, MARS, Raichur and College of Agriculture, Bheemarayanagudi for two successive years in *kharif* of 2021 and 2022. Augmented design was used for evaluation along with five checks (BGDS-1033, BGDS-1063, SCS-1061, SCS-1062 and SCS-793) and observations on different quantitative traits such as ~~Plant~~ plant height (PH), ~~Number~~ number of monopodia per plant (NM), ~~Number~~ number of sympodia per plant (NS), ~~Number~~ number of bolls per plant (NB), ~~Boll~~ boll weight (BW), ~~Seed~~ seed cotton yield per plant (SCY), ~~Lint~~ lint yield (LY), ~~Ginning~~ ginning out turn (GOT), ~~Lint~~ lint index (LI) and ~~Seed~~ seed index (SI) were recorded. Seed cotton yield being a complex trait is affected by many genetic and non-genetic factors. In order to identify the independent variables like yield attributes, association studies serve as an effective tool. The correlation based on Pearson method and diversity analysis using K Means clustering were performed in R software using *metan* and *factoextra* packages, respectively.

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RESULTS AND DISCUSSION

The results on correlation studies of seed cotton yield with yield attributing traits revealed that seed cotton yield was positively significantly correlated with number of sympodia per plant (SN) (r=0.40**), number of bolls per plant (NBP) (r=0.91**), lint yield (LY) (0.94) at 1% probability level ~~of significance~~, whereas boll weight (BW) (0.28) and lint

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index (LI) (0.32) were found to be significant at 5% probability level ~~of significance~~ (Table 1). Other traits were also found to be associated with seed cotton yield but not in a significant amount. It indicated that the seed yield of cotton could be enhanced in a significant manner by improving these strongly associated traits, mainly formerly mentioned three traits (Fig.1 and 2). Similarly, LY was significantly positive correlated with other traits such as LI (0.41) and GOT (0.40). Seed ~~Index~~ index was also found to be associated with BW (0.62). Number of bolls per plant (NB) ~~NB~~ was associated with NS (0.41). However, PH was positively correlated with NS (0.67) and SI (0.28) in a significant manner. It was observed that non-~~existence of significant association of NM with any of the traits.~~

Table1. ~~Estimates of c~~ Correlation coefficients between yield and its components ~~traits~~ among germplasm accessions

	PH	NM	NS	NB	LY	SI	BW	GOT	LI	SCY
PH	1.00									
NM	0.20ns	1.00								
NS	0.67**	0.19	1.00							
NB	0.20ns	0.20	0.41**	1.00						
LY	0.15ns	0.19	0.35**	0.91**	1.00					
SI	0.28*	0.07	0.17	0.02	0.09	1.00				
BW	0.09ns	-0.05	0.03	-0.03	0.21	0.62**	1.00			
GOT	-0.22ns	-0.01	-0.05	0.22	0.40**	-0.43	-0.13	1.00		
LI	0.08ns	0.06	0.12	0.18	0.41**	0.66**	0.53**	0.39**	1.00	
SCY	0.25ns	0.20	0.40**	0.91**	0.94**	0.26	0.28*	0.07	0.32*	1.00

Ns, * and **: Non significant, significant at 5 and 1 % probability levels, respectively.

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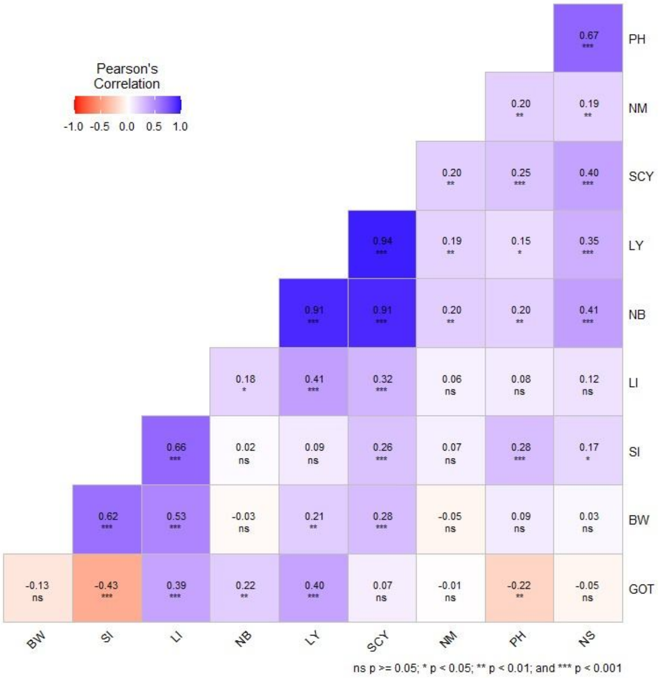

Fig 1. Heatmap depicting estimates of correlation coefficients between yield and its components ~~traits~~ among germplasm accessions

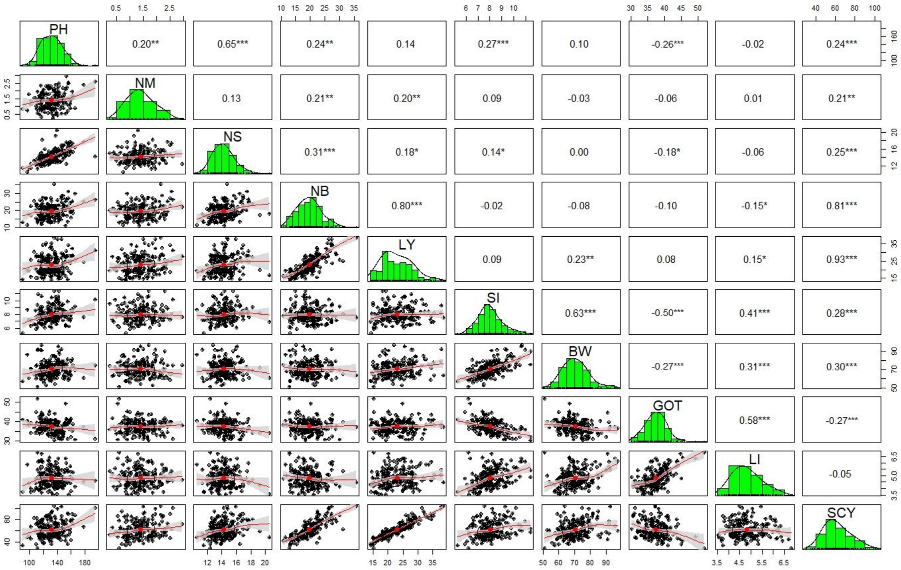

Fig 2. Corrplot depicting estimates of correlation coefficients between yield and its components ~~traits~~ among germplasm accessions

Genetic diversity is referred to as any variation at the phenotypic, DNA or genomic level of an individual, population or species. The appraisal of diversity is important to understand its pattern and evolutionary relationships between germplasms or genotypes, which will aid in sampling the genetic resources in a more systematic manner for conservation and crop improvement ~~Revanasiddayya~~ [4]. The diversity analysis based on K Means clustering classified the complete set of 192 germplasm lines into eight different clusters (Fig. 3) *viz*., cluster I, cluster II, cluster III, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII with a cluster size of 13, 47, 21, 26, 31, 19, 27 and 8, respectively. First two clusters share similarity more than the next six clusters, which share quite common similarity. Cluster I have germplasm lines which are distant from the germplasm lines of cluster VIII. These results indicated the existence of adequate genetic diversity among the germplasm lines (Fig.4), that could be exploited for further development of hybrids or varieties by selecting individuals in segregating generations of a cross between distant germplasm lines. The better hybrids can be expected when the germplasm lines of cluster I are crossed with the germplasm lines of cluster VIII. High yielding varieties can also be produced from the selections in segregating generations of the cross between the distant lines belong to cluster I and cluster VIII.

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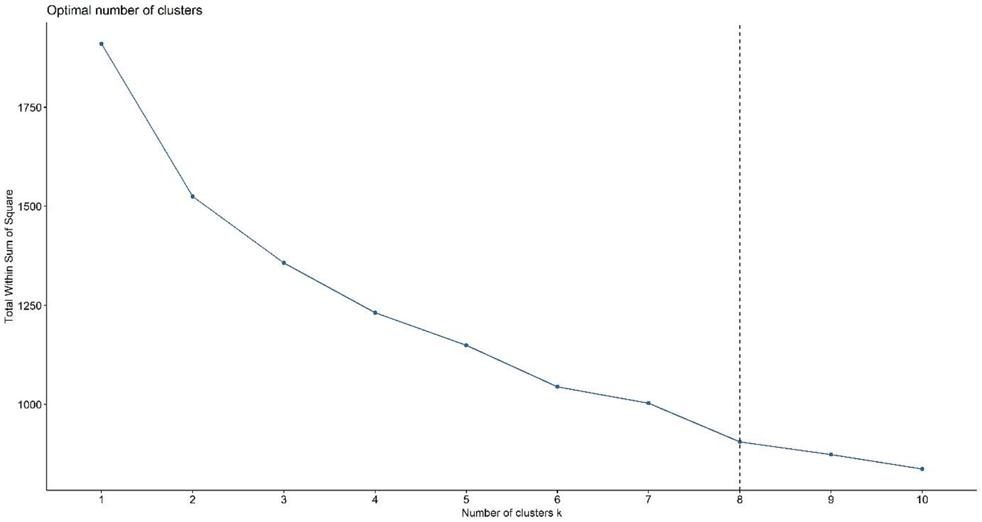

Fig 3. Optimum number of clusters defined using K Means clustering

The information about the contribution of these characters to genetic divergence is essential for understanding which traits are driving the differences among the cotton germplasms. This knowledge can guide breeding programs and helps prioritize specific traits for improvement or selection of diverse germplasm for hybridization. Meanwhile, ~~Similar~~ similar results were obtained by Bhimate [5], Santos [6], Rajendrakumar [7], Gururajan and Manickam [8], Kiran [9] and Karunakar [10].

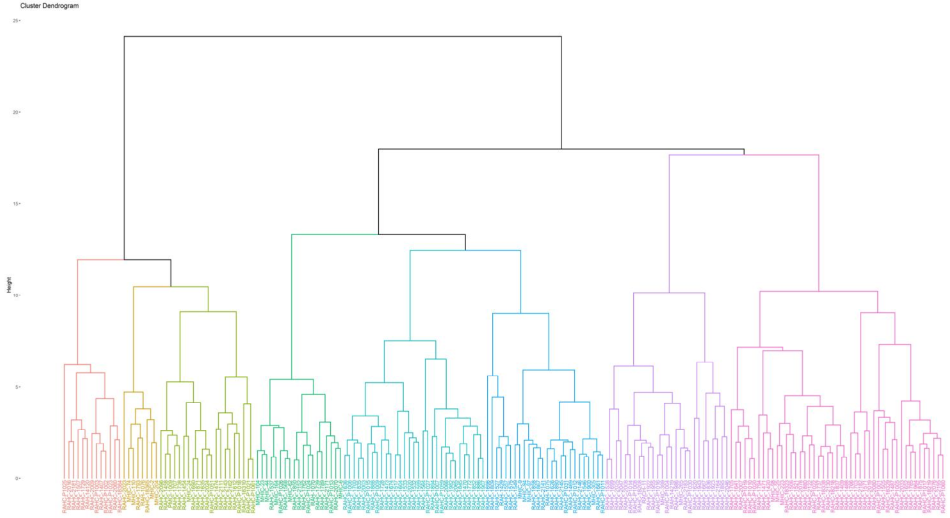

Fig 4. Dendrogram deciphering different clusters of cotton germplasm accessions

The correlation analysis indicates that several traits are significantly and positively associated with ~~seed cotton yield (~~SCY~~)~~, suggesting that indirect selection for these yield-related traits could be effective for genetic improvement in cotton. In this investigation, SCY was found to be significantly associated with ~~lint yield (~~LY~~)~~, ~~number of bolls per plant (~~NB~~)~~, ~~number of sympodia per plant (~~NS~~)~~, ~~boll weight (~~BW~~)~~, and ~~lint index (~~LI~~)~~. This means that enhancing SCY could be achieved by selecting for any of these traits. Similar trends were observed in previous studies by Deshmukh [11], Selvaraj [12], Hampannavar [13], Chapepa [14] and Jangid [15], which also reported significant associations between SCY and these traits.

Additionally, the significant genetic diversity exhibited by the germplasm lines can be harnessed to achieve a higher magnitude of heterosis through the hybridization of genotypes from distant clusters. The diversity analysis categorized the germplasm lines into distinct clusters, suggesting that crossing lines from genetically diverse clusters could result in superior hybrids with enhanced yield potential. This finding aligns with the results of previous studies by Nishanth [16], Nikhil [17], Vinodhana and Gunasekaran [18] and Sarwar [19], who also highlighted the importance of genetic diversity in breeding programs.

CONCLUSION

This study provides valuable insights into the nature of the association between yield and its components~~ traits~~, emphasizing the potential of indirect selection for seed yield improvement in cotton. By leveraging both the significant trait associations and the genetic diversity within the germplasm, breeders can develop high-yielding, resilient cotton varieties. The findings underscore the importance of comprehensive genetic analyses in guiding effective cotton breeding strategies aimed at enhancing productivity and sustainability in cotton cultivation.

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