GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN COTTON (*Gossypium hirsutum* L.)

A THESIS SUBMITTED TO
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE

OF

MASTER OF SCIENCE
(Agriculture)

IN

GENETICS AND PLANT BREEDING

BY

VARMA KEVAN NATVARBHAI
B.Sc. (Hons.) Agriculture

कृषिमित् कृषस्व

DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506

DECEMBER-2021

[Registration No. 04-AGRMA-02092-2019]

ABSTRACT

GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN COTTON (*Gossypium hirsutum* L.)

Name of Student	**Major Advisor**
VARMA KEVAN NATVARBHAI	**DR. J. M. PATEL**

DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506

ABSTRACT

Cotton (*Gossypium hirsutum* L.) belongs to *Malvaceae* family which is a self-pollinated and often cross-pollinated (5-25% cross pollination) crop. The present investigation on **"Genetic variability and character association studies in cotton (*Gossypium hirsutum* L.)"** was carried out using thirty-five genotypes for fourteen traits of cotton to determine the extent of variability, correlation coefficient and path coefficient analysis. The material was evaluated in randomized block design with three replications during *kharif*-2020 at Cotton Research Station, S. D. Agricultural University, Talod. The characters *viz.*, days to flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of boll per plant, seed cotton yield per plant (g), boll weight (g), seed index (g), lint index (g), ginning out-turn (%), upper half mean length (mm), fibre fineness (µg/inch), fibre strength (g/tex) and uniformity ratio (%) were included in the present study.

The analysis of variance reveled significant differences among the genotypes for all the characters studied indicating the presence of adequate amount of variability among thirty-five genotypes. High genotypic and phenotypic coefficient of variations were exhibited by number of monopodia per plant followed by number of boll per plant and seed cotton yield per plant which suggests the possibility of improving these traits through simple selection. The highest heritability was recorded for number of monopodia per plant followed by seed cotton yield per plant, number of boll per plant, lint index and boll weight. The highest genetic advance as per cent of mean was recorded for number of monopodia per plant followed by seed cotton yield per plant, number of boll per plant and lint index. High heritability associated with high genetic advance as per cent of mean was observed for the characters *viz.*, number of monopodia per plant, number of boll per plant, seed cotton yield per plant and lint index which indicates that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects.

The correlation coefficient analysis revealed the positive and highly significant correlation of seed cotton yield per plant with number of boll per plant and boll weight at both genotypic and phenotypic level whereas, the trait plant height exhibited positive and significant correlation with seed cotton yield per plant only at genotypic level. This suggested that these characters could be considered as criteria for improving seed cotton yield.

The path coefficient analysis revealed that the characters *viz.*, plant height, number of sympodia per plant, boll weight, upper half mean length, fibre fineness and fibre strength recorded high and positive direct effect towards seed cotton yield per plant. Present findings for path analysis suggests that for the traits bearing positive direct effects with seed cotton yield per plant, the direct selection would be rewarding for improvement in yield.

On the source of all the above studies, it can be concluded that more emphasis should be given to number of monopodia per plant, number of boll per plant and boll weight while doing selection for genetic improvement in cotton. Based on the mean performance of seed cotton yield per plant, genotypes *viz.*, GBHV 217, GBHV 241, GJHV 560, GN. Cot. 22 and GSHV 235 were categorized as high seed cotton yielding genotypes. Also, the genotypes like GSHV 208 and GSHV 191 produced fine fibre compared to rest of the genotypes, which can be utilized in the development of cotton genotypes with superior fibre quality.

SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR 385 506

CERTIFICATE – I

Date: 24/12/2021

This is to certify that the thesis entitled, **"GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN COTTON (*Gossypium hirsutum* L.)"** submitted for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** is a record of bonafide research work carried out by **VARMA KEVAN NATVARBHAI** under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associate ship, fellowship or other similar titles. The assistance and help received during the course of investigation have been fully acknowledged.

(J. M. PATEL)
Major Advisor

(K. P. PRAJAPATI)
Minor Advisor

(R. M. PATEL)
Advisor

(G. K. CHAUDHARY)
Advisor

SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR 385 506

CERTIFICATE – II

Date:24/12/2021

This is to certify that **VARMA KEVAN NATVARBHAI,** Department of Genetics and Plant Breeding, C. P. College of Agriculture, Sardarkrushinagar has made all corrections/modifications in the thesis entitled, **"GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN COTTON (*Gossypium hirsutum* L.)"** as suggested by the External Examiner and the Advisory Committee in the oral examination held on **23rd DECEMBER, 2021.**

(J. M. PATEL)
Associate Research Scientist,
Wheat Research Station,
S. D. Agricultural University,
Vijapur-382 870

Professor and Head,
Department of Genetics and Plant Breeding,
C. P. College of Agriculture,
S. D. Agricultural University,
Sardarkrushinagar-385 506

Principal and Dean,
C. P. College of Agriculture,
S. D. Agricultural University,
Sardarkrushinagar-385 506

APPROVED (Seal and Date)

24/12/'21

Director of Research and
Dean, Post-Graduate Studies,
S. D. Agricultural University,
Sardarkrushinagar-385 506

ACKNOWLEDGEMENT

Accomplishment of this thesis is the result of benevolence of Almighty, my parents, guidance of my teachers and help of my friends.

I take the opportunity to express high regard, a deep sense of gratitude and indebtedness to industrious, magnificent and courteous personality **Dr. J. M. Patel**, Associate Research Scientist, Wheat Research Station, S. D. A. U., Vijapur my Major Advisor, for his valuable guidance, timely motivation and insightful suggestions during the investigation and in preparation of thesis manuscript.

I emphatically express my venerable thanks to my Minor Advisor, **Mr. K. P. Prajapati**, Assistant Research Scientist, Castor-Mustard Research Station, S. D. A. U., Sardarkrushinagar for his cooperation in all respects throughout the study. I am very grateful and indebtedness to **Dr. R. M. Patel**, Assistant Research Scientist, Maize Research Station, S. D. A. U., Bhiloda and **Dr. G. K. Chaudhary**, I/c. Professor and Head, Department of Agril. Statistics, C. P. College of Agriculture, S. D. A. U., Sardarkrushinagar for their unceasing interest and inspiring guidance as to the members of my advisory committee.

I would like to express my sincere thanks to **Dr. J. A. Patel**, Ex. Assistant Research Scientist, Cotton Research Station, S. D. A. U., Talod for his constant encouragement, sustained interest, talented guidance in breeding work, valuable suggestions and critical review to complete this manuscript.

I have a great pleasure in expressing my sincere gratitude to **Dr. S. D. Solanki**, Professor and Head, **Dr. N. B. Patel**, **Dr. H. S. Bhadauria**, **Dr. N. V. Soni**, **Dr. P. C. Patel**, **Dr. K. K. Tiwari**, **Dr. H. N. Zala**, **Dr. A. K. Singh** and other staff members of the Department of Genetics and Plant Breeding for their immense knowledge, fruitful advices and persistent support during tenure of my study.

I really feel short of words to express my heartfelt gratitude towards **Dr. R. M. Chauhan**, Honourable Vice Chancellor and **Dr. B. S. Deora**, Director of Research, S. D. Agricultural University for providing facilities for conducting the research work.

I wish to place on record my humble gratitude to **Dr. D. G. Patel**, Associate Research Scientist, Cotton Research Station, S. D. A. U., Talod and **Mr. J. N. Hingu**, Agriculture Officer, Cotton Research Station, S. D. A. U., Talod for their valuable help and co-operation whenever needed during my research work.

I am very grateful to **Harsiddhi madam**, **Ravibhai** and **Parthbhai** staff members of Cotton Research Station, S. D. A. U., Talod for helping me during my experiment work. Also, I am thankful to **Nikul**, **Krupan**, **Mahipal** and **Jigar** for their considerable help and all the farm labors for helping me in farm practices during my research work.

No scholar can complete the work on his own. He or she has to get a little help from their friends for one or another item of works and no words can describe the unending love, care and moral support by my friends **Maulik, Dipen, Mayur, Jackieson, Jay, Trushna, Dinesh, Dhaval, Pratik, Jasmin, Jay (Sindhav), Ashita, Kalpesh, Ravi, Rutul** and my seniors **Mr. Parthsinh, Mr. Ravindra** and **Mr. Ravinder**. I also want to take a moment to thank my school friend **Abhishek** for his valuable help regarding my experiment.

I am short of words to express my feelings, special esteems and deep-seated obligations to my beloved father **Mr. Natvarbhai Vankar**, mother **Mrs. Rekhaben Vankar** and brother **Vidhan** for their everlasting love which made this endeavor possible. I also want to express my gratitude towards my grandfather **Mr. Khemabhai Parmar**, late grandmother **Kodiben Parmar**, uncle **Mr. Nareshbhai Parmar**, aunt **Mrs. Devikaben Parmar** and cousins **Dr. Jay** and **Gritiksha** for the constant support and unending encouragement.

Thanks to all those who cannot find a separate name, but helped me directly or indirectly to achieve my goal.

Last but not the least, I bow my head in extreme regards to the almighty goddess **Maa Saraswati** whose blessings enabled me to reach this destination.

Place: Sardarkrushinagar
Date: 24 / 12 / 2021

[Varma Kevan N.]

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

ACRONYMS SYMBOLS AND ABBREVIATIONS USED

%	:	Per cent
/	:	Per
2n	:	Somatic chromosome number
@	:	At the rate of
σ^2_g	:	Genotypic variance
σ^2_p	:	Phenotypic variance
σ^2_e	:	Environmental variance
ºC	:	Degree Celsius
C.D.	:	Critical Difference
C.V.	:	Coefficient of variation
cm	:	Centimeter
CIRCOT	:	Central Institute for Research on Cotton Technology
d.f.	:	Degree of freedom
e.g.	:	Example
et al.	:	And others (*et alibi*)
Fig.	:	Figure
g	:	Gram
GCV	:	Genotypic coefficient of variation
PCV	:	Phenotypic coefficient of variation
GOT	:	Ginning out-turn
HVI	:	High volume instrument
GA	:	Genetic advance
GAM	:	Genetic advance as per cent of mean
h^2_b	:	Broad sense heritability
ha	:	Hectare
hrs	:	Hours
m	:	Meter
Max.	:	Maximum
Min.	:	Minimum
mm	:	Millimetre
RH	:	Relative humidity
r_g	:	Genotypic correlation
r_p	:	Phenotypic correlation
S.Em.±	:	Standard error of mean
Sr. No.	:	Serial number
Spp.	:	Species
Via	:	Through
viz.	:	Namely (*videlicet*)

INTRODUCTION

I. INTRODUCTION

Cotton is the King of the fibre crops commonly known as the “White gold”. It is the main economic and industrial crop of our country serving prime raw material for textile mills. The genus Gossypium belongs to the family Malvaceae and there are about 50 different species of cotton among which four species are cultivated having spinnable lint and the remaining 46 species are in wild form. India has the distinction of growing all the four spinnable lint bearing species of Gossypium viz., *G. hirsutum*, *G. barbadense* (New World, tetraploid with 2n=4x=52) and *G. arboreum*, *G. herbaceum* (Old World, diploid with 2n=2x=26). Among four cultivated species, *Gossypium hirsutum* L. is cultivated on more than 90% of the area throughout the world. It is having wide range of yield components and fibre quality traits.

Simpson (1954) classified cotton as predominantly self-pollinated and often cross-pollinated crop (The percentage of cross pollination varies from 5-25%) and is amenable for heterosis breeding. The hybrid cotton era has started with the release of Hybrid 4 in Gujarat during early 1970’s. Today, several hybrids have been released in long and extra-long staple groups. Although, their productivity is higher than varieties in most of the areas, however, there is a scope for further improvement in productivity as apparent from the substantial gap in the yield of demonstration plots, research fields and progressive farmer’s fields under rainfed and irrigated conditions in the country.

Cotton is one of the most important fibre and cash crops of India and plays a dominant role in the industrial and agricultural economy of the country. It provides the basic raw material (cotton fibre) to cotton textile industry. Cotton in India provides direct livelihood to 6 million farmers and about 40-50 million people are employed in cotton trade and its processing. In India, there are ten major cotton growing states which are divided into three zones, *viz*. north zone, central zone and south zone. North zone consists of Punjab, Haryana and Rajasthan. Central zone includes Madhya Pradesh, Maharashtra and Gujarat. South zone comprises Andhra Pradesh, Telangana, Karnataka and Tamil Nadu. Besides these ten states, cotton cultivation has gained momentum in the Eastern State of Orissa. Cotton is also cultivated in small areas of non-traditional states such as Uttar Pradesh, West Bengal and Tripura.

Cotton occupies a prime position as fibre crop of masses of the world in general and of India in particular. The sufficient production of cotton for meeting the fibre requirements of the world’s exploding population is now universally realized. Keeping in view the future needs of the country, cotton research needs to be versatile and accelerated to develop more productive cotton genotypes.

Cotton is being cultivated in 70 countries of the world with a total coverage of 33.14 m ha. China, India, USA and Pakistan are the major cotton producing countries in the world accounting for 70 per cent of the world’s cotton area and production. India is the largest cotton growing country in the world with 35.29 per cent of world cotton area followed by China (15.23%). China and India are the major cotton consuming countries in the world (around 55%). USA and India constitute 27 and 19.5 per cent of the world’s cotton exports respectively. Among the major cotton growing countries, Australia tops the productivity level of 2151 kg lint/ha followed by Turkey (1484 kg lint/ha) and Brazil (1465 kg lint/ha). In India, cotton is cultivated on an area of 129.57 lakh ha with a production of 371 lakh bales with average productivity of 486.76 kg lint/ha during the year 2020-21 (Anonymous, 2021). In Gujarat, it is cultivated over 26.53 lakh ha with a production of 89.00 lakh bales with average productivity of 570.30 kg lint/ha during the year 2019-20 (Anonymous, 2020).

It has become necessary to exploit the germplasm properly and to add new germplasm in the existing genetic pool. These practices have enough potential to create sufficient variations to evolve superior genotypes.

Crop improvement primarily refers to the evolution and development of resistant and high yielding crop varieties. The breeding programmes are executed generally with the intension to develop varieties with superior qualitative and quantitative traits. However, selection is the most powerful tool for considering a particular trait, which entirely depends on the extent of correlation between yield related traits and seed yield.

Crop yield is a complex character hence, its genetic analysis is rather difficult, seed cotton yield and fiber quality are very important to fulfill the requirement of the farming community, ginning industries and textile industries (spinning and weaving units). Seed cotton yield is a resultant effect of component characters, which are not under direct control of one single gene. Therefore, the complexity of the crop yield characters makes its genetic analysis quite difficult. Characters contributing to yield and quality are presumed to be controlled by a large number of genes and are greatly influenced by environment. It is therefore important to know the types and nature of cotton yield components and inter-relationship amongst themselves. Thus, improvement of component characters lead to the improvement in yield for achieving rational improvement in yield and fibre quality.

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of variability helps in selecting a desirable genotype. Therefore, for successful improvement of any crop, it is necessary to have knowledge of variability present in the available genetic material. Substantial genetic variances and high heritability estimates implied that characters could be improved through selection from segregating populations (Baloch, 2004). High genetic advance coupled with high heritability estimates offers a most effective response to selection (Larik *et al*., 1997). In order to enhance the yield potential of the cotton varieties, an understanding on relationship among different characters is more important (McCarty *et al*., 2008).

Cotton breeders have continued their efforts to exploit the cotton germplasm to develop high yielding cotton varieties with acceptable fibre quality. Peohlman and Selper (1995) clarified that the yield contributing and fibre quality traits are heritable in nature. Thus, the quantitative and qualitative traits can be improved by utilizing appropriate breeding programme by developing new cross combinations. For this purpose, breeders are interested to have sufficient knowledge of genetic components such as genetic variability, coefficient of variation, heritability and genetic advance to devise the breeding plan in accordance to their breeding objectives (Dhamayanathi *et al.*, 2010; Ali and Khan, 2007).

The magnitude of relationship between various plant characters is measured by correlation coefficient analysis that determines the component characters on which selection can be made for improvement in seed cotton yield and fibre quality. Direction and magnitude of correlation between yield and yield contributing characters must be considered for selecting the superior genotypes from diverse genetic population. In breeding, genotypic and phenotypic correlations are applied to determine the extent of relationship between yield and yield contributing characters.

But correlation does not provide information about direct and indirect effects of independent variables on the dependent one. For this, path coefficient analysis is carried out. Path analysis splits correlation coefficient into the measures of direct and indirect effects, which reveals whether the association of these characters with yield is due to their direct effect on yield or is a consequence of their indirect effects via other component characters. Thus, it measures cause of association between two variables and effect situation. The main objective was to study the variability, correlation and path analysis of various yield and its attributing characters.

Keeping these aspects in view, the present research work on Genetic variability and character association studies in Cotton (*Gossypium hirsutum* L.) was planned by using 35 various genotypes of cotton with following objectives:

1. To study genetic variability for seed cotton yield, its attributing characters and fibre quality traits
2. To access correlation and path coefficient analysis among yield and its component traits

REVIEW OF LITERATURE

II. REVIEW OF LITERATURE

A brief resume of research work done on various aspects related to the present investigation has been reviewed here under. The available literature has been summarized under following heads:

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation coefficient analysis

2.3 Path coefficient analysis

2.1 Genetic variability, heritability and genetic advance:

The information on the nature and magnitude of variability for different quantitative and qualitative traits in any crop species plays a vital role for formulating the efficient breeding programmes. Importance of estimates of genotypic and phenotypic variability in evolving superior cultivars in cotton have been emphasized by Hutchinson (1940) and Miller *et al.* (1958).

Superior genotypes can be isolated by selection if considerable genetic variation is present within the population. In general, the total variability can be partitioned into the heritable and non-heritable components with the help of genetic parameters like genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV) and heritability. The literature on genetic variability, heritability and genetic advance studies on cotton are considered here.

Joshi *et al.* (2006) estimated variability parameters for 36 hybrids and showed that genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were comparatively high for lint yield (31.37%, 34.25%) and seed cotton yield (30.56%, 33.07%). Moderate GCV and PCV values were recorded for sympodia per plant (13.40%, 15.05%) and plant height (17.40%, 17.48%) whereas, low values were observed for days to first flowering (7.16%, 7.97%) and ginning percentage (7.63%, 7.80%), respectively. High heritability values were recorded for plant height (99.0%), ginning percentage (95.7%), seed cotton yield (85.4%) and lint yield (83.9%) while moderate heritability was observed in boll weight (66.4%) which indicated that selection was effective. A high estimate of heritability together with high genetic advance as per cent of mean was recorded for seed cotton yield (58.17), lint yield (59.18), number of sympodia per plant (24.60) and plant height (35.67) revealing the influence of additive gene action for these four traits.

Ranganatha *et al.* (2013) observed that genotypic (GCV) and phenotypic coefficients of variation (PCV) value was high for seed cotton yield per plant (25.10%, 26.83) while moderate value was recorded for plant height (11.8% and 12.9%). Moderate to high values of GCV and PCV were reported for number of boll per plant (19.1%, 21.3%) and boll weight (18.05%, 20.46%). High heritability along with high genetic gain as per cent mean was recorded for number of boll plant per plant (81.00%, 35.39%), boll weight (78.00%, 32.79%) and seed cotton yield per plant (87.00%, 48.37%), respectively.

An experiment was conducted by Dhivya *et al.* (2014) during winter 2010 and results showed high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in single plant yield (25.8% and 25.9%) while moderate GCV and PCV were observed for plant height (10.2% and 17.0%), number of sympodia per plant (12.1% and 14.8%), number of boll per plant (10.9% and 14.4%), lint index (11.2% and 17.0%) and seed index (13.5% and 17.7%), respectively. The values of GCV and PCV were estimated low for days to 50% flowering (3.5% and 4.5%). High heritability along with high genetic advance in traits *viz.*, number of sympodia per plant (66.9%, 26.2%) and single plant yield (89.1%, 27.3%) whereas, moderate heritability was recorded in seed index (58.00%). The moderate heritability along with low genetic advance was observed in days to 50% flowering (58.5% and 7.0%) and ginning out-turn (31.6% and 9.0%), respectively. The combinations of high heritability with high genetic advance will provide a clear base on the reliability of that particular character in selection of variable entries.

Erande *et al*. (2014) studied genetic parameters for fibre quality traits in diploid cotton. High estimates of genotypic and phenotypic coefficient of variation (GCV and PCV) were observed for number of sympodia (24.54%, 25.20%), number of boll per plant (25.30%, 26.20%) and seed cotton yield per plant (29.67%, 38.57%). The lower GCV and PCV were observed for plant height (8.63%, 9.67%), days to 50% flowering (3.56%, 3.78%), fibre strength (3.80%, 4.25%), uniformity ratio (2.79%, 3.42%) and ginning out-turn (3.41%, 4.19%), respectively. Low GCV (8.56%) and moderate PCV (10.47%) was recorded for seed index whereas, moderate GCV and PCV was exhibited by lint index (11.99%, 14.22%) and micronaire (10.15%, 12.11%). High heritability coupled with high expected genetic advance were observed for the characters number of boll per plant (93.20%, 50.34%), number of sympodia (94.80%, 49.24%) and seed cotton yield per plant (60.70, 45.03%), respectively indicating additive gene action.

An investigation was carried out by Malagouda *et al.* (2014) to study genetic parameters of fibre quality traits in diploid cotton comprising of *Gossypium herbaceum* var. Jayadhar and *G. arboreum* var. DLSa17 along with their recombinant inbred lines (RILs). Lower values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for all the traits *viz.*, uniformity ratio (2.71%, 3.59%), fibre strength (5.64%, 7.76%) and micronaire (4.86%, 9.91%). Moderate heritability with low genetic advance as per cent mean was recorded for uniformity ratio (56.83%, 5.39%). Low heritability coupled with low genetic advance was observed for micronaire (24.00%, 6.28%) indicating that this trait is controlled by non-additive genes and simple selection would not be effective.

Ahsan *et al.* (2015) observed highest genotypic (GCV) and phenotypic coefficient of variation (PCV) exhibited by the number of boll per plant (28.99%, 29.07%) while low value of GCV and PCV was observed in plant height (9.4%, 9.4%). Moderate value of GCV and PCV was recorded for seed cotton yield per plant (19.7%, 19.8%) and boll weight (15.42%, 15.67%). High heritability and high genetic advance was observed for lint index (54.51%), number of boll per plant (40.46%) and seed cotton yield per plant (35.84%). The combination of the high heritability and high genetic advance provide the clear image of the trait in the selection process.

Two hundred and two progenies of cotton were evaluated by Wadeyar *et al.* (2015) at two locations. The analysis of variance revealed the presence of sufficient variability in the material for seven traits at both the locations. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was recorded for number of boll per plant and seed cotton yield per plant while, moderate variability estimate was recorded for plant height and low PCV and GCV were noticed for ginning out turn, seed index and lint index at both the locations. High heritability coupled with high genetic advance as per cent mean was observed for plant height, number of boll per plant and seed cotton yield per plant whereas, moderate genetic advance as percent mean along with high heritability was noticed for boll weight and seed index at both the locations.

Naik *et al.* (2016) evaluated fifty genotypes of american cotton for estimation of variability parameters based on 15 characters. Results showed moderate estimates of genotypic coefficient of variation (GCV) and high phenotypic coefficient of variation (PCV) values for the trait number of monopodia per plant (15.79%, 21.88%). Low GCV and PCV were recorded for the characters *viz.*, days to 50% flowering (6.41%, 6.57%), ginning out turn (1.91%, 2.11%), seed index (5.42%, 6.02%) and uniformity ratio (0.40%, 0.96%), respectively. Moderate GCV and PCV were observed for the characters *viz.*, number of boll per plant (10.85%, 16.13%), boll weight (10.47%, 11.26%) and micronaire (10.31%, 11.20%). High heritability coupled with high genetic advance as per cent of mean was observed for plant height, boll weight and micronaire. High heritability coupled with moderate genetic advance as per cent of mean was observed in case of seed index and lint index while, moderate heritability coupled with moderate genetic advance genetic advance as per cent of mean was observed for number of sympodia per plant and number of boll per plant. Number of monopodia per plant and seed cotton yield per plant exhibited moderate heritability with high genetic advance as per cent mean.

Twenty-five germplasm lines of cotton were evaluated by Adsare and Abhay (2017), they observed moderate genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) value for plant height (14.19%). High value of PCV along with moderate value of GCV was exhibited by seed cotton yield per plant (21.74%, 10.70%) whereas, ginning out-turn (3.20%, 4.06%) and seed index (3.94%, 4.67%) recorded low GCV and PCV values. High heritability along with low genetic advance as percent of mean was recorded by seed index (70.20%, 6.70%). However, the character days to 50 % flowering showed low heritability coupled with low genetic advance as per cent mean (9.77%, 4.38%).

Devidas *et al.* (2017) conducted an experiment using ten germplasm lines of cotton and revealed that the highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for the character number of boll per plant (33.37%, 36.10%) whereas, lower value of GCV and PCV was observed in plant height (8.21%, 8.92%), uniformity ratio (4.55%, 4.67%) and fibre strength (8.52%, 9.89%). The moderate estimates of GCV and PCV was observed for average boll weight (11.77%, 14.20%). Number of boll per plant, ginning out-turn and days to 50% flowering showed high heritability coupled with high genetic advance as per cent of mean indicates selection could be effective for improvement in these characters.

An experiment was conducted by Eswari *et al.* (2017) in cotton and they reported the highest magnitude of both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for number of boll per plant (24.20%, 21.68%). The characters number of sympodia per plant (16.46%, 11.14%), micronaire value (16.23%, 11.61%), boll weight (15.61%, 12.92%) and seed cotton yield per plant

(15.57%, 12.82%) recorded for moderate magnitudes of both PCV and GCV, respectively. The traits days to 50% flowering (4.25%, 5.20%), ginning percentage (9.76%, 8.18%) and uniformity ratio (5.59%, 3.04%) recorded for low magnitudes of both PCV and GCV, respectively. High heritability coupled with high genetic advance as percent of mean was observed for number of boll per plant, boll weight and seed cotton yield per plant whereas, number of sympodia per plant and micronaire value recorded moderate heritability coupled with moderate genetic advance.

Sunayana *et al.* (2017) reported high estimate of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for seed cotton yield per plant (27.89%, 25.63%) whereas, moderate estimates of PCV and GCV were estimated for traits like plant height (15.04%, 10.35%) and number of monopodia per plant (12.19%, 10.78%). Seed index (6.12%, 4.84%) and ginning out-turn (4.35%, 4.06%) exhibited low PCV and GCV values. High heritability coupled with high genetic advance was noticed in number of boll per plant (85.63%, 36.63%) and seed cotton yield per plant (84.44%, 48.52%) whereas, high heritability along with moderate genetic advance was observed in case of boll weight (86.39%, 16.39%) and lint index (81.75%, 17.27%).

Aarthi *et al.* (2018) evaluated 399 germplasm lines of upland cotton and revealed that the highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for the number of monopodia (55.14%, 36.81%) followed by seed cotton yield (43.43%, 35.14%). For the characters *viz.*, boll weight (14.55%, 13.54%), lint index (16.11%, 15.5%) and micronaire value (13.40%, 12.78%) moderate PCV and GCV values were observed. Characters like days to 50 % flowering (5.55%, 4.34%), bundle strength (9.47%, 8.46%), ginning out-turn (9.11%, 8.19%) and uniformity ratio (7.48%, 7.10%) had shown low PCV and GCV values. High heritability coupled with high genetic advance as per cent of mean was observed for number of monopodia, number of sympodia, boll weight, lint index, micronaire value and seed cotton yield per plant. The characters like plant height, ginning out-turn, uniformity ratio and micronaire value had shown high heritability with moderate genetic advance as per cent of mean.

An investigation was carried out by Gnanasekaran *et al.* (2018) in cotton and they recorded the highest magnitude of both phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for number of monopodia per plant (59.66% and 39.57%) followed by seed cotton yield (32.55%, 30.50%). Boll weight (12.95%, 11.24%), micronaire value (17.25%, 14.66%) showed moderate estimates of PCV and GCV. Low values of PCV and GCV were observed for days to 50% flowering (4.76%, 4.18%), ginning percentage (6.38%, 4.84%), bundle strength (6.08%, 6.01%) and upper half mean length (UHML) (6.93%, 6.85%). High heritability coupled with high genetic advance was observed for boll weight, seed cotton yield and micronaire value whereas, moderate heritability coupled with low genetic advance was observed in ginning out-turn (57.62%, 7.57%) and number of sympodia per plant (37.74%, 6.84%).

Monisha *et al.* (2018) evaluated total of fifty-four cotton (*Gossypium hirsutum* L.) F_1 for seed cotton yield and fibre quality traits. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for number of monopodial branches per plant (47.31%, 47.20%) and single plant yield (24.42%, 24.25%). Moderate PCV and GCV values were recorded for plant height (12.32%, 11.00%), number of sympodial branches per plant (11.09%, 10.96%), number of boll per plant (17.21%, 16.99%) and boll weight (13.21%, 10.97%). Low PCV and GCV were observed for days to first flowering (4.69%, 3.95%), ginning out turn (6.95%, 5.49%), uniformity ratio (4.63%, 3.94%) and fibre fineness (6.67%, 4.24%). High heritability coupled with high genetic advance as per cent mean was observed for characters *viz.*, number of monopodial branches per plant (97.53%, 47.00%), number of sympodial branches per plant (97.5%, 22.29%), number of boll per plant (97.36%, 34.53%) and single plant yield (98.65%, 49.62%). High heritability coupled with low genetic advance was noticed for character *viz.*, ginning out turn (62.26%, 8.92%). Moderate heritability coupled with low genetic advance was observed in uniformity index (47.46%, 5.67%). High heritability coupled with moderate genetic advance was observed for characters *viz.*, boll weight (68.97%, 18.77%) and seed index (92.56%, 17.21%).

Nawaz *et al.* (2019) recorded the highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for monopodial branches per plant (51.52%, 52.87%) followed by bolls per plant (24.19%, 24.24%). The traits like boll weight (3.44%, 3.52%), fiber uniformity (5.32%, 5.32%) and fiber strength (5.39%, 5.39%) showed low GCV and PCV values. Moderate values of GCV and PCV was observed for lint index (15.92%, 16.20%). High heritability along with high genetic advance as per cent of mean was recorded by plant height (99.78%, 22.46%), monopodial branches per plant (94.96%, 103.42%), bolls per plant (99.52%, 49.71%), seed cotton yield (98.85%, 32.24%) and lint index (96.61%, 32.25%).

Reddy *et al.* (2019) carried out an experiment and reported high value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for number of monopodia per plant (25.78% 33.24%). The traits *viz.*, days to 50% flowering (4.39%, 6.86%), plant height (6.95%, 8.42%), ginning out turn (7.23%, 7.80%) and uniformity ratio (1.31%, 3.34%) recorded low GCV and PCV values, respectively which indicates presence of low genetic variability among the genotypes studied. Moderate values of GCV and PCV was exhibited by lint index (13.40%, 14.52%) and seed cotton yield (10.37%, 16.27%). High heritability with high genetic advance as per cent mean was recorded by seed index (86.40%, 20.87%), number of monopodia per plant (60.0%, 41.19%) and lint index (85.10%, 25.46%). Medium heritability with low genetic advance was exhibited by bundle strength (51.40%, 7.04%). The traits plant height (68.00%, 11.83%), boll weight (76.90%, 13.74%) and ginning out turn (87.10%, 13.98%) showed high heritability and medium genetic advance as per cent of mean indicates these traits influenced by both additive and non-additive type of gene actions.

An experiment comprised of 40 elite genotypes of upland cotton with one check was carried out by Jangid *et al.* (2019). They reported moderate estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for seed cotton yield per plant (12.76%, 14.66%), lint index (13.21%, 15.14%) and number of boll per plant (13.48%, 16.74%). The low GCV and PCV were recorded for ginning out turn % (7.67%, 8.67%), seed index (7.92%, 9.05%) and plant height (4.41%, 7.82%), respectively. High heritability coupled with high genetic advance was observed in seed cotton yield per plant (75.7%, 22.88), lint index (76.1%, 23.73%) and number of boll per plant (64.9%, 22.36%) whereas, moderate heritability coupled with low genetic advance was reported in plant height (31.8%, 5.12%).

Shruti *et al.* (2019) observed that number of monopodia per plant (20.13%, 26.88%) and number of boll per plant (20.60%, 21.90%) showed high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), respectively while upper half mean length (UHML) (5.55%, 5.94%), fibre strength (6.13%, 6.28%), and micronaire (6.81%, 9.60%) showed comparatively low GCV and PCV, respectively. Moderate values of GCV and PCV were exhibited by number of sympodia per plant (18.00%, 18.48%), boll weight (10.03%, 11.34%), lint index

(16.09%, 19.72%) and seed cotton yield (18.85, 19.57%). High heritability coupled with high genetic advance as per cent of mean were observed for plant height, number of boll per plant, boll weight and lint index indicating the existence of additive gene action hence selection on phenotypic basis might be productive. Moderate heritability with low genetic advance was observed in micronaire indicating the preponderance of non-additive gene action.

An experiment was laid out by Balci *et al.* (2020) in cotton and they observed that seed index (78.9%), ginning out-turn (75.8%), boll weight (64.4%) and boll number (61.7%) exhibited a high degree of heritability whereas, the lowest heritability degree was registered in seed cotton yield (28.6%). High heritability coupled with high genetic advance was observed for boll number (28.93%) and sympodial branch number (16.73%) whereas, moderate heritability with low genetic advance as per cent mean was recorded for boll weight (64.4%, 7.93%) and plant height (56.9%, 9.88%).

Sahar *et al.* (2021) reported the highest genotypic coefficient of variation (GCV) for seed cotton yield (42.71%) followed by the number of monopodial branches (40.05%), plant height (28.16%), the number of boll per plant (26.44%) and boll weight (23.15%). A similar trend was also observed for the phenotypic coefficient of variation (PCV). The characters *viz.*, lint index (19.06%, 20.19%), seed index (11.47%, 12.07%) and ginning out-turn (8.84%, 9.28%) exhibited moderate GCV and PCV whereas, fibre fineness (6.60%, 6.91%), fibre strength (5.66%, 5.93%), upper half mean length (UHML) (3.79%, 4.10%) and uniformity index (1.33%, 1.40%) showed low values of GCV and PCV, respectively. High heritability with maximum genetic advance as percent mean was recorded in monopodial branches, the number of boll, lint index, seed index, and seed cotton yield. The trait upper half mean length (UHML) recorded low genetic advance as per cent mean which indicates operation of non-additive gene action.

2.2 Correlation coefficient analysis:

Correlation studies provide better understanding of yield components which helps the plant breeder during selection (Johnson *et al.* 1955). Thus, the review pertaining to the correlation among the different yield contributing traits with yield and fibre quality traits in cotton is summarised as under.

Ahmad *et al.* (2008) concluded that the parameters *viz.*, plant height, number of sympodia per plant, number of boll per plant and boll weight manifested positive correlation with seed cotton yield whereas, number of monopodia per plant showed negative correlation with it.

Khan *et al.* (2009) conducted an experiment in cotton and reported that plant height, number of boll per plant and boll weight expressed significantly positive correlation with seed cotton yield per plant.

An investigation was carried out by Salahuddin *et al.* (2010) using fifteen genotypes (six parents and nine crosses) of upland cotton (*G. hirsutum* L.) and results exhibited that sympodial branches, number of boll per plant, boll weight and ginning out-turn were found to be positively correlated with seed cotton yield per plant in all the genotypes at 1.0 percent level of probability.

Sixty-two progenies of an interspecific backcross population of cotton were evaluated by Magadum *et al.* (2012). Genotypic correlation studies revealed that number of boll per plant, boll weight, seed index, days to flowering and plant height had significant positive association with seed cotton yield per plant. The trait, number of sympodia per plant also had positive significant association with number of boll per plant whereas, lint index and fibre fineness had significant positive association with ginning out-turn. The significant positive correlation of fibre strength with uniformity index was observed at both genotypic and phenotypic levels.

Tulasi *et al.* (2012) revealed that number of boll per plant and boll weight expressed significant positive association with seed cotton yield per plant whereas, ginning out-turn had significant positive association with lint index at both phenotypic and genotypic levels. Also, a highly significant and positive correlation was observed between seed index and lint index at both phenotypic and genotypic levels.

Alkuddsi *et al.* (2013) reported that seed cotton yield per plant was significantly and positively correlated with days to flowering, plant height, number of boll per plant, mean boll weight and ginning out-turn at genotypic level whereas, the association of number of monopodia per plant with seed cotton yield per plant was positive and non-significant. At both genotypic and phenotypic level, seed index was significantly and positively correlated with the lint index.

An experiment was conducted by Rao and Gopinath (2013) in cotton and they concluded that number of boll per plant, boll weight, number of monopodia per plant, number of sympodia per plant and plant height had significant positive association with seed cotton yield per plant. The trait seed index and ginning out-turn had positive and significant association with lint index. A significantly positive association was found between number of sympodia per plant and number of boll per plant as well as ginning out-turn and uniformity index.

Punitha *et al.* (2013) reported that seed cotton yield had positive significant correlation with number of boll per plant and fibre length. The value of genotypic correlation coefficient was higher than phenotypic correlation coefficient, which denoted that there was strong association between these two characters genetically but the phenotypic value was lessened by the significant interaction of environment. Number of boll per plant had significant positive association with plant height and fibre length. The positive significant correlation was observed for seed index and ginning out-turn with lint index at genotypic and phenotypic levels. The trait, fibre fineness had significant but negative association with fibre strength. Thus, for increasing seed cotton yield in cotton due emphasis should be given to number of boll per plant, boll weight, seed index, lint index and fibre length characters.

Farooq *et al.* (2014) reported that seed cotton yield had positive genotypic correlation with bolls per plant, plant height, boll weight and ginning out-turn. Considering number of sympodia per plant, its significant positive genotypic and phenotypic association was found with bolls per plant, plant height, fiber fineness and ginning out-turn while, it showed negative and significant phenotypic correlation with number of monopodia per plant.

An investigation was carried out by Malagouda *et al.* (2014) to study genetic parameters of fibre quality traits in diploid cotton and results revealed that fibre strength was significantly and positively associated with uniformity index. Significant negative correlation was observed between fibre strength and fibre fineness (micronaire). Thus, for undertaking selection programme for fibre quality traits in interspecific cross combinations, selection based on fibre strength and micronaire can be considered for improvement of fibre quality.

Pujer *et al.* (2014) observed that seed cotton yield was positively and significantly correlated with traits like plant height and number of boll per plant whereas, boll weight and fibre fineness had significantly negative association with seed index and fibre strength (bundle strength), respectively. The number of monopodia per plant and lint index traits were positively and significantly associated with at both genotypic and phenotypic levels.

An experiment was conducted by Asha *et al.* (2015) using 40 genotypes of upland cotton for 15 characters to analyse correlation coefficient and results revealed that plant height, sympodia per plant, bolls per plant, boll weight, fibre strength (bundle strength) and fibre elongation recorded significant positive association with seed cotton yield per plant whereas, lint index exhibited significant and positive association with seed index and ginning out-turn at both genotypic and phenotypic levels. The negative and non-significant association was observed between days to flowering and seed cotton yield per plant at genotypic level while, positive but non-significant correlation was recorded between monopodia per plant and seed cotton yield per plant. The traits, sympodia per plant and bolls per plant exhibited positive and significant correlation at both genotypic and phenotypic levels whereas, uniformity index had positive significant correlation with ginning out-turn at genotypic level.

Reddy *et al.* (2015) observed that number of monopodia per plant, number of boll per plant, boll weight, and lint yield per plant were associated positively with seed cotton yield per plant at both phenotypic and genotypic levels. The characters, seed index and ginning out-turn also showed positive and significant correlation with lint index.

Babu *et al.* (2017) reported that seed cotton yield had significant positive association with number of boll per plant and boll weight whereas, number of sympodia per plant showed positive and significant association with number of boll per plant at both genotypic and phenotypic levels indicating their true association. Uniformity index also showed significant positive association with ginning out-turn at genotypic level and with lint index at both genotypic and phenotypic levels. Fibre fineness exhibited significant negative association with fibre strength (bundle strength).

Seed cotton yield depicted positive and significant correlation with traits *viz.*, lint yield per plant, number of boll per plant, boll weight, number of monopods per plant, plant height and days to first flower. The trait *viz.*, seed index was positively and significantly correlated with number of monopods per plant and lint index at both genotypic as well as phenotypic level whereas, ginning out-turn had positive and significant correlation with lint index, as observed by Sunayana *et al.* (2017).

Khalid *et al.* (2018) revealed that plant height showed positive correlation with number of sympodial branches per plant, number of boll per plant, fiber length and yield of seed cotton while plant height was negatively correlated with fiber fineness. Number of sympodial branches per plant had positive correlation with number of boll per plant and yield of seed cotton. Number of boll per plant had positive correlation with yield of seed cotton, while number of boll per plant had negative association with fiber length. Boll weight exhibited positive correlation with yield of seed cotton. Ginning out-turn showed positive correlation with fiber length while this trait had negative correlation with fiber fineness. Fiber length showed positive correlation with fiber strength while fiber length showed negative association with fiber fineness. Fiber strength had negative correlation with fiber fineness.

Nikhil *et al.* (2018) observed that at phenotypic level, seed cotton yield per plant has shown significant positive correlation with number of monopodia per plant, number of boll per plant, boll weight and lint index followed by non-significant positive correlation with micronaire, ginning out-turn and seed index. Upper half mean length (UHML) showed significantly negative association with boll weight and ginning out-turn whereas, lint index exhibited significantly positive association with seed index and ginning out-turn. The trait, fibre strength was positively and significantly correlated with upper half mean length (UHML) at phenotypic level. Seed cotton yield per plant recorded significant negative phenotypic correlation with upper half mean length (UHML).

Thirty-three cotton genotypes were evaluated by Kumar *et al.* (2019) to study the association among the seed cotton yield and yield contributing traits. Correlation studies revealed that plant height, number of sympodial branches per plant, number of boll per plant and boll weight registered significant positive association with seed cotton yield while, the traits *viz.*, seed index and ginning out-turn had positive and significant association with lint index at both genotypic and phenotypic levels.

Nawaz *et al.* (2019) observed that seed cotton yield was positively correlated with all yield contributing traits like plant height, monopodial branches per plant, number of boll per plant, boll weight, lint weight, seed index, lint index, fiber fineness, fiber strength and fiber uniformity at both genotypic and phenotypic level whereas, it depicted negative relationship with staple length. The trait, monopodial branches per plant had positive and significant association with seed index while, sympodial branches was positively and significantly correlated with number of boll per plant. The fibre quality parameter, fibre strength recorded positive and significant association with uniformity index.

Jangid *et al.* (2019) concluded that seed cotton yield per plant exhibited positively and highly significant association with lint yield per plant, number of boll per plant, plant height and seed index at both genotypic as well as phenotypic level. Seed cotton yield per plant recorded positive and significant association with boll weight at genotypic level and also positive correlation with boll weight at phenotypic level. It has also exhibited negative and highly significant association with ginning out-turn (%) at both genotypic as well as phenotypic level. Lint index showed positive and significant correlation with lint index at both genotypic and phenotypic levels.

A total of one hundred and sixty germplasm accessions of cotton (*Gossypium barbadense*) were evaluated by Premalatha *et al.* (2020) for sixteen traits. The correlation analysis revealed that the number of boll per plant, number of sympodia per plant and boll weight showed positive and significant correlation with seed cotton yield per plant whereas, the association between days to flowering and seed cotton yield per plant was non-significant. Number of sympodia per plant showed positive and highly significant genotypic correlation with number of boll per plant. Boll weight showed highly significant positive genotypic correlation with upper half mean length (UHML) and fibre strength. Lint index showed positive and highly significant genotypic correlation with seed index and ginning out-turn. Seed index showed positive and highly significant genotypic correlation with fibre strength. Upper half mean length (UHML) showed positive and highly significant genotypic correlation with fibre strength and elongation percentage whereas, ginning out-turn recorded negative and significant association with upper half mean length (UHML).

Balci *et al.* (2020) recorded significantly positive genotypic correlation of seed cotton yield with boll number, boll weight, fiber strength, sympodial branch number, days to first flower and seed index. Monopodial branch number also exhibited positive and significant association with seed index. Thus, it was concluded that greater response in seed cotton yield can be achieved through indirect selection on boll number and weight in early segregating generation of cotton breeding.

Sahar *et al.* (2021) reported positive and significant association of seed cotton yield with plant height, the number of monopodial branches, the number of sympodial branches, ginning out-turn (%), the number of boll per plant, seed index and uniformity index at genotypic level, and at phenotypic level, it was positively and significantly associated with sympodial branches, plant height, ginning out-turn (%) and the number of boll per plant. Plant height was significantly positively correlated with the number of sympodial branches and uniformity index while, a negatively significant correlation was observed with ginning out-turn, the number of boll per plant, upper half mean length (UHML) and boll weight at the genotypic level. The number of sympodial branches were highly significantly and positively associated with fiber fineness while, boll weight was significantly and negatively correlated with upper half mean length (UHML).

2.3 Path coefficient analysis:

Path coefficient analysis devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning the correlation coefficient into direct and indirect effects of independent variables on dependent variables. Path analysis helps to elucidate the intrinsic nature of the observed associations and imparts a degree of confidence in the selection schemes adopted for a given situation (Dewey and Lu, 1959).

Joshi *et al.* (2006) reported significant and positive association between lint yield and seed cotton yield was mainly due to high positive direct effect of lint yield. The traits *viz.*, plant height, number of sympodia per plant and boll weight showed low direct effect on seed cotton yield.

An investigation was carried out by Magadum *et al.* (2012) using sixty-two progenies of an interspecific backcross population of cotton and they concluded that number of boll per plant contributed maximum direct effect to seed cotton yield per plant followed by boll weight and lint index whereas, days to flowering and uniformity index exhibited low positive direct effect. The highest positive indirect effect on seed cotton yield per plant was also observed through number of boll per plant. This indicated that seed cotton yield per plant was highly influenced by number of boll per plant directly and indirectly.

Tulasi *et al.* (2012) reported that the characters seed index, number of boll per plant, ginning out-turn and plant height recorded high positive direct effect while, boll weight, number of monopodia per plant and lint index had high negative direct effect. With regard to indirect effects, all traits recorded high indirect effects *via* number of boll per plant, ginning out-turn and seed index and negative and moderate indirect effects via boll weight and number of sympodia per plant. Hence, number of boll per plant, boll weight, ginning out-turn, seed index and lint index should be considered as selection indices for seed cotton yield per plant.

Alkuddsi *et al.* (2013) observed high positive direct effect of monopodia per plant and mean boll weight on seed cotton yield whereas, number of boll per recorded negative direct effect on seed cotton yield. Sympodia per plant exhibited high positive indirect effect on seed cotton yield via seed index, the result of this mean boll weight had high positive correlation with seed cotton yield and sympodia per plant recorded low positive correlation with seed cotton yield.

Rao and Gopinath (2013) reported that number of boll per plant exhibited maximum direct effect on seed cotton yield per plant followed by boll weight, number of sympodia per plant, lint index and uniformity ratio. The maximum positive indirect effect on seed cotton yield per plant was observed through number of boll per plant. Thus, due emphasis should be given to number of boll per plant, boll weight and lint index for improvement in seed cotton yield.

Eight lines and seven testers and their fifty-six F_1s made with the parents of *G. hirsutum* and *G. barbadense* genotypes of diverse origin were evaluated by Punitha *et al.* (2013). Path coefficient analysis revealed that number of sympodia per plant, number of boll per plant, boll weight, seed index and lint index directly influenced the seed cotton yield with high direct effects. It was concluded that these characters could be considered as significant selection criteria for seed cotton yield improvement in cotton.

Erande *et al.* (2014) reported that seed index, ginning out-turn, plant height, lint index and fibre fineness (micronaire value) exerted high direct effect on seed cotton yield whereas, weak positive indirect effects were observed for the characters *viz.*, number of sympodia per plant, average boll weight, 2.5% span length, uniformity index and negative indirect effects were showed by the traits *viz*, days to flowering, number of monopodia and fibre strength with seed cotton yield. The fibre quality traits like 2.5% span length, micronaire value and uniformity ratio exhibited direct effect on seed cotton yield per plant, while fibre strength showed negative indirect effects.

An experiment was conducted by Farooq *et al.* (2014) in cotton crop, results revealed that the traits like sympodia per plant, plant height, boll weight and ginning out-turn showed positive direct effect on seed cotton yield, while remaining traits *viz.*, monopodia per plant, bolls per plant, fibre fineness (micronaire value), fibre strength and days to first flower showed negative estimates.

Pujer *et al.* (2014) observed that days to first flower, number of monopodial branches, number of boll per plant, boll weight, seed index, lint index, ginning out turn and uniformity ratio showed positive direct effect on seed cotton yield. Indirect effects of plant height influenced the seed cotton yield through lint index, boll weight, ginning out turn, bundle strength, number of boll per plant, number of monopods per plant and seed index.

An investigation was carried out by Latif *et al.* (2015) on cotton and they observed that bolls per plant showed high direct effect on yield. Therefore, it is suggested that selection based on bolls per plant will help plant breeder in the improvement of cotton yield. Also, positive indirect effect of ginning out turn on high yield *via* bolls per plant appeared.

Reddy *et al.* (2015) conducted an experiment on cotton and revealed that number of boll per plant, boll weight, seed index and lint yield per plant had shown direct positive effect on seed cotton yield per plant at both phenotypic and genotypic levels whereas, traits like days to flowering, number of sympodia per plant, lint index and ginning out-turn exhibited negative direct effect on seed cotton yield per plant.

Chaudhari *et al.* (2017) observed that number of boll per plant and boll weight had high direct effect on seed cotton yield per plant whereas, seed index, ginning out-turn and 2.5% span length had negative direct effect on seed cotton yield per plant. The traits like days to flowering, fibre strength and fibre fineness recorded low to moderate positive direct effect on seed cotton yield per plant. Number of sympodia per plant showed positive indirect effects on seed cotton yield per plant through a number of boll per plant, plant height, boll weight, seed index, 2.5% span length, fibre strength and fibre fineness.

An experiment was carried out by Sunayana *et al.* (2017) to study twelve quantitative traits in three genotypes of cotton (*Gossypium arboreum* L.) during the year 2015-‘16. Results revealed that lint index exhibited negative direct effect on seed cotton yield per plant whereas, lint yield per plant exhibited maximum positive direct effect on seed cotton yield followed by number of boll per plant, seed index, boll weight and plant height. Hence, selection for these traits would be quite effective to improve the seed cotton yield.

Nikhil *et al.* (2018) reported that boll weight and number of boll per plant had high direct effect on seed cotton yield per plant whereas, traits like plant height, upper half mean length (UHML), fibre strength and lint index had negative direct effect on yield. The direct effect of other component traits *viz.*, number of monopodia per plant, number of sympodia per plant, micronaire, ginning out-turn and seed index on seed cotton yield were positive but low.

Kumar *et al.* (2019) observed that among the yield component characters, number of boll per plant had recorded maximum positive direct effect on seed cotton yield per plant followed by lint index, single boll weight, 2.5 percent span length, number of sympodial branches per plant and days to fifty percent flowering. Negative direct effect of seed index followed by ginning out turn, micronaire, biological yield and plant height towards seed cotton yield per plant was recorded.

A study was undertaken by Manonmani *et al.* (2019) to study the variability and association parameters in cotton, they reported that days to first flowering, number of monopodia, number of boll per plant and number of sympodia showed very high direct effect on single plant yield. High direct effect on single plant yield was contributed by seed index, 2.5 per cent span length and uniformity ratio. Lint index and ginning out turn showed moderate direct effect while plant height, fibre strength (bundle strength) and fibre fineness had negative direct effect on yield.

An experiment was laid out by Nawaz *et al.* (2019) using selected F_3 populations of upland cotton along with parents. They observed that maximum direct positive effect was found of lint weight on seed cotton yield followed by fiber fineness, seed index, bolls per plant, sympodial branches per plant, plant height, lint index and fibre strength.

Jangid *et al.* (2019) conducted an experiment on cotton and observed that the maximum positive value for direct effect was found for seed index and number of boll per plant. The highest negative effect was shown by lint index followed by ginning out turn and plant height. Number of boll per plant followed by plant height, lint index, ginning out-turn, seed index and boll weight had indirect effects on seed cotton yield per plant through lint yield per plant.

Chapepa *et al.* (2020) carried out an experiment to determine degree of association between seed cotton yield and its component traits and revealed that ginning out-turn had the highest indirect contribution to seed cotton yield through lint yield, followed by fibre strength through plant height, seed weight through boll weight, fibre fineness through boll weight indicating the importance of these traits to plant height, boll weight and seed cotton yield. The negative direct effect of characters like ginning out-turn, boll weight, upper half mean length (UHML) and micronaire was observed on seed cotton yield.

Saritha and Patil (2020) reported high positive direct effects on seed cotton yield from micronaire value, elongation value, upper half mean length (UHML), number of sympodia per plant, boll weight and lint index whereas, traits *viz.*, uniformity index, number of monopodia per plant and seed index had moderate to low direct effect on seed cotton yield. The characters, fibre strength and maturity ratio had negative indirect effects on seed cotton yield.

A study was performed by Sahar *et al.* (2021) to assess the associations of yield and fiber quality traits in cotton. They observed that traits like number of monopodial branches, plant height, ginning out-turn and boll weight impacted positively and directly on seed cotton yield. The remaining traits *viz.*, sympodial branches, total number of boll per plant, seed index, lint index, uniformity index, fibre strength, fibre fineness and upper half mean length (UHML) exerted negative direct effects on yield.

MATERIAL AND METHODS

III. MATERIAL AND METHODS

The present investigation on "**Genetic variability and character association studies in cotton (*Gossypium hirsutum* L.)**" was carried out at Cotton Research Station, S. D. Agricultural University, Talod during *kharif* season 2020. The fibre quality traits were analyzed at Central Institute for Research on Cotton Technology (CIRCOT), Mumbai. The details of material used, methodology and statistical analysis adopted in the present study are described here as under:

3.1 Experimental material

The experimental material comprised 35 genotypes of *G. hirsutum* (American cotton) which were procured from the Cotton Research Station, S.D.A.U., Talod. The list of genotypes has been presented in **Table 3.1**.

Table 3.1 List of cotton genotypes

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	GSHV 234	19.	GTHV 19/7
2.	GSHV 235	20.	GTHV 18/6
3.	GSHV 236	21.	GN. Cot. 32
4.	GSHV 238	22.	G. Cot. 38
5.	GISV 328	23.	GSHV 223
6.	GISV 342	24.	GSHV 224
7.	GSHV 191	25.	GISV 332
8.	GBHV 217	26.	GSHV 208
9.	GBHV 218	27.	GJHV 548
10.	GBHV 234	28.	GJHV 568
11.	GBHV 241	29.	GJHV 534
12.	GBHV 242	30.	GHHV 60/2013
13.	GHHV 34/2013	31.	GTHV 18/17
14.	GJHV 562	32.	GTHV 18/19
15.	GJHV 567	33.	GTHV 15/34
16.	GJHV 584	34.	GTHV 15/220
17.	GJHV 560	35.	GN. Cot. 22
18.	GTHV 19/6		

3.2 Experimental details

3.2.1 Experimental design

A set of thirty-five genotypes of cotton were evaluated in *Kharif*-2020 using Randomized Block Design (RBD) with three replications. The plot size of the experiment was 5.4 m × 1.2 m and each genotype was sown with spacing of 120 cm between rows and 45 cm between plants.

3.2.2 Date of sowing

The experimental material was sown on 19th June, 2020 by dibbling 2-3 seeds per hill and one seed per hill was kept after thinning.

3.2.3 Cultural practices

Recommended agronomical and plant protection practices were followed throughout the crop season. The fertilizer @ 120:60:60 kg NPK/ha were applied to the crop, out of which 60:60:60 kg NPK/ha was given at the time of sowing and remaining 60 kg N/ha was applied 45 days after sowing.

3.2.4 Climate and weather conditions

The standard week-wise meteorological data for the period of investigation recorded at the Cotton Research Station, S.D.A.U., Talod, district Sabarkantha are presented in **Appendix A**.

The data indicate that the mean maximum temperature ranged between 18.6 to 38.1 °C, while mean minimum temperature ranged between 11.3 to 30.6 °C with an average of 30.88 to 20.77 °C. The mean relative humidity ranged between 76.9 to 96.6 per cent with an average of 87.85 per cent. Total rainfall during the period of experimentation was recorded 961.6 mm in the year 2020.

3.3 Observations recorded

Observations were recorded on five randomly selected competitive plants of each genotype in each replication for different characters as mentioned below and their mean values were used for statistical analysis.

Yield contributing characters:

3.3.1 Days to flowering

Number of days required from sowing to the flowering of 50% plants in each plot was recorded.

3.3.2 Plant height (cm)

Height of each selected plant was recorded in centimetre from base of plant to tip of the main stem after the first picking.

3.3.3 Number of monopodia per plant

The number of monopodia was taken as a number of primary branches or vegetative branches on which secondary fruiting branches are grown on each randomly selected plant.

3.3.4 Number of sympodia per plant

The number of fruiting branches appearing on main stem on each randomly selected plant was counted at maturity stage.

3.3.5 Number of boll per plant

Total number of matured boll actually picked over all pickings was recorded on each randomly selected plant.

3.3.6 Seed cotton yield per plant (g)

Total weight of seed cotton in grams obtained from each randomly selected plant was recorded separately and average was taken as seed cotton yield per plant.

3.3.7 Boll weight (g)

At the time of second picking, seed cotton from five well opened representative bolls from each randomly selected plant was picked & average boll weight in gram was recorded.

3.3.8 Seed index (g)

The absolute weight of 100 matured seeds in grams obtained from each of the individual selected plants was recorded as seed index and averaged over all the plants.

3.3.9 Lint index (g)

It is the absolute weight of lint obtained from 100 seeds in grams. It was computed from the formula as follows:

$$\text{Lint index} = \frac{\text{Ginning out-turn (\%)} \times \text{Seed index}}{100 - \text{Ginning out-turn (\%)}}$$

Where,

Ginning out-turn = ratio of weight of lint (g) and weight of total seed cotton (g)

Seed index = weight of 100 matured seeds of cotton (g)

3.3.10 Ginning out-turn (%)

The produce of each selected plant was bulked separately and clean representative sample was drawn. The seed cotton was ginned out on ginning machine and weight of lint and seed cotton was taken separately. The ginning percent was obtained by the formula.

$$\text{Ginning out-turn (\%)} = \frac{\text{Weight of lint (g)}}{\text{Weight of total seed cotton (g)}} \times 100$$

Fibre quality characters:

All the major fibre characteristics were tested with HFT-9000 system. In the HFT-9000 system, various conventional instruments are integrated into a single computer operating system by using the state of the art technology in mechanize, optics and electronics. The HFT-9000 system provides accurate and precise measurements of length, micronaire value and fibre strength.

3.3.11 Upper half mean length (UHML) (mm)

It is defined as the distance spanned by a specified percentage (50%) of fibre in the specimen being tested. Upper half mean length was estimated by using High Volume Instrument (HVI) and expressed in millimeters. UHML is the average length by the longer half (50%) of the fibre distributed by weight.

3.3.12 Fibre fineness (Micronaire) (µg/inch)

Fibre fineness is a weight of one-inch fibre. If weight of one-inch fibre is more then fibre fineness is less and if weight is less then fineness is more. Fineness tester, air perimeter and arealometer was used to determine the fibre fineness (micronaire). The principle is based on the permeability-to-air. Lower value is preferable.

3.3.13 Fibre strength (Tenacity) (g/tex)

Fibre strength was measured at 3.2 mm or 1/8 gauge on the stelometer. It denotes the strength of the fibre and was measured with HFT-9000.

3.3.14 Uniformity index (%)

Ratio of 50% span length to 2.5% span length. It indicates uniformity of fibre length. Fibre uniformity index was estimated by using High Volume Instrument (HVI) and expressed in percentage. If it is less than 47%, there will be increase in short fibres. (Source: CIRCOT, Mumbai)

$$\text{Uniformity index (\%)} = \frac{\text{50 \% span length}}{\text{2.5 \% span length}} \times 100$$

3.4 Statistical analysis

Mean values of the five plants selected at random in each plot were used for statistical analysis.

The data were subjected to following statistical analysis.

1. Analysis of variance
2. Estimation of mean and range
3. Genetic variability
4. Heritability and Genetic advance
5. Correlation coefficient
6. Path coefficient

3.4.1 Analysis of variance

Analysis of variance was performed to test the significance of differences between the genotypes for all the characters. The analysis of variance is set out under ANOVA table:

Table 3.2 Analysis of variance for experimental design

Source of Variation	d.f.	Mean sum of squares	
		Observed	Expected
Replication	(r-1)	RMS	$\sigma^2e+\sigma^2r$
Treatment	(t-1)	TRMS	$\sigma^2e+r\sigma^2g$
Error	(r-1) (t-1)	EMS	σ^2e
Total	(rt-1)		

Where,

r = number of replication

t = number of treatment

The mean squares were tested against error variance by usual 'F' test. The standard error of difference for comparing any two genotypic means was estimated by formula.

Standard Error (SE) = $\sqrt{EMSS/r}$

Where,

EMSS = error mean sum of squares

r = number of replication

C.D. = S.E. × $\sqrt{2 \times t}$

Where,

t = table value of 't' at error d.f. at 5 and 1 per cent level of significance.

3.4.2 Estimation of mean and range

The mean values of all the treatments for the characters under study were worked out by dividing the total by corresponding number of observations.

Mean (X) = $\frac{1}{n}[\sum \text{Xi}]$

Where,

i = 1…….n

X = mean of character

Xi = i^{th} observation of population

n = number of observations per replication

The lowest and highest values of mean of each character represented range.

3.4.3 Genetic variability

Various parameters of genetic variability were calculated by using appropriate formula.

The genotypic and phenotypic variance was calculated by using the respective mean squares from variance table.

1. Genotypic variance ($\sigma^2 g$)

   $$\sigma^2 g = \frac{TRMSS - EMSS}{R}$$

2. Error variance = $\sigma^2 e$ = EMSS
3. Phenotypic variance ($\sigma^2 p$)

   $$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

TRMSS = treatment mean sum of squares

EMSS = error mean sum of squares

R = number of replication

The genotypic and phenotypic coefficient of variation (GCV and PCV) was calculated according to method suggested by Burton (1952).

4. Phenotypic coefficient of variation (PCV)

   $$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100$$

5. Genotypic coefficient of variation (GCV)

   $$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\overline{X}$ = general mean of character

GCV and PCV were categorized by Shivasubramanian and Menon (1973). It is as follows

0-10 % = Low

10-20 % = Moderate

20 % and above = High

3.4.4 Heritability and Genetic advance

Heritability (broad sense) was calculated according to the method suggested by Allard (1960).

1. Heritability (h^2_b) = $\frac{\sigma^2 g}{\sigma^2 p} \times 100$

Where,

σ^2g = genotypic variance

σ^2p = phenotypic variance

Heritability percentage categories was demonstrated by Robinson (1966).

0-30 % = Low

30-60% = Moderate

60 % and above = High

The genetic advance (at 5 per cent selection intensity) was calculated for each character using the formula suggested by Johnson *et al.* (1955).

2. Genetic advance = $h^2{}_b \times K \times \sqrt{\sigma^2 p}$

Where,

h^2_b = heritability (broad sense)

K = selection difference at 5 per cent selection intensity, the value of K is 2.06.

$\sqrt{\sigma^2 p}$ = phenotypic standard deviation

The expected genetic advance (EGA) in per cent of mean is calculated as,

3. EGA = $\frac{GA}{\overline{X}} \times 100$

Where,

EGA = expected genetic advance

GA = genetic advance

The genetic advance as percent mean categories was suggested by Johnson *et al.* (1955).

0-10 % = Low

10-20 % = Moderate

20 % and above = High

3.4.5 Correlation coefficient

In order to study the extent of association between different traits, the genotypic and phenotypic simple correlation coefficients were worked out from the respective variances and covariances. The formula as suggested by Johnson *et al.*, (1955) were used for calculating simple correlation coefficients as given below:

1. Genotypic correlation coefficient (rg_{xy})

$$rg_{xy} = \frac{Cov\ (gx \cdot gy)}{\sqrt{\sigma^2 gx \cdot \sigma^2 gy}}$$

Where,

Cov ($g_x.g_y$) = genotypic covariance between character x and y

$\sigma^2 g_x$ and $\sigma^2 g_y$ = genotypic variance of character x and y, respectively.

Similarly,

2. Phenotypic correlation coefficient (rp_{xy})

$$rp_{xy} = \frac{Cov\ (px \cdot py)}{\sqrt{\sigma^2 px \cdot \sigma^2 py}}$$

Where,

Cov ($p_x.p_y$) = phenotypic covariance between character x and y

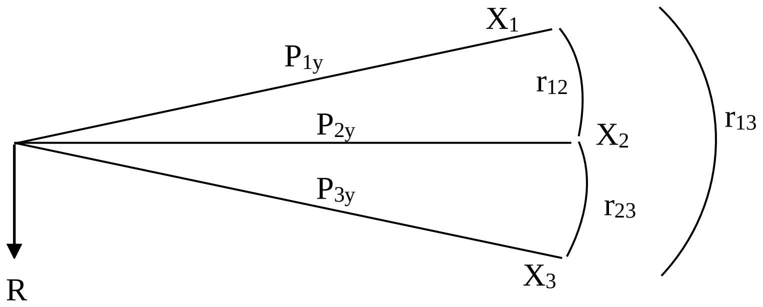
$\sigma^2 p_x$ and $\sigma^2 p_y$ = phenotypic variance of character x and y, respectively.

Significance of correlation coefficient was determined from the Fisher and Yates table ‘correlation coefficient’ at 5 and 1 per cent level of significance. The ‘r’ values were compared against (n-2) degrees of freedom.

3.4.6 Path coefficient

The genotypic correlation coefficients between yield and its components were further partitioned into direct and indirect effects with the help of path coefficient analysis given by Dewey and Lu (1959). The first step in path analysis is to prepare the path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as effect *e.g.* the function of various components like X_1, X_2, X_3 and these components show following type of association with each other.

In path diagram, the seed cotton yield is the result of X_1, X_2, X_3 and some other undefined factors designated by R. The double arrowed lines indicate mutual association as measured by correlation coefficient (r_{ij}) and the single arrowed line represents direct influence as measured by path coefficient (P_{ij}).



Path diagram showing the factors influencing yield

Direct and indirect contribution of variables to seed cotton yield were calculated by solving a set of simultaneous equations of the form as per Dewey and Lu (1959).

r_{ny} = $p_{ny} + r_{n2}p_{2y} + r_{n3}p_{3y} + \ldots\ldots.$

Where,

r_{ny} = represents correlation coefficient between one component and seed cotton yield

r_{n2} = represents correlation coefficient between that character and each of other components

p_{ny} = represents path coefficient between that character and seed cotton yield

Matrix-A Matrix-B

$$\begin{pmatrix} r_{1\text{-}y} \\ r_{2\text{-}y} \\ . \\ . \\ . \\ . \\ r_{n\text{-}y} \end{pmatrix} = \begin{pmatrix} P_1 \\ P_2 \\ . \\ . \\ . \\ . \\ P_n \end{pmatrix} \begin{pmatrix} r_{2,1} & r_{1,2}\ldots\ldots r_{1,n} \\ r_{2,1} & r_{2,2}\ldots\ldots r_{2,n} \\ . & . \quad\quad . \\ . & . \quad\quad . \\ . & . \quad\quad . \\ . & . \quad\quad . \\ r_{n,1} & r_{n,2}\ldots\ldots 1 \end{pmatrix}$$

The matrix B was inverted (B^{-1}) and path coefficients (P_{ij}) were obtained as

$$P_{ij} = A \times B^{-1}$$

The coefficients P_1, $P_2\ldots\ldots P_n$ are estimates of direct effects of character while the indirect effects of ith character on seed cotton yield through jth character is $r_{ij}P_{ij}$.

The residual factor i.e. variation in yield unaccounted by these associations, was calculated from following formula.

Residual factor (Rx) = $\sqrt{1 - R^2}$

Where,

R = (P_{1y}, r_{1y} + P_{2y}, r_{2y} + ………+ P_{ny}, r_{ny})

Where,

P_{1y}, P_{2y}……P_{ny} = path values

r_{1y}, r_{2y}…… r_{ny} = correlation coefficients

RESULTS AND DISCUSSION

IV. RESULTS AND DISCUSSION

The present investigation entitled "**Genetic variability and character association studies in cotton (*Gossypium hirsutum* L.)**" was carried out using thirty-five cotton genotypes to study the variability, heritability, genetic advance as per cent of mean, character association, direct and indirect effects of yield components on seed cotton yield. Possibility of improving economic traits through selection in crop depends mainly on the magnitude and nature of genetic variability. For any successful breeding programme, variability is the prime factor required for the selection of elite genotypes. Genotypic and phenotypic coefficient of variation gives the idea about the range of variability present in genetic population, whereas heritability is helpful in speculating the role of transmission factors in phenotypes expression and eventually selection of elite genotypes from the segregating population. Heritability along with genetic advance favours the fixation of genetic factors for any particular trait. Correlation and path analysis help in determining the nature and dependency of yield and yield attributing traits. The results along with statistical analysis of the data are discussed and presented under the following headings.

4.1 Variance components analysis

4.2 Correlation coefficient analysis

4.3 Path coefficient analysis

4.1 Variance components analysis

All the 35 genotypes were ascertained by analysis of variance of mean for all the characters as a magnitude of variability. The results disclosed a noteworthy difference and presence of adequate variability among all the genotypes for all the characters *viz.*, days to flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of boll per plant, seed cotton yield per plant (g), boll weight (g), seed index (g), lint index (g), ginning out-turn (%), upper half mean length (mm), fibre fineness (micronaire) (μg/inch), fibre strength (tenacity) (g/tex) and uniformity index (%). The analysis of variance depicting mean sum of squares for all the characters studied are presented in **Table 4.1**.

In any successful crop improvement programme, the availability of adequate variability in basic genetic stocks and their proper use through breeding for building up improved strains are very necessary. The genetic improvement of plant population

Table 4.1: Analysis of variance (mean sum of squares) for yield contributing and fibre quality characters in cotton

Source of variation	d.f.	Days to flowering	Plant height	Number of monopodia per plant	Number of sympodia per plant	Number of boll per plant	Seed cotton yield per plant	Boll weight
		1	**2**	**3**	**4**	**5**	**6**	**7**
Replications	2	4.838	13.779	0.002	0.083	3.659	4.844	0.060
Treatments	34	7.861**	223.565**	0.722**	11.763**	61.415**	380.446**	0.562**
Error	68	3.661	64.470	0.043	2.669	5.043	26.017	0.097

Source of variation	d.f.	Seed index	Lint index	Ginning out-turn	Upper half mean length	Fibre fineness	Fibre strength	Uniformity index
		8	**9**	**10**	**11**	**12**	**13**	**14**
Replications	2	0.026	0.308	2.255	0.332	0.052	1.886	0.200
Treatments	34	1.417**	1.402**	17.318**	2.919**	0.409**	3.529**	3.340**
Error	68	0.301	0.211	4.632	0.861	0.106	1.079	1.219

* and ** indicates significance at 0.05 and 0.01 levels of probability, respectively.

Where, d.f. = degree of freedom

Plate I: General view of experiment plot depends on the existence of magnitude of genetic variability and the extent to which the desirable traits are transmissible. Thus, besides genetic variability knowledge on heritability and expected genetic advance plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. The higher the heritability, the greater would be the response to selection that is gain in yield as heritability is directly proportional to genetic advance making selection more effective. This was supported by Burton (1952) as well as Swarup and Chaugle (1962). So, the magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship on to response to selection (Panse, 1957).

The *per se* performance of thirty-five genotypes over three replications for the characters studied with all the variability parameters *viz*., mean, range, genotypic coefficient of variation (GCV%), phenotypic coefficient of variation (PCV%), heritability in broad sense ($h^2{}_b$) and genetic advance as per cent mean analysed from variance components and mean sum of square values are given in **Table 4.2** and **Fig. 4.1** whereas, standard error of mean (S. Em.), critical difference (C.D.) at 5% and coefficient of variation (CV%) are presented in **Appendix B**.

4.1.1 Days to flowering

Analysis of variance revealed that all the genotypes exhibited a significant difference for days to flowering, suggesting the presence of variability in the genotypes which provides the chance for further improvement in the trait. The variation present in all genotypes for the days to flowering ranged between 49.33 to 55.33 days with an average mean of 52.45 days. The genotype GBHV 241 (49.33 days) was the earliest among all the genotypes and the genotype GTHV 19/6 (55.33 days) was late for flowering (Appendix B). The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were low (2.26% and 4.29% respectively) indicating less variability among the genotypes studied. Similar results were reported by Joshi *et al.* (2006), Dhivya *et al.* (2014), Erande *et al*. (2014), Naik *et al.* (2016), Eswari *et al.* (2017), Aarthi *et al.* (2018), Gnanasekaran *et al.* (2018), Monisha *et al.* (2018) and Reddy *et al.* (2019).

Low heritability (27.66%) coupled with low genetic advance as per cent mean (2.44%) was observed for days to flowering indicating the presence of non-additive gene action which means the trait is highly influenced by environmental effects and selection would be ineffective. Similar results were reported by Adsare and Abhay (2017).

Table 4.2: Genetic parameters of variation for seed cotton yield and its contributing characters in cotton

Sr. No.	Character	Mean	Range		σ^2g	σ^2p	Coefficient of variation		h^2_b (%)	GA	GAM (%)
			Min.	Max.			GCV (%)	PCV (%)			
1.	**Days to flowering**	52.45	49.33	55.33	1.40	5.06	2.26	4.29	27.66	1.28	2.44
2.	**Plant height (cm)**	118.37	96.43	133.56	53.03	117.50	6.15	9.16	45.13	10.08	8.51
3.	**Number of monopodia per plant**	1.89	1.08	3.10	0.22	0.26	24.82	26.98	84.61	0.89	47.08
4.	**Number of sympodia per plant**	16.10	11.39	19.49	3.03	5.70	10.81	14.83	53.16	2.61	16.21
5.	**Number of boll per plant**	20.27	11.75	33.09	18.79	23.83	21.38	24.08	78.85	7.93	39.12
6.	**Seed cotton yield per plant (g)**	50.11	29.59	73.22	118.14	144.16	21.69	23.96	81.95	20.26	40.43
7.	**Boll weight (g)**	3.79	3.02	4.63	0.16	0.26	10.55	13.45	61.54	0.64	16.89
8.	**Seed index (g)**	8.00	6.50	9.38	0.37	0.67	7.60	10.23	55.22	0.93	11.62
9.	**Lint index (g)**	4.91	3.57	6.57	0.39	0.60	12.72	15.78	65.00	1.03	20.98
10.	**Ginning out-turn (%)**	37.96	31.75	43.09	4.22	8.85	5.41	7.84	47.68	2.92	7.70
11.	**Upper half mean length (mm)**	25.77	23.83	27.87	0.68	1.54	3.20	4.82	44.16	1.13	4.38
12.	**Fibre fineness (µg/inch)**	4.62	3.60	5.33	0.10	0.20	6.84	9.68	50.00	0.46	9.96
13.	**Fibre strength (g/tex)**	25.95	24.00	28.20	0.81	1.89	3.47	5.30	42.86	1.21	4.71
14.	**Uniformity index (%)**	82.03	80.33	84.00	0.70	1.92	1.03	1.69	36.46	1.04	1.27

Where, σ^2g and σ^2p are the genotypic and phenotypic variance, respectively. GCV and PCV are genotypic and phenotypic coefficient of variation, respectively. h^2_b = heritability in broad sense, GA = Genetic advance, GAM = Genetic advance as per cent mean

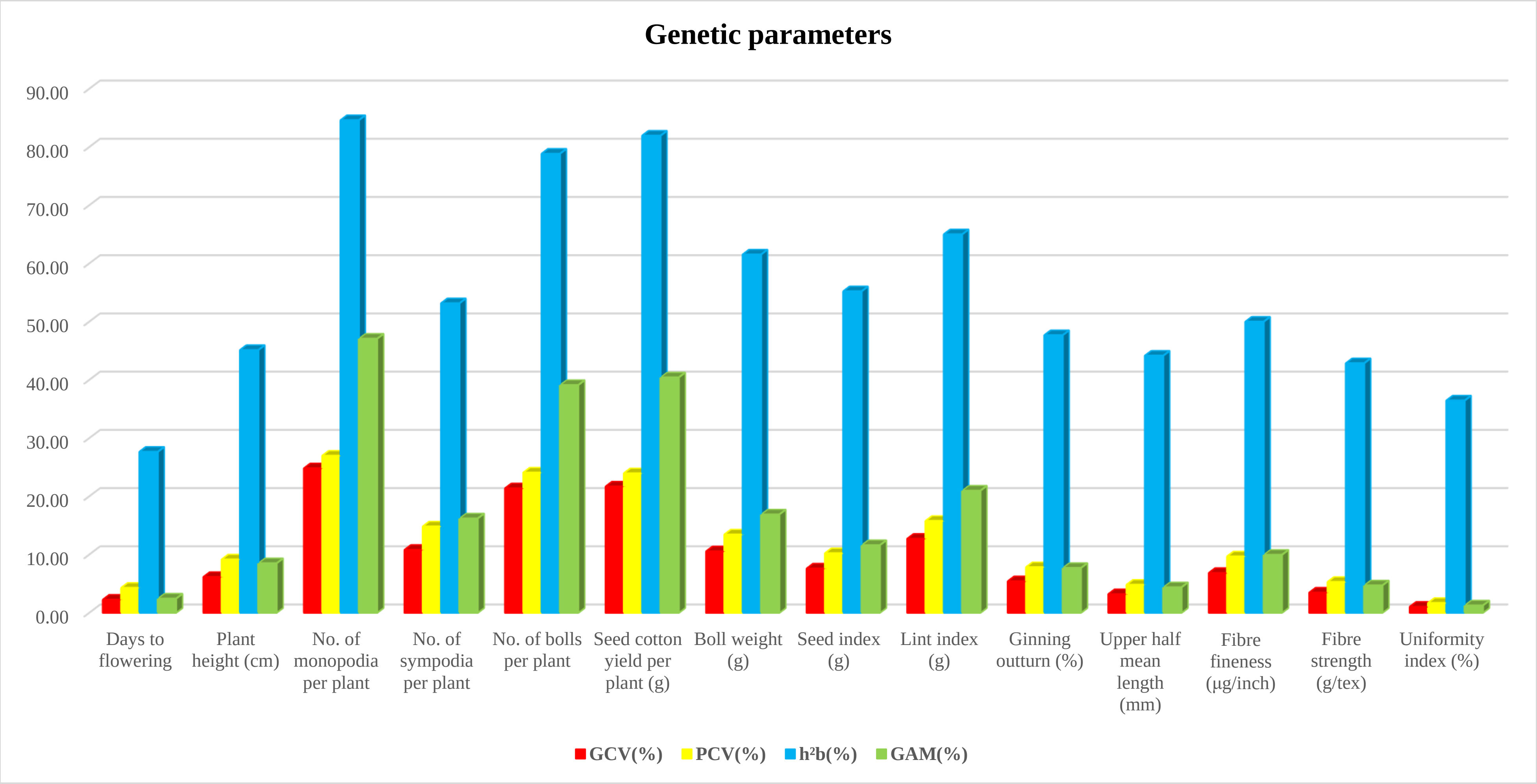


Fig. 4.1: Genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent mean for fourteen characters in cotton (*Gossypium hirsutum* L.)

4.1.2 Plant height (cm)

The plant height ranged from 96.43 cm (GJHV 568) to 133.56 cm (GN. Cot. 22) with a mean of 118.37 cm. The estimates of GCV (6.15%) and PCV (9.16%) were low indicating presence of less variation among the genotypes for the plant height. Similar results were reported by Erande *et al.* (2014), Ahsan *et al.* (2015), Devidas *et al.* (2017), Jangid *et al.* (2019), Reddy *et al.* (2019).

The moderate estimate of heritability (45.13%) coupled with low genetic advance (8.51%) was observed for the trait indicating the preponderance of non-additive gene action. The similar estimates were observed by Jangid *et al.* (2019) and Balci *et al.* (2020).

4.1.3 Number of monopodia per plant

The mean value recorded for the trait number of monopodia per plant was 1.89 with the range of 1.08 to 3.10 monopodia per plant. Genotype GJHV 548 (3.10) recorded the maximum and the genotype GISV 332 (1.08) recorded minimum number of monopodia per plant. High GCV (24.82%) and PCV (26.98%) values were measured, suggesting the presence of good amount of variability among the genotypes for the trait. Similarity between both values suggest the little influence of environment on the traits. Similar results were recorded by Aarthi *et al.* (2018), Gnanasekaran *et al.* (2018), Monisha *et al.* (2018), Nawaz *et al.* (2019), Shruti *et al.* (2019), Reddy *et al.* (2019) and Sahar *et al.* (2021).

High heritability (84.61%) accompanied with high genetic advance (47.08%) indicates the presence of additive gene effect, least environmental influence on the trait and leading to fast genetic improvement. The trait can be utilized for selection by fixing the genes of the traits. High genetic advance coupled with high heritability was also recorded by Monisha *et al.* (2018), Nawaz *et al.* (2019), Reddy *et al.* (2019) and Sahar *et al.* (2021).

4.1.4 Number of sympodia per plant

The number of sympodia per plant ranged from 11.39 (GBHV 234) to 19.49 (GN. Cot. 22) with a mean of 16.10 for the trait. Moderate GCV (10.81%) and PCV (14.83%) were recorded which suggest the presence of moderate amount of variability which can be utilized through selection for efficient breeding programme. The results are in support with the findings of Joshi *et al.* (2006), Dhivya *et al.* (2014), Eswari *et al.* (2017), Monisha *et al.* (2018) and Shruti *et al.* (2019).

Moderate estimates of heritability (53.16%) coupled with moderate genetic advance (16.21%) suggests the operation of both additive and non-additive gene action and desired results may not be obtained by simple selection. The result of moderate heritability is in agreement with the findings of Naik *et al.* (2016) and Eswari *et al.* (2017).

4.1.5 Number of boll per plant

The number of boll per plant recorded the lowest for GTHV 19/6 (11.75) and the highest for GN. Cot. 22 (33.09) with an average of 20.27 (Appendix B). The GCV and PCV were estimated high (21.38% and 24.08% respectively) reveals the presence of good amount of variability. Similar results were reported by Erande *et al.* (2014), Ahsan *et al.* (2015), Wadeyar *et al.* (2015), Devidas *et al.* (2017), Eswari *et al.* (2017), Nawaz *et al.* (2019), Shruti *et al.* (2019) and Sahar *et al.* (2021).

High heritability (78.85%) coupled with high genetic advance as per cent mean (39.12%) indicating presence of additive genes action and a better scope for selection. Ranganatha *et al.* (2013), Erande *et al.* (2014), Ahsan *et al.* (2015), Wadeyar *et al.* (2015), Devidas *et al.* (2017), Eswari *et al.* (2017), Sunayana *et al.* (2017), Monisha *et al.* (2018), Jangid *et al.* (2019), Nawaz *et al.* (2019), Shruti *et al.* (2019) and Sahar *et al.* (2021) reported similar results for high heritability coupled with high genetic advance for this trait.

4.1.6 Seed cotton yield per plant (g)

All the genotypes showed significant difference ranging from 29.59 g to 73.22 g with an average of 50.11 g. The genotype GBHV 217 (73.22 g) recorded the maximum seed cotton yield per plant, whereas the genotype GSHV 224 (29.59 g) recorded the lowest seed cotton yield per plant (Appendix B). High GCV (21.69%) and PCV (23.96%) values were measured, which is due to presence of huge amount of variability amongst all the genotypes studied for this trait. Similarity between both the values depicts the least influence of environment on seed cotton yield. These results are in agreement with the findings of Joshi *et al.* (2006), Ranganatha *et al.* (2013), Dhivya *et al.* (2014), Erande *et al*. (2014), Wadeyar *et al.* (2015), Sunayana *et al.* (2017), Monisha *et al.* (2018) and Sahar *et al.* (2021).

High heritability (81.95%) coupled with high genetic advance as per cent mean (40.43%) was observed which suggest the influence of additive genes and selection could be beneficial by utilizing the fixable genes for improvement. High heritability with high genetic advance as per cent mean was also recorded by Joshi *et al.* (2006), Ranganatha *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Ahsan *et al.* (2015), Wadeyar *et al.* (2015), Eswari *et al.* (2017), Aarthi *et al.* (2018), Jangid *et al.* (2019), Nawaz *et al.* (2019) and Sahar *et al.* (2021).

4.1.7 Boll weight (g)

The range of variation observed for boll weight was from 3.02 g (GSHV 191) to 4.63 g (GJHV 562) with a mean of 3.79 g. The values of GCV (10.55%) and PCV (13.45%) for this trait were moderate which suggest the moderate amount of variability which can be utilized through selection for efficient breeding programme. The difference between them is high which indicates that there is influence of environment in the expression of this trait. The results are in support with the findings of Ahsan *et al.* (2015), Naik *et al.* (2016), Devidas *et al.* (2017), Eswari *et al.* (2017), Aarthi *et al.* (2018), Gnanasekaran *et al.* (2018), Monisha *et al.* (2018) and Shruti *et al.* (2019).

High heritability (61.54%) accompanied with moderate magnitude of genetic advance (16.89%) was observed for this trait indicating the involvement of both additive and non-additive gene action and desired results may not be obtained by simple selection. Similar findings were reported by Joshi *et al.* (2006), Wadeyar *et al.* (2015), Sunayana *et al.* (2017), Monisha *et al.* (2018) and Reddy *et al.* (2019).

4.1.8 Seed index (g)

Variance due to genotypes for seed index was significant indicating the presence of sufficient variability. All the genotypes showed a significant difference ranging from 6.50 g to 9.38 g. The genotype GTHV 18/17 recorded the maximum seed index (9.38g), whereas genotype GTHV 15/34 recorded the minimum seed index (6.50g) with a mean of 8.00 g (Appendix B). The estimates of GCV (7.60%) and PCV (10.23%) were low and moderate, respectively which indicates presence of moderate to low amount of variability in the genotypes. The similar findings were reported by Erande *et al.* (2014).

Moderate heritability (55.22%) with moderate genetic advance as per cent of mean (11.62%) were observed for seed index indicating the role of both additive and non-additive gene action in the expression of this trait and desired results may not be obtained by simple selection. The result of moderate heritability is in agreement with the findings of Dhivya *et al.* (2014).

4.1.9 Lint index (g)

The highest value of lint index was measured 6.57 g for GN. Cot. 32 and the lowest was recorded with 3.57 g for GSHV 191 with a mean of 4.91 g. The estimates of GCV (12.72%) and PCV (15.78%) were moderate, that indicates the presence of moderate amount of variability in the genotypes which can be utilized through selection for efficient breeding programme. The results are in accordance with the findings of Dhivya *et al.* (2014), Erande *et al*. (2014), Aarthi *et al.* (2018), Jangid *et al.* (2019), Nawaz *et al.* (2019), Shruti *et al.* (2019) and Reddy *et al.* (2019).

High heritability (65.00%) coupled with high genetic advance as per cent mean (20.98%) was observed for this character exhibiting the presence of additive gene action and a better scope for selection. Similar findings were reported by Ahsan *et al.* (2015), Aarthi *et al.* (2018), Jangid *et al.* (2019), Nawaz *et al.* (2019), Shruti *et al.* (2019), Reddy *et al.* (2019) and Sahar *et al.* (2021).

4.1.10 Ginning out-turn (%)

The range of variation for ginning out-turn was from 31.75 % (GSHV 191) to 43.09 % (GISV 342) with an average of 37.96 %. The estimates of GCV (5.41%) and PCV (7.84%) were low indicating that there is less variability among the genotypes studied for this trait. Similar results were reported by Joshi *et al.* (2006), Erande *et al*. (2014), Wadeyar *et al.* (2015), Naik *et al.* (2016), Adsare and Abhay (2017), Sunayana *et al.* (2017), Aarthi *et al.* (2018), Monisha *et al.* (2018), Jangid *et al.* (2019), Reddy *et al.* (2019) and Sahar *et al.* (2021).

Moderate heritability (47.68%) coupled with low genetic advance as per cent of mean (7.70%) was observed for this trait which indicates the preponderance of non-additive gene action. Similar results were also reported by Dhivya *et al.* (2014) and Gnanasekaran *et al.* (2018).

4.1.11 Upper half mean length (UHML) (mm)

Upper half mean length (UHML) in all the genotypes ranged from 23.83 mm to 27.87 mm with the mean of 25.77 mm. The genotype GSHV 191 showed the highest value of UHML (27.87 mm), whereas the minimum value was recorded for GISV 342 (23.83 mm) (Appendix B). The estimates of GCV (3.20%) and PCV (4.82%) were low indicating less variation among the genotype studied. Similar findings were reported by Gnanasekaran *et al.* (2018), Shruti *et al.* (2019) and Sahar *et al.* (2021).

Moderate heritability (44.16%) accompanied with low genetic advance (4.38%) as per cent mean was observed for UHML indicating the operation of non-additive gene action. The heritability is being exhibited due to favourable influence of environment rather than genotype indicating the possibility of improvement of this trait through heterosis breeding, rather than simple selection. The low genetic advance as per cent mean was also observed by Sahar *et al.* (2021).

4.1.12 Fibre fineness (µg/inch)

The range of variation for the fibre fineness (micronaire) value was obtained from 3.60 µg/inch (GSHV 208) to 5.33 µg/inch (GBHV 242) with a mean of 4.62 µg/inch. The magnitude of genotypic (6.84%) and phenotypic (9.68%) coefficient of variation were low indicating presence of less variation among the genotypes for the trait. Low GCV and PCV values were also reported by Malagouda *et al.* (2014), Monisha *et al.* (2018), Shruti *et al.* (2019) and Sahar *et al.* (2021).

Moderate measures of heritability (50.00%) coupled with low genetic advance as per cent mean (9.96%) which indicates the presence of both fixable and non-fixable genes which offers a limited scope of improvement for the trait suggesting selection may not be rewarding for improvement. Similar results for moderate heritability and low genetic advance were also obtained by Monisha *et al.* (2018) and Shruti *et al.* (2019).

4.1.13 Fibre strength (g/tex)

The fibre strength (tenacity) ranged from 24.00 g/tex (GJHV 548) to 28.20 g/tex (GBHV 241) with an average mean of 25.95 g/tex. The estimates of GCV (3.47%) and PCV (5.30%) were low indicating that there is a less variability among the genotypes studied. The results are in agreement with Erande *et al*. (2014), Malagouda *et al.* (2014), Devidas *et al.* (2017), Aarthi *et al.* (2018), Gnanasekaran *et al.* (2018), Nawaz *et al.* (2019), Shruti *et al.* (2019) and Sahar *et al.* (2021).

Moderate heritability (42.86%) coupled with low genetic advance as per cent of mean (4.71%) was observed for fibre strength indicating the operation of non-additive gene action. This is in agreement with the findings of Reddy *et al.* (2019).

4.1.14 Uniformity index (%)

The range of variation for uniformity index was from 80.33 per cent to 84.00 per cent with an average mean of 82.03 per cent. The genotypes GBHV 218 and GTHV 15/34 showed the lowest value (80.33%) while highest value was recorded by the genotype GN. Cot. 32 (84.00%) (Appendix B). The magnitude of genotypic (1.03%) and phenotypic (1.69%) coefficient of variation were low indicating presence of less variation among the genotypes for the trait. Low GCV and PCV values were also reported by Erande *et al*. (2014), Malagouda *et al.* (2014), Naik *et al.* (2016), Devidas *et al.* (2017), Eswari *et al.* (2017), Aarthi *et al.* (2018), Monisha *et al.* (2018), Nawaz *et al.* (2019), Reddy *et al.* (2019) and Sahar *et al.* (2021).

Moderate heritability (36.46%) coupled with low genetic advance as per cent of mean (1.27%) was observed for the uniformity index which indicates the preponderance of non-additive gene action. Same results were also reported by Malagouda *et al.* (2014) and Monisha *et al.* (2018).

4.2 Correlation coefficient analysis

Correlation coefficient analysis is used to find out the association between two or more characters. It measures the type and magnitude of association between a pair of characters. This association provides the information about the economic characters like yield and yield contributing characters which are useful for the selection and improvement of yield which is beneficial for the plant breeder to select a desirable genotype from the diverse plant genotypes.

Correlation coefficient analysis is based on two levels genotypic (r_g) and phenotypic level (r_p). the observable association between a pair of traits, is the phenotypic correlation which includes both genotypic and environmental effects. Genotypic correlation is the inherent association with dependent character, which improves the genetic make-up of the genotypes through the selection of the economic and its contributing traits. If the correlation between seed cotton yield and a character is due to the direct effect of the character, it reflects a true relationship between them and selection can be practiced for such characters in order to improve yield. But, if the correlation is mainly due to indirect effect of the characters through another component trait, the breeder has to select for the trait through which the indirect effect is expected. So, correlation coefficients are useful if indirect selection of a secondary trait is to be used for improving the primary trait of interest. A great yield response is obtained when the character for which indirect selection is practiced has a high heritability and a positive correlation with yield. Thus, correlation is an improvement asset to cotton breeder helping him in deciding the breeding procedure for genetic improvement of seed cotton.

In the present investigation, the genotypic and phenotypic correlation coefficients for all fourteen characters for thirty-five cotton genotypes to determine the degree and direction of association of seed cotton yield with other related component traits were estimated and presented in **Table 4.3**.

4.2.1 Days to flowering

Days to flowering showed highly significant positive association with number of sympodia per plant (r_g = 0.3989*), seed index (r_g = 0.457**), lint index (r_g = 0.4643**), ginning out-turn (r_g = 0.425*) and uniformity index (r_g = 0.4505**) at only genotypic level indicating that increase in one character will lead to increase in second and *vice* *versa* whereas, it showed highly significant but negative association with boll weight (r_g = -0.552** and r_p = -0.2294**) at both genotypic and phenotypic levels. The trait exhibited non-significant association with plant height, number of monopodia per plant, number of boll per plant, boll weight, upper half mean length, fibre fineness, fibre strength and seed cotton yield.

The non-significant negative and positive association with seed cotton yield per plant (r_g = -0.1009 and r_p = 0.016) was observed at genotypic and phenotypic level, respectively. The values of genotypic correlation coefficient (r_g) were higher than phenotypic correlation coefficient (r_p) for sympodia per plant, seed index, lint index, and uniformity index indicated that there is sturdy affiliation between these characters genetically but the phenotypic correlation lessened by the significant interaction of environment.

The results are in agreement with the findings of Asha *et al.* (2015) at genotypic level and Reddy *et al.* (2015), Premalatha *et al.* (2020) at phenotypic level for association of days to flowering with seed cotton yield per plant.

4.2.2 Plant height (cm)

The plant height showed highly significant positive association with number of boll per plant (r_g = 0.5927** and r_p = 0.3898**) and ginning out-turn (r_g = 0.5132** and r_p = 0.2008*) at both genotypic and phenotypic levels whereas, positively significant correlation with sympodia per plant (r_g = 0.3569*) and seed cotton yield per plant (r_g = 0.3344*) at genotypic level. Number of monopodia per plant, seed index, lint index, upper half mean length, fibre fineness, fibre strength and uniformity index showed non-significant association with plant height at both genotypic and phenotypic levels.

The trait showed positive significant association with seed cotton yield per plant at genotypic level which was also reported by Magadum *et al.* (2012), Farooq *et al.* (2014), Kumar *et al.* (2019) at genotypic level.

4.2.3 Number of monopodia per plant

At both genotypic and phenotypic levels, number of monopodia per plant was found to have significant positive correlation with seed index (r_g = 0.3918* and r_p = 0.2993**) while at phenotypic level, it showed positive and significant association with number of boll per plant (r_p = 0.2067*). Non-significant negative association was observed for boll weight (r_g = -0.2283, r_p = -0.1594), fibre strength (r_g = -0.1128, r_p = -0.0884) and uniformity index (r_g = -0.1294, r_p = -0.0095) whereas, positive non-significant association was found in days to flowering, plant height, number of sympodia, lint index,

Table 4.3: Genotypic and phenotypic correlation coefficient among the different characters in cotton

		DF	**PH**	**MP/P**	**SP/P**	**B/P**	**BW**	**SI**	**LI**	**GOT**	**UHML**	**FF**	**FS**	**UI**	**SCY/P**
DF	**G**	**1.00**	-0.1168	0.077	0.3989*	0.1427	-0.552**	0.457**	0.4643**	0.425*	0.1581	0.0463	0.0555	0.4505**	-0.1009
	P	**1.00**	0.0707	0.0378	0.056	0.1017	-0.2294*	0.0543	0.2332*	0.0558	0.0727	0.0729	0.0245	0.1869	0.016
PH	**G**		**1.00**	0.0829	0.3569*	0.5927**	0.3277	-0.1799	0.2456	0.5132**	-0.1599	0.1057	0.1679	0.0332	0.3344*
	P		**1.00**	0.0915	0.1541	0.3898**	0.1775	-0.0932	0.0803	0.2008*	-0.1325	0.0858	-0.0356	0.059	0.1769
MP/P	**G**			**1.00**	0.0029	0.2306	-0.2283	0.3918*	0.227	-0.024	0.0495	0.1661	-0.1128	-0.1294	0.0268
	P			**1.00**	0.0043	0.2067*	-0.1594	0.2993**	0.1594	0.0084	0.0100	0.1100	-0.0884	-0.0095	0.0491
SP/P	**G**				**1.00**	0.5935**	0.1108	-0.125	0.0791	0.1679	-0.2043	-0.1438	-0.1496	0.0399	0.2124
	P				**1.00**	0.439**	0.08	-0.0079	0.042	0.1417	-0.1049	-0.0816	-0.0676	0.0698	0.157
B/P	**G**					**1.00**	0.1332	0.0772	0.0667	-0.0324	0.1192	0.152	0.0877	0.1677	0.4748**
	P					**1.00**	0.1125	0.0636	0.0213	0.0132	0.0766	0.094	-0.0203	0.0805	0.3975**
BW	**G**						**1.00**	-0.3498*	-0.1121	0.2249	-0.3999*	0.1867	-0.108	-0.1144	0.363*
	P						**1.00**	-0.2386*	-0.0626	0.0822	-0.3109**	0.1599	-0.0954	-0.0974	0.3916**
SI	**G**							**1.00**	0.8677**	0.1034	0.4835**	0.2336	0.355*	0.3687*	-0.0006
	P							**1.00**	0.4747**	0.0839	0.1713	0.1079	0.1372	0.0931	-0.0087
LI	**G**								**1.00**	0.8693**	-0.0613	0.3014	0.2024	0.4279*	-0.0743
	P								**1.00**	0.6826**	0.0588	0.343**	0.1129	0.2035*	-0.0575
GOT	**G**									**1.00**	-0.4447**	0.3505*	0.0306	0.3442*	-0.0942
	P									**1.00**	-0.2363*	0.2561**	-0.1004	0.0561	-0.1163
UHML	**G**										**1.00**	-0.6825**	0.6782**	0.081	0.1171
	P										**1.00**	-0.3264**	0.6039**	0.2304*	0.0145
FF	**G**											**1.00**	-0.467**	-0.203	-0.0956
	P											**1.00**	-0.3663**	0.0042	-0.0352
FS	**G**												**1.00**	0.356*	0.2888
	P												**1.00**	0.3311**	0.1624
UI	**G**													**1.00**	-0.0063
	P													**1.00**	-0.004

Significant at 5% level of significance** and *-Significant at 1% level of significance**

Where, DF= Days to flowering, PH= Plant height, MP/P= No. of monopodia/plant, SP/P= No. of sympodia/plant, B/P= No. of boll/plant, BW= Boll weight, SI= Seed index, LI= Lint index, GOT= Ginning out-turn, UHML= Upper half mean length, FF= Fibre fineness, FS= Fibre strength, UI= Uniformity index, SCY/P= Seed cotton yield/plant ginning out-turn, upper half mean length, fibre fineness and seed cotton yield per plant.

Similar findings were reported by Alkuddsi *et al.* (2013), Asha *et al.* (2015) for association with seed cotton yield and by Pujer *et al.* (2014), Sunayana *et al.* (2017), Nawaz *et al.* (2019), Balci *et al.* (2020) for association with seed index.

4.2.4 Number of sympodia per plant

The character showed highly significant positive association with number of boll per plant ($r_g = 0.5935^{**}$ and $r_p = 0.439^{**}$) at genotypic as well as phenotypic level. It showed non-significant negative correlation with seed index ($r_g = -0.125$, $r_p = -0.0079$), upper half mean length ($r_g = -0.2043$, $r_p = -0.1049$), fibre fineness ($r_g = -0.1438$, $r_p = -0.0816$), fibre strength ($r_g = -0.1496$, $r_p = -0.0676$) and non-significant positive association with boll weight, lint index, ginning out-turn, uniformity index and seed cotton yield per plant at both genotypic and phenotypic levels.

Positive and highly significant correlation between number of sympodia per plant and number of boll per plant was also reported by Magadum *et al.* (2012), Rao and Gopinath (2013), Asha *et al.* (2015), Babu *et al.* (2017), Khalid *et al.* (2018), Nawaz *et al.* (2019) and Premalatha *et al.* (2020).

4.2.5 Number of boll per plant

Number of boll per plant had a significantly positive phenotypic and genotypic correlation with seed cotton yield per plant ($r_g = 0.4748^{**}$, $r_p = 0.3975^{**}$), plant height ($r_g = 0.5927^{**}$, $r_p = 0.3898^{**}$) and number sympodia per plant ($r_g = 0.5935^{**}$, $r_p = 0.439^{**}$) at genotypic as well as phenotypic level. The trait exhibited significant positive phenotypic correlation with number of monopodia per plant ($r_p = 0.2067^{*}$). Association with other component traits was non-significant at both phenotypic and genotypic levels.

The selection for high seed cotton yield per plant based on number of boll per plant is beneficial as their association is significantly positive at genotypic and phenotypic level. The results are in conformity with the reports of Khan *et al.* (2009), Magadum *et al.* (2012), Tulasi *et al.* (2012), Alkuddsi *et al.* (2013), Rao and Gopinath (2013), Punitha *et al.* (2013), Pujer *et al.* (2014), Asha *et al.* (2015), Reddy *et al.* (2015), Babu *et al.* (2017), Sunayana *et al.* (2017), Khalid *et al.* (2018), Nikhil *et al.* (2018), Kumar *et al.* (2019), Nawaz *et al.* (2019), Jangid *et al.* (2019), Premalatha *et al.* (2020) and Sahar *et al.* (2021) for association of number of boll per plant with seed cotton yield.

4.2.6 Boll weight (g)

The trait, boll weight has shown significant and highly significant positive correlation with seed cotton yield per plant ($r_g = 0.363^{*}$, $r_p = 0.3916^{**}$) at both phenotypic and genotypic levels, respectively. The trait had a significant negative correlation with seed index (r_g = -0.3498*, r_p = -0.2386*) and upper half mean length (r_g = -0.3999**, r_p = -0.3109**) at genotypic as well as phenotypic level. The association of boll weight with lint index (r_g = -0.1121 and r_p = -0.0626), fibre strength (r_g = -0.108, r_p = -0.0954) and uniformity index (r_g = -0.1144, r_p = -0.0974) was negative and non-significant whereas, with ginning out-turn and fibre fineness it was positive but non-significant at both phenotypic and genotypic levels.

Significant negative association of boll weight with seed index was also reported by Pujer *et al.* (2014) while significant negative association with upper half mean length was reported by Nikhil *et al.* (2018) and Sahar *et al.* (2021). Similar findings of association of this trait with seed cotton yield per plant was recorded by Khan *et al.* (2009), Magadum *et al.* (2012), Tulasi *et al.* (2012), Alkuddsi *et al.* (2013), Rao and Gopinath (2013), Asha *et al.* (2015), Reddy *et al.* (2015), Babu *et al.* (2017), Sunayana *et al.* (2017), Khalid *et al.* (2018), Kumar *et al.* (2019), Nawaz *et al.* (2019), Premalatha *et al.* (2020) and Balci *et al.* (2020).

4.2.7 Seed index (g)

The character, seed index was highly significantly and positively correlated with lint index (r_g = 0.8677**, r_p = 0.4747**) at both phenotypic and genotypic levels whereas, its association with upper half mean length (r_g = 0.4835**), fibre strength (r_g = 0.355*) and uniformity index (r_g = 0.3687*) was significantly positive only at genotypic level. Seed cotton yield per plant showed non-significant negative correlation with this trait at both genotypic and phenotypic levels.

The correspondence result of seed index with lint index was observed by Tulasi *et al.* (2012), Alkuddsi *et al.* (2013), Rao and Gopinath (2013), Punitha *et al.* (2013), Pujer *et al.* (2014), Asha *et al.* (2015), Reddy *et al.* (2015), Sunayana *et al.* (2017), Nikhil *et al.* (2018), Kumar *et al.* (2019), Jangid *et al.* (2019) and Premalatha *et al.* (2020).

4.2.8 Lint index (g)

Lint index has established a significant and positive genotypic and phenotypic association with ginning out-turn (r_g = 0.8693**, r_p = 0.6826**) and uniformity index (r_g = 0.4279*, r_p = 0.2035*). The trait had a highly significant positive phenotypic correlation with fibre fineness (r_p = 0.343**). The association of lint index with seed cotton yield per plant was negative and non-significant whereas, with fibre strength it was positive but non-significant at both genotypic and phenotypic levels, clearly indicating the independent nature of these traits and selection for high seed cotton yield per plant based on lint index is not reliable.

Magadum *et al.* (2012), Tulasi *et al.* (2012), Rao and Gopinath (2013), Punitha *et al.* (2013), Asha *et al.* (2015), Reddy *et al.* (2015), Sunayana *et al.* (2017), Nikhil *et al.* (2018), Kumar *et al.* (2019) and Premalatha *et al.* (2020) also observed highly positive and significant association of lint index with ginning out-turn trait.

4.2.9 Ginning out-turn (%)

Ginning out-turn had significant positive association with fibre fineness (r_g = 0.3505*, r_p = 0.2561**) and significant negative association with upper half mean length (r_g = -0.4447**, r_p = -0.2363**) at both phenotypic and genotypic levels. It showed positive genotypic correlation with uniformity index (r_g = 0.3442*) whereas, non-significant association was exhibited with seed cotton yield per plant and fibre strength.

The results are in accordance with the findings of Magadum *et al.* (2012) for association of ginning out-turn with fibre fineness. Rao and Gopinath (2013), Asha *et al.* (2015) and Babu *et al.* (2017) recorded similar results for association of the trait with uniformity index whereas, the negative association of upper half mean length with the trait was also reported by Nikhil *et al.* (2018) and Premalatha *et al.* (2020).

4.2.10 Upper half mean length (UHML) (mm)

The trait, upper half mean length (UHML) has shown highly significant and positive correlation with fibre strength (r_g = 0.6782**, r_p = 0.6039**) and highly significant negative correlation with fibre fineness (r_g = -0.6825**, r_p = -0.3264**) at both genotypic and phenotypic levels. The trait had a significant positive phenotypic correlation with uniformity index (r_p = 0.2304*). Upper half mean length had a non-significant association with seed cotton yield per plant at both genotypic and phenotypic levels, clearly indicating the independent nature of the trait and selection for high seed cotton yield per plant based on upper half mean length is not reliable.

Nikhil *et al.* (2018) and Premalatha *et al.* (2020) also observed positive significant association between upper half mean length and fibre strength.

4.2.11 Fibre fineness (µg/inch)

The fibre quality parameter, fibre fineness (micronaire value) has shown a highly significant negative genotypic and phenotypic correlation with fibre strength (r_g = -0.467**, r_p = -0.3663**) and upper half mean length (r_g = -0.6825**, r_p = -0.3264**). The trait had a significant and positive genotypic and phenotypic association with ginning out-turn (r_g = 0.3505*, r_p = 0.2561**). Significant positive associations of fibre fineness was observed at phenotypic level with lint index (r_p = 0.343**). The rest of the traits including seed cotton yield per plant had non-significant association with this trait.

The correspondence result of fibre fineness with fibre strength (bundle strength) was reported by Punitha *et al.* (2013), Malagouda *et al.* (2014), Pujer *et al.* (2014), Babu *et al.* (2017) and Khalid *et al.* (2018).

4.2.12 Fibre strength (g/tex)

The trait, fibre strength (tenacity) has shown significant positive genotypic and phenotypic association with uniformity index (r_g = 0.356*, r_p = 0.3311**) and upper half mean length (r_g = 0.6782**, r_p = 0.6039**). It has also shown significant negative genotypic and phenotypic correlation with fibre fineness (r_g = -0.467**, r_p = -0.3663**). Non-significant positive association was observed for seed cotton yield per plant indicating that selection of high seed cotton yield per plant based on this character is not preferable.

The significant positive genotypic and phenotypic association of fibre strength with uniformity index was also observed by Magadum *et al.* (2012), Malagouda *et al.* (2014) and Nawaz *et al.* (2019).

4.2.13 Uniformity index (%)

Uniformity index had a highly significant positive correlation with lint index (r_g = 0.4279*, r_p = 0.2035*) and fibre strength (r_g = 0.356*, r_p = 0.3311**) at genotypic as well as phenotypic level. At genotypic level the trait had significant positive association with days to flowering (r_g = 0.4505**) and seed index (r_g = 0.3685**) whereas, at phenotypic level it had positive significant association with upper half mean length (r_p = 0.2304*).

The genotypic and phenotypic correlation between uniformity index and seed cotton yield per plant was negative and non-significant which clearly exhibits that selection for high seed cotton yield per plant based on uniformity index is not reliable. The positive significant correlation of uniformity index with lint index was reported by Babu *et al.* (2017).

4.3 Path coefficient analysis

Seed cotton yield is economically important trait which is improved through the direct and indirect contribution of various traits by studying the correlation and mutual association among the different traits. Path coefficient analysis helps to measure the magnitude and nature of direct and indirect effect of each trait on the dependent trait *i.e.*, yield. Causes of associations between seed cotton yield per plant with all the other thirteen traits were measured using genotypic correlation coefficient. Further, residual effect is calculated which signifies the role of other independent traits on the dependent trait which were not included in the study. Path analysis helps to find out the superior genotypes through selection from diverse genetic population.

With the increase in number of variables, it becomes imperative to measure the contribution of each variable towards the observed correlation. Therefore, partitioning the observed correlation coefficients into unidirectional pathways and alternate pathway would facilitate the characterization of more complex traits like seed cotton yield as devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes. In light of above inferences, path coefficient analysis, which splits the correlation coefficients to provide precise information on the direct and indirect effects in order to perceive the most influencing characters can be utilized as selection criteria in cotton breeding programme.

As a guideline for interpretation of the results of path analysis, the following broad points were kept in view (Singh and Chaudhary, 1977).

- If the correlation coefficient between a casual factor and the effects is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.
- If the correlation coefficient is positive but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the direct casual factors are to be considered simultaneously for selection.
- Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e.*, the restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.
- If the correlation coefficient is negative and direct effect is also negative, then we have to drop the idea of selection based on the character.

The residual effect determines how best the casual factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered in the study need to be included in the analysis to account fully for the variation in yield.

So, in the present study, direct and indirect effects of different yield component traits on seed cotton yield per plant were estimated through path coefficient analysis at genotypic level and presented in **Table 4.4**. The genotypic path diagrams given in **Fig. 4.2**.

4.3.1 Days to flowering vs. Seed cotton yield per plant

The genotypic correlation between days to flowering and seed cotton yield per plant was negative and non-significant (-0.1009). Results of path coefficient analysis revealed that days to flowering had positive and negligible direct effect (0.0169) on seed cotton yield per plant. The negative correlation with seed cotton yield along with positive direct effect suggesting imposition of restricted simultaneous selection model to nullify the undesirable effects in order to make use of the direct effect. The positive indirect effect on seed cotton yield per plant through number of monopodia per plant (0.0013), number of sympodia per plant (0.0067), number of boll per plant (0.0024), seed index (0.0077), lint index (0.0079), ginning out-turn (0.0072), upper half mean length (0.0027), fibre fineness (0.0008), fibre strength (0.0009) and uniformity index (0.0076) was negligible whereas, negative and negligible indirect effect was recorded for plant height (-0.0020) and boll weight (-0.0093).

The positive direct effect of days to flowering on seed cotton yield per plant was also reported by Magadum *et al.* (2012), Chaudhari *et al.* (2017) and Kumar *et al.* (2019).

4.3.2 Plant height vs. Seed cotton yield per plant

The character plant height exhibited positive and significant correlation with seed cotton yield per plant (0.3344*). The plant height had positive high direct effect (0.3440) on seed cotton yield per plant. The positive correlation along with positive direct effect on seed cotton yield per plant was recorded indicating better scope for direct selection through this trait. The positive indirect effect of this trait on seed cotton yield per plant *via* number of monopodia per plant (0.0285), lint index (0.0845), fibre fineness (0.0363), fibre strength (0.0578) and uniformity index (0.0114) was negligible whereas, positive low indirect effect was observed through number of sympodia per plant (0.1228), boll weight (0.1127) and ginning out-turn (0.1766). This trait also showed positive moderate indirect effect on seed cotton yield per plant through number of boll per plant (0.2039). The negative indirect effect of this trait on seed cotton yield per plant *via* days to flowering (-0.0402), seed index (-0.0619) and upper half mean length (-0.0450) was negligible.

Tulasi *et al.* (2012), Erande *et al.* (2014), Nawaz *et al.* (2019) and Sahar *et al.* (2021) also observed positive high direct effect of this trait on seed cotton yield per plant.

Table 4.4: Path coefficient analysis showing direct and indirect effects of various traits on seed cotton yield in cotton on genotypic level

	DF	PH	MP/P	SP/P	B/P	BW	SI	LI	GOT	UHML	FF	FS	UI	SCY/P (r_g)
DF	**0.0169**	-0.0402	0.0132	0.1908	-0.0410	-0.2454	0.0812	-0.2444	-0.0417	0.0669	0.0231	0.0169	0.1030	-0.1009
PH	-0.0020	**0.3440**	0.0142	0.1707	-0.1701	0.1457	-0.0320	-0.1293	-0.0504	-0.0677	0.0525	0.0511	0.0076	0.3344*
MP/P	0.0013	0.0285	**0.1713**	0.0014	-0.0662	-0.1015	0.0696	-0.1195	0.0024	0.0209	0.0826	-0.0344	-0.0296	0.0268
SP/P	0.0067	0.1228	0.0005	**0.4782**	-0.1703	0.0492	-0.0222	-0.0416	-0.0165	-0.0865	-0.0715	-0.0456	0.0091	0.2124
B/P	0.0024	0.2039	0.0395	0.2838	**-0.2870**	0.0592	0.0137	-0.0351	0.0032	0.0505	0.0756	0.0267	0.0383	0.4748**
BW	-0.0093	0.1127	-0.0391	0.0530	-0.0382	**0.4446**	-0.0621	0.0590	-0.0221	-0.1693	0.0929	-0.0329	-0.0262	0.363*
SI	0.0077	-0.0619	0.0671	-0.0598	-0.0222	-0.1555	**0.1776**	-0.4568	-0.0102	0.2047	0.1162	0.1081	0.0843	-0.0006
LI	0.0079	0.0845	0.0389	0.0378	-0.0191	-0.0499	0.1541	**-0.5264**	-0.0854	-0.0260	0.1499	0.0616	0.0978	-0.0743
GOT	0.0072	0.1766	-0.0041	0.0803	0.0093	0.1000	0.0184	-0.4576	**-0.0982**	-0.1882	0.1743	0.0093	0.0787	-0.0942
UHML	0.0027	-0.0550	0.0085	-0.0977	-0.0342	-0.1778	0.0859	0.0323	0.0437	**0.4233**	-0.3394	0.2065	0.0185	0.1171
FF	0.0008	0.0363	0.0284	-0.0688	-0.0436	0.0830	0.0415	-0.1587	-0.0344	-0.2889	**0.4973**	-0.1422	-0.0464	-0.0956
FS	0.0009	0.0578	-0.0193	-0.0716	-0.0252	-0.0480	0.0630	-0.1065	-0.0030	0.2871	-0.2322	**0.3045**	0.0814	0.2888
UI	0.0076	0.0114	-0.0222	0.0191	-0.0481	-0.0509	0.0655	-0.2253	-0.0338	0.0343	-0.1010	0.1084	**0.2286**	-0.0063

Residual effect = 0.6186

*** - Significant at 5% level of significance**
**** - Significant at 1% level of significance**

Where, DF= Days to flowering, PH= Plant height, MP/P= No. of monopodia/plant, SP/P= No. of sympodia/plant, B/P= No. of boll/plant, BW= Boll weight, SI= Seed index, LI= Lint index, GOT= Ginning out-turn, UHML= Upper half mean length, FF= Fibre fineness, FS= Fibre strength, UI= Uniformity index, SCY/P= Seed cotton yield/plant

4.3.3 Number of monopodia per plant vs. Seed cotton yield per plant

The genotypic correlation between number of monopodia per plant and seed cotton yield per plant was positive and non-significant (0.0268). Its direct effect on seed cotton yield per plant was positive and low (0.1713). The positive indirect effect of this trait on seed cotton yield per plant *via* days to flowering (0.0132), plant height (0.0142), number of sympodia (0.0005), number of boll per plant (0.0395), seed index (0.0671), lint index (0.0389), upper half mean length (0.0085) and fibre fineness (0.0284) was negligible. The negative indirect effect of this character *via* boll weight (-0.0391), ginning out-turn (-0.0041), fibre strength (-0.0193) and uniformity index (-0.0222) was also negligible.

Positive direct effect of number of monopodia per plant on seed cotton yield per plant was also reported by Nikhil *et al.* (2018) and Saritha and Patil (2020).

4.3.4 Number of sympodia per plant vs. Seed cotton yield per plant

The trait, number of sympodia per plant has shown positive and non-significant genotypic correlation with seed cotton yield per plant (0.2124). Number of sympodia per plant exhibited positive and high direct effect (0.4782) on seed cotton yield per plant and positive indirect effect *via* number of monopodia per plant (0.0014), boll weight (0.0530), lint index (0.0378), ginning out-turn (0.0803) and uniformity index (0.0191) was negligible. The positive and low indirect effect of this character on seed cotton yield per plant *via* days to flowering (0.1908) and plant height (0.1707) was recorded although, the positive indirect effect of this trait on seed cotton yield per plant *via* number of boll per plant (0.2838) was moderate. Negative indirect effect was noticed through seed index (-0.0598), upper half mean length (-0.0977), fibre fineness (-0.0688) and fibre strength (-0.0716) which were also negligible.

The results are in agreement with the findings of Punitha *et al.* (2013) and Nawaz *et al.* (2019) for direct positive effect of this trait on seed cotton yield per plant.

4.3.5 Number of boll per plant vs. Seed cotton yield per plant

The genotypic correlation between number of boll per plant and seed cotton yield per plant was positive and highly significant (0.4748**). The direct effect of number of boll per plant on seed cotton yield per plant was observed to be negative and moderate (-0.2870). The positive correlation along with negative direct effect on seed cotton yield per plant was exhibited by the trait suggesting indirect effect to be cause for positive correlation and the trait should be considered simultaneously for selection. The trait exhibited positive and negligible indirect effect on seed cotton yield per plant through ginning out-turn (0.0093)

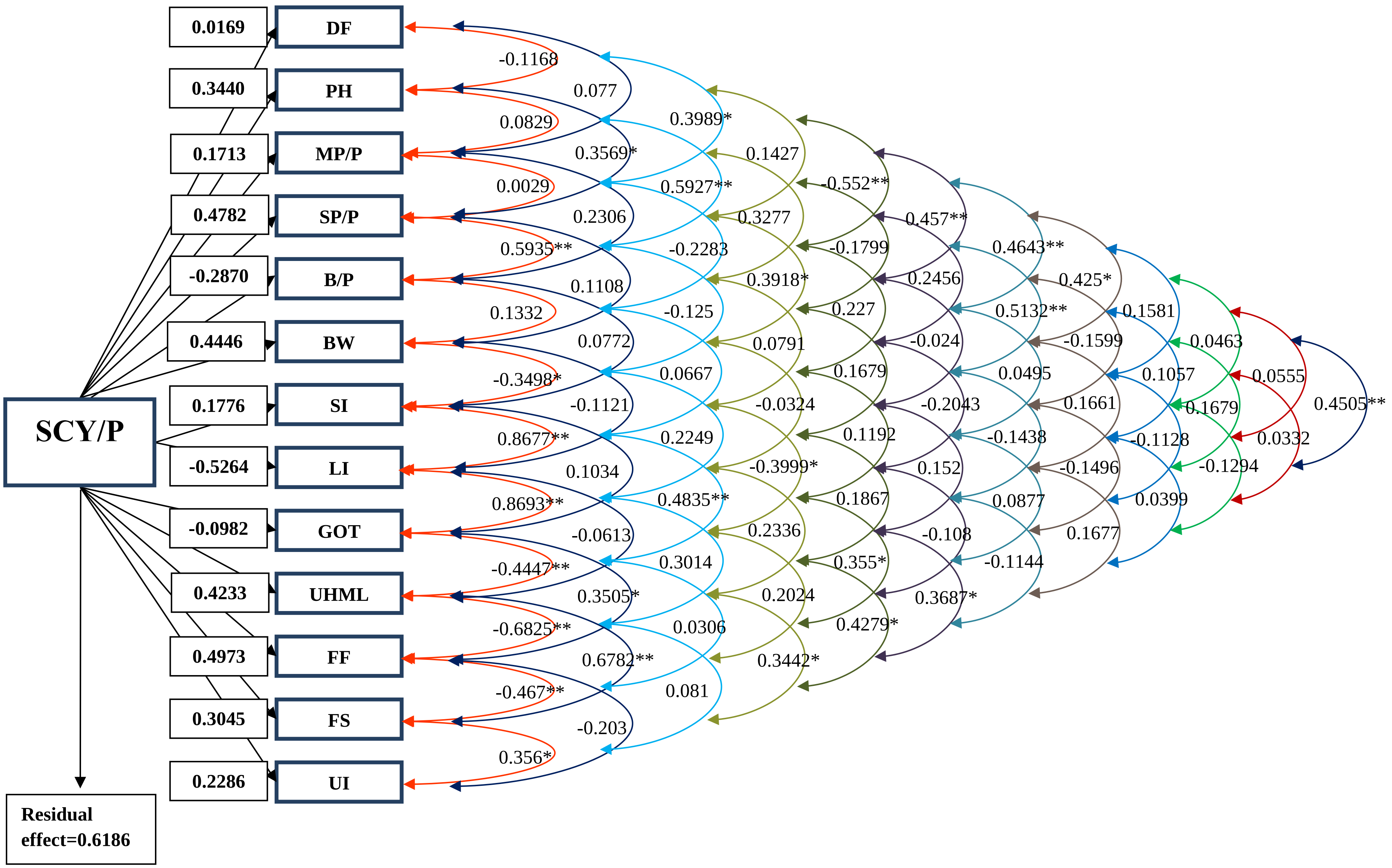


Fig. 4.2: Genotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

whereas, negative and negligible effect of the trait on seed cotton yield per plant was observed *via* days to flowering (-0.0410), number of monopodia per plant (-0.0662), boll weight (-0.0382), seed index (-0.0222), lint index (-0.0191), upper half mean length (-0.0342), fibre fineness (-0.0436), fibre strength (-0.0252) and uniformity index (-0.0481). The negative indirect effect of the trait on seed cotton yield per plant *via* plant height (-0.1701) and number of sympodia per plant (-0.1703) was moderate.

The negative direct effect of number of boll per plant on seed cotton yield was also observed by Alkuddsi *et al.* (2013), Farooq *et al.* (2014) and Sahar *et al.* (2021).

4.3.6 Boll weight vs. Seed cotton yield per plant

The trait, boll weight has shown significant and positive genotypic correlation with seed cotton yield per plant (0.363*). Its direct positive effect on seed cotton yield per plant was found to be high (0.4446). The positive correlation along with positive direct effect on seed cotton yield per plant was recorded which indicates that direct selection through this trait would be effective. The trait also showed positive and low indirect effect on seed cotton yield per plant *via* plant height (0.1457) and ginning out-turn (0.1000) whereas, negative and low indirect effect of this characters on seed cotton yield per plant was observed *via* number of monopodia per plant (-0.1015), seed index (-0.1555) and upper half mean length (-0.1778). The negative indirect effect of the trait on seed cotton yield per plant *via* days to flowering (-0.2454) was moderate whereas, negative indirect effect exhibited by lint index (-0.0499), fibre strength (-0.0480) and uniformity index (-0.0509) was negligible. The positive indirect effect of this character on seed cotton yield per plant *via* number of sympodia per plant (0.0492), number of boll per plant (0.0592) and fibre fineness (0.0830) was negligible.

Similar positive direct effect of boll weight on seed cotton yield per plant was observed by Magadum *et al.* (2012), Alkuddsi *et al.* (2013), Rao and Gopinath (2013), Punitha *et al.* (2013), Chaudhari *et al.* (2017), Nikhil *et al.* (2018) and Sahar *et al.* (2021).

4.3.7 Seed index vs. Seed cotton yield per plant

The genotypic correlation between the trait seed index and seed cotton yield per plant was negative and non-significant (-0.0006). The trait exhibited positive and low direct effect on seed cotton yield per plant (0.1776). The positive indirect effect of this trait on seed cotton yield per plant was *via* lint index (0.1541) was moderate. The negative indirect effect of the character on seed cotton yield per plant *via* plant height (-0.320), number of sympodia per plant (-0.0222) and boll weight (-0.0621) was observed to be negligible and the positive indirect effect of the trait on seed cotton yield per plant through days to flowering (0.0812), number of monopodia per plant (0.0696), number of boll per plant (0.0137), ginning out-turn

(0.0184), upper half mean length (0.0859), fibre fineness (0.0415), fibre strength (0.0630) and uniformity index (0.0655) was also negligible.

Similar result for positive direct effect of seed index on seed cotton yield per plant was reported by Saritha and Patil (2020).

4.3.8 Lint index vs. Seed cotton yield per plant

The trait, lint index has established a negative and non-significant genotypic correlation with seed cotton yield per plant (-0.0743). The character exerted negative and high direct effect on seed cotton yield per plant (-0.5264). The negative correlation with seed cotton yield along with negative direct effect suggesting no reward through direct selection of this trait for the improvement. Its negative indirect effect on seed cotton yield per plant *via* plant height (-0.1293), number of monopodia per plant (-0.1195), fibre fineness (-0.1587) and fibre strength (-0.1065) was observed to be low whereas, moderate and high negative indirect effect was exhibited by the trait on seed cotton yield per plant through days to flowering (-0.2444), uniformity index (-0.2253) and seed index (-0.4568), respectively. The trait showed negative and negligible indirect effect on seed cotton yield per plant *via* number of sympodia per plant (-0.0416) and number of boll per plant (-0.0351). Its positive but negligible indirect effect on seed cotton yield per plant was also observed *via* boll weight (0.0590) and upper half mean length (0.0323).

Negative direct effect of lint index on seed cotton yield was also recorded by Tulasi *et al.* (2012), Sunayana *et al.* (2017) and Sahar *et al.* (2021).

4.3.9 Ginning out-turn vs. Seed cotton yield per plant

The genotypic correlation between the character ginning out-turn and seed cotton yield per plant was negative and non-significant (-0.0942). Its negative direct effect on seed cotton yield per plant was negligible (-0.0982). The positive indirect effect of the trait on seed cotton yield per plant *via* number of monopodia per plant (0.0024), number of boll per plant (0.0032) and upper half mean length (0.0437) was negligible whereas, negative and negligible indirect effect of ginning out-turn on seed cotton yield per plant was also observed *via* days to flowering (-0.0417), plant height (-0.0504), number of sympodia per plant (-0.0165), boll weight (-0.0221), seed index (-0.0102), lint index (-0.0854), fibre fineness (-0.0344), fibre strength (-0.0030) and uniformity index (-0.0338).

Similar results for negative direct effect of ginning out-turn on seed cotton yield per plant was also reported by Reddy *et al.* (2015) and Chaudhari *et al.* (2017).

4.3.10 Upper half mean length vs. Seed cotton yield per plant

The trait, upper half mean length (UHML) showed positive and non-significant correlation with seed cotton yield per plant (0.1171). Its positive direct effect on seed cotton yield per plant was observed to be high (0.4233). The positive indirect effect of the trait on seed cotton yield per plant *via* seed index (0.2047) and fibre strength (0.2871) was moderate and negative indirect effect of UHML on seed cotton yield per plant through fibre fineness (-0.2889) was moderate too. Low and negative indirect effect of the trait on seed cotton yield per plant was observed *via* boll weight (-0.1693) and ginning out-turn (-0.1882). The positive indirect effect of UHML on seed cotton yield per plant *via* days to flowering (0.0669), number of monopodia per plant (0.0209), number of boll per plant (0.0505) and uniformity index (0.0343) was negligible and negative indirect effect of the character on seed cotton yield per plant was also negligible *via* plant height (-0.0677), number of sympodia per plant (-0.0865) and lint index (-0.0260).

The results are in conformity with the findings of Saritha and Patil (2020) for the positive direct effect of UHML on seed cotton yield per plant.

4.3.11 Fibre fineness vs. Seed cotton yield per plant

The genotypic correlation of fibre fineness (micronaire) with seed cotton yield per plant was negative and non-significant (-0.0956). The positive direct effect of fibre fineness on seed cotton yield per plant was high (0.4973). Its positive direct effect on seed cotton yield per plant through seed index (0.1162), lint index (0.1499) and ginning out-turn (0.1743) was low whereas, moderate negative indirect effect of the trait on seed cotton yield per plant *via* fibre strength (-0.2322) was observed. High, low and negligible negative indirect effects of the trait on seed cotton yield per plant was recorded *via* upper half mean length (-0.3394), uniformity index (-0.1010) and number of sympodia per plant (-0.0715), respectively. Positive indirect effect of the trait on seed cotton yield per plant through days to flowering (0.0231), plant height (0.0525), number of monopodia per plant (0.0826), number of boll per plant (0.0756) and boll weight (0.0929) was negligible.

Positive direct effect of fibre fineness on seed cotton yield per plant was also reported by Erande *et al.* (2014) and Nawaz *et al.* (2019).

4.3.12 Fibre strength vs. Seed cotton yield per plant

The character, fibre strength (bundle strength) has shown positive and non-significant correlation with seed cotton yield per plant (0.2888). Its positive direct effect on seed cotton yield per plant was high (0.3045). Positive and low indirect effect of the trait on seed cotton yield per plant was observed *via* seed index (0.1081) whereas, positive and moderate indirect effect of the trait on seed cotton yield per plant was exhibited through upper half mean length (0.2065). Negative and low indirect effect of the trait on seed cotton yield per plant was showed by fibre fineness (-0.1422). The traits *viz.*, days to flowering (0.0169), plant height (0.0511), number of boll per plant (0.0267), lint index (0.0616) and ginning out-turn (0.0093) showed negative and negligible positive indirect effect on seed cotton yield per plant and the remaining traits *viz.*, number of monopodia per plant (-0.0344), number of sympodia per plant (-0.0456) and boll weight (-0.0329) exhibited negative and negligible indirect effect on seed cotton yield per plant.

Similar results of positive direct effect of fibre strength on seed cotton yield was also reported by Chaudhari *et al.* (2017) and Nawaz *et al.* (2019).

4.3.13 Uniformity index vs. Seed cotton yield per plant

The genotypic correlation between uniformity index and seed cotton yield per plant was negative and non-significant (-0.0063). The trait had positive and moderate direct effect on seed cotton yield per plant (0.2286). Its positive indirect effect on seed cotton yield per plant *via* days to flowering (0.1030) was low whereas, positive and negligible indirect effect of the trait on seed cotton yield per plant through plant height (0.0076), number of sympodia per plant (0.0091), number of boll per plant (0.0383), seed index (0.0843), lint index (0.0978), ginning out-turn (0.0787), upper half mean length (0.0185) and fibre strength (0.0814) was observed. The remaining character *viz.*, number of monopodia per plant (-0.0296), boll weight (-0.0262) and fibre fineness (-0.0464) had negative and negligible indirect effect through uniformity index on seed cotton yield per plant.

The results are in agreement with the findings of Rao and Gopinath (2013), Erande *et al.* (2014), Pujer *et al.* (2014) and Saritha and Patil (2020) for positive direct effect of the trait on seed cotton yield per plant.

The effect of residual factor on seed cotton yield per plant suggested that, there might be few more characters, other than those studied in the present investigation, which might have also contributed for yield.

SUMMARY AND CONCLUSIONS

V. SUMMARY AND CONCLUSIONS

The present investigation on "**Genetic variability and character association studies in cotton (*Gossypium hirsutum* L.)**" was carried out at Cotton Research Station, S. D. Agricultural University, Talod during *kharif*-2020. The experiment was conducted using thirty-five genotypes which were procured from the Cotton Research Station, S. D. A. U., Talod. Seeds were planted on 19th June, 2020 using randomized block design with three replications. The mean, genetic variability, heritability, genetic advance as per cent of mean, character association and the magnitude of direct and indirect effects of yield component traits on seed cotton yield were studied for fourteen characters *viz.*, days to flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of boll per plant, seed cotton yield per plant (g), boll weight (g), seed index (g), lint index (g), ginning out-turn (%), upper half mean length (mm), fibre fineness (µg/inch), fibre strength (g/tex) and uniformity ratio (%).

The *per se* performance of all the genotypes varied between 49.33 to 55.33 days with a mean of 52.45 days to flowering and 96.43 cm to 133.56 cm with a mean of 118.37 cm for plant height. Number of monopodia per plant varied from 1.08 to 3.10 with general mean 1.89, number of sympodia per plant ranged from 11.39 to 19.49 with an average of 16.10, number of boll per plant were in range of 11.75 to 33.09 with an average mean 20.27, seed cotton yield per plant recorded in a range from 29.59 g to 73.22 g with an average mean 50.11 g, boll weight lies between 3.02 g to 4.63 g with mean 3.79 g, seed index was recorded 6.50 g to 9.38 g with an average of 8.00 g, lint index ranged from 3.57 g to 6.57 g with a mean 4.91 g and ginning out-turn varied from 31.75% to 43.09% with the general mean of 37.96%. The *per se* performance of the fibre quality traits varied from 23.83 mm to 27.87 mm with a mean of 25.77 mm for upper half mean length, fibre fineness (micronaire) values ranged from 3.60 µg/inch to 5.33 µg/inch with an average mean of 4.62 µg/inch, fibre strength observed in the range of 24.00 g/tex to 28.20 g/tex with the general mean of 25.95 g/tex and uniformity index was ranged from 80.33% to 84.00% with an average of 82.03%.

Variance components

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of diverse material in the present study.

The high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for number of monopodia per plant, number of boll per plant and seed cotton yield per plant which suggests the possibility of improving these traits through simple selection.

High heritability estimates coupled with high expected genetic advance were observed for the characters number of monopodia per plant, number of boll per plant, seed cotton yield per plant and lint index. This indicated the additive nature of genetic variation was transmitted from parents to progeny. Moreover, these traits can easily be fixed in the genotypes by selection of early generation.

The trait, boll weight recorded high heritability along with the moderate genetic advance which indicated the involvement of both additive and non-additive gene action and improvement in seed cotton yield may not be obtained by simple selection.

Correlation coefficient

The correlation coefficient studies revealed positive and highly significant genotypic and phenotypic association of number of boll per plant and boll weight with seed cotton yield per plant and also the trait plant height had positive and significant correlation with seed cotton yield per plant but only at genotypic level suggesting selection for high seed cotton yield per plant is beneficial.

Path coefficient

The path coefficient analysis revealed that, the traits *viz.*, days to flowering, plant height, number of monopodia per plant, number of sympodia per plant, boll weight, seed index, upper half mean length, fibre fineness, fiber strength and uniformity index exerted direct positive effect on seed cotton yield. The negative direct effect coupled with highly positive significant correlation was exhibited by number of boll per plant whereas, lint index and ginning out-turn showed negative direct effect along with negative non-significant correlation with seed cotton yield per plant. The residual factor however, indicated that it requires some more study with a greater number of parameters, so that the breeder can have better choice for selection.

Conclusion

It can be concluded from the present findings that in a breeding programme aiming to improve seed cotton yield per plant in cotton, more weightage should be mainly given to number of monopodia per plant, number of boll per plant and lint index as they exhibited high heritability coupled with high genetic advance as per cent mean.

The traits, number of boll per plant and boll weight has showed positive and significant correlation with seed cotton yield per plant which indicates that these characters are the most important ones in the process of effective selection of superior cotton genotypes. Whereas, high positive direct effect along with positive correlation was exerted by boll weight which suggests direct selection through this trait would be effective.

Based on the mean performance of seed cotton yield per plant, genotypes *viz.*, GBHV 217, GBHV 241, GJHV 560, GN. Cot. 22 and GSHV 235 were categorized as high seed cotton yielding genotypes which can be selected for further breeding programme. Also, the genotypes like GSHV 208 and GSHV 191 produced fine fibre (lower micronaire value which is preferable) compared to rest of the genotypes, which can be utilized in the development of cotton genotypes with superior fibre quality. So, for the improvement of seed cotton yield and their component traits more emphasis could be given to these genotypes and with planning of research for more number of seasons and locations to get more precise results.

REFERENCES

REFERENCES

Aarthi, V., AmalaBalu, P., and Premelatha, N. (2018). Genetic variability studies in germplasm of upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, **9**(4), 1600-1605.

Adsare, A. N., and Abhay, N. S. (2017). Study on genetic variability for the quantitative traits in some genotypes of upland cotton (*Gossypium hirsutum* L.). *Bioscience Discovery*, **8**(3), 365-368.

Ahmad, W., Khan, N. U., Khalil, M. R., Parveen, A., Saeed, M., and Shah, S. A. (2008). Genetic variability and correlation analysis in upland cotton. *Sarhad Journal of Agriculture (Pakistan)*.

Ahsan, M. Z., Majidano, M. S., Bhutto, H., Soomro, A. W., Panhwar, F. H., Channa, A. R., and Sial, K. B. (2015). Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. *Journal of Agricultural Science*, **7**(2), 147.

Ali, M. A. and I. A. Khan (2007). Assessment of genetic variation and inheritance mode of some metric traits in cotton (*Gossypium hirsutum* L.). *Journal of Agriculture and Social Sciences*. **3**: 112-116.

Alkuddsi, Y., Rao, M. G., Patil, S. S., Joshi, M., and Gowda, T. H. (2013). Correlation and path coefficient analysis between seed cotton yield and its attributing characters in intra hirsutum cotton hybrids. *Molecular Plant Breeding*, *4*.

Allard R.W. 1960. Principles of plant breeding. John Wiley and Sons. Inc., NewYork: 84-85.

Anonymous. (2020). Cotton Advisory Board Report. 2019-20.

Anonymous. (2021). Committee on Cotton Production and Consumption (COCPC). 2020-21.

Asha, R., Ahamed, M. L., Babu, D. R., and Kumar, P. A. (2015). Character association and path coefficient analysis for yield and component traits in upland cotton. *Journal of Cotton Research and Development*, **29**(1), 31-35.

Babu, B. J., Satish, Y., Ahamed, M., and Rao, V. S. (2017). Correlation and path coefficient analysis for yield and yield component traits in upland cotton (*Gossypium hirsutum* L.). *The journal of research ANGRAU*, 46.

Balci, Ş., Çinar, V. M., and Aydın, Ü. N. A. Y. (2020). A study on genetic advance and heritability for quantitative traits in cotton (*Gossypium hirsutum* L.). *Adnan Menderes Üniversitesi Ziraat Fakültesi Dergisi*, **17**(1), 81-84.

Baloch, M. J., and Baloch, Q. B. (2004). Plant characters in relation to earliness in cotton (*Gossypium hirsutum*). *Proceedings of the Pakistan Academy of Sciences*, **41**(2), 103-108.

Burton, G. W. (1952, August). Qualitative inheritance in grasses. Vol. 1. In *Proceedings of the 6th International Grassland Congress, Pennsylvania State College* (pp. 17-23).

Chapepa, B., Mubvekeri, W., Mare, M., and Kutywayo, D. (2020). Correlation and path coefficient analysis of polygenic traits of upland cotton genotypes grown in Zimbabwe. *Cogent Food and Agriculture*, **6**(1), 1823594.

Chaudhari, M. N., Faldu, G. O., and Ramani, H. R. (2017). Genetic variability, correlation and path coefficient analysis in cotton (*Gossypium hirsutum* L.). *Advances in Bioresearch*, **8**(6), 226-233.

Devidas, A. A., Narayan, S. A., and Prakash, P. N. (2017). Study of genetic variability, heritability and genetic advance in some genotypes of Egyptian cotton (*Gossypium barbadense* L.). *Journal Global Biosciences*, **6**(4), 4954-7.

Dewey, D. R., and Lu, K. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production 1. *Agronomy Journal*, **51**(9), 515-518.

Dhamayanathi, K. P. M., Manickam, S., and Rathinavel, K. (2010). Genetic variability studies in *Gossypium barbadense* L. genotypes for seed cotton yield and its yield components. *Electronic Journal of Plant Breeding*, **1**(4), 961-965.

Dhivya, R., Amalabalu, P., Pushpa, R., and Kavithamani, D. (2014). Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *African Journal of Plant Science*, **8**(1), 1-5.

Erande, C. S., Kalpande, H. V., Deosarkar, D. B., Chavan, S. K., Patil, V. S., Deshmukh, J. D., and Puttawar, M. R. (2014). Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboreum* L.). *African Journal of Agricultural Research*, **9**(29), 2278-2286.

Eswari, K. B., Sudheer Kumar, S. Gopinath and Rao, MVB 2017. Genetic variability heritability and genetic advance studies in cotton. *International Journal of Development Research*, **7**, 10902-10904.

Farooq, J., Anwar, M., Riaz, M., Farooq, A., Mahmood, A., Shahid, M. T. H., and Ilahi, F. (2014). Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). *JAPS: Journal of Animal and Plant Sciences*, **24**(3).

Gnanasekaran, M., Thiyagu, K., and Gunasekaran, M. (2018). Genetic variability heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, **9**(1), 377-382.

Hutchinson, J. B. (1940). The application of genetics to plant breeding. The genetic interpretation of plant breeding problems. *Journal of Genetics*. **40**: 271-282.

Jangid, K., Reddy, B., Nimbal, S., Sangwan, R. S., Kumar, P. and Sagar (2019). Genetic parameters, correlation and path analysis of agro-morphological traits in elite genotypes of upland cotton (*Gossypium hirsutum* L.). *International Journal of Crop Science*, **7**(5), 1885-1889.

Johnson, H. W., Robinson, H. F., and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy Journal*, **47**(7), 314-318.

Joshi, H. J., Chovatia, P. K., and Mehta, D. R. (2006). Genetic variability, character association and component analysis in upland cotton. *Indian Journal of Agricultural Research*, **40**(4), 302-305.

Khalid, M. A., Malik, T. W., Fatima, N., Sahkeel, A., Karim., I., Arfan, M., Merrium, S., and Khanum, P. (2018). Correlation for economic traits in upland cotton. *ACTA Scientific Agriculture*, **2**, 59-62.

Khan, N. U., Hassan, G., Marwat, K. B., Farhatullah, S. B., Makhdoom, K., Khan, I., and Ahmad, W. (2009). Genetic variability and heritability in upland cotton. *Pakistan Journal of Botany*, **41**(4), 1695-1705.

Kumar, C. P. S., Prasad, V., Rajan, R. E. B., Joshi, J. L., and Thirugnanakumar, S. (2019). Studies on correlation and path-coefficient analysis for seed cotton yield and its contributing traits in cotton (*Gossypium hirsutum* L.). *Plant Archives*, **19**(1), 683-686.

Larik, A. S., Ansari, S. R., and Kumbhar, M. B. (1997). Heritability analysis of yield and quality components in *Gossypium hirsutum* L. *Pakistan Journal of Botany (Pakistan)*.

Latif, A., Bilal, M., Hussain, S. B., and Ahmad, F. (2015). Estimation of genetic divergence, association, direct and indirect effects of yield with other attributes in cotton (*Gossypium hirsutum* L.) using biplot correlation and path coefficient analysis. *Tropical Plant Research*, **2**(2), 120-126.

Magadum, S., Banerjee, U., Ravikesavan, R., Thiyagu, K., Boopathi, N. M., and Rajarathinam, S. (2012). Association analysis of yield and fibre quality characters in interspecific population of cotton (*Gossypium spp.*). *Journal of Crop Science and Biotechnology,* **15**(3), 239-243.

Malagouda, P., Khadi, B. M., Basamma, K., and Katageri, I. S. (2014). Genetic variability and correlation analysis for fibre quality traits in diploid cotton (*Gossypium spp*). *American-Eurasian Journal of Agricultural and Environmental Sciences*, **14**(5), 392-395.

Manonmani, K., Mahalingam, L., Malarvizhi, D., Sritharan, N., and Premalatha, N. (2019). Genetic variability, correlation and path analysis for seed cotton yield improvement in upland cotton (*Gossypium hirsutum* L.). *Journal of Pharmacognosy and Phytochemistry*, **8**(4), 1358-1361.

McCarty, J. C., Wu, J., and Jenkins, J. N. (2008). Genetic association of cotton yield with its component traits in derived primitive accessions crossed by elite upland cultivars using the conditional ADAA genetic model. *Euphytica,* **161**(3), 337-352.

Miller, P. A.; Williams, J. C.; Robinson, H. F. and Comstock, R. R. (1958). Estimates of genotypic and environmental variance and covariance in upland and their implications in selection. *Agronomy Journal*. **50**: 126-131.

Monisha, K., Premalatha, N., Sakthivel, N. and Kumar, M., (2018). Genetic variability and correlation studies in upland cotton (*Gossypium hirsutum* L). *Electronic Journal of Plant Breeding*, **9**(3), 1053-1059.

Naik, B. M., Satish, Y., and Babu, D. R. (2016). Genetic variability, heritability and genetic advance studies for yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). *The Journal of Research ANGRAU*, 14.

Nawaz, B., Sattar, S., and Malik, T. A. (2019). Genetic analysis of yield components and fiber quality parameters in upland cotton. *International Multidisciplinary Research Journal*, 13-19.

Nikhil, P. G., Nidagundi, J. M., and Anusha, H. A. (2018). Correlation and path analysis studies of yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Pharmacognosy Phytochemistry*, **7**(5), 2596-2599.

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*. **17**(3): 318-328.

Poehlman, J. M. and Selper, D. A. (1995). Breeding of field crops. 4th Edition. Panima Publishing Corporation. New Delhi, India.

Premalatha, N., Mahalingam, L., Kumar, M., and Rajeswari, S. (2020). Genetic variability studies in *Gossypium barbadense* L. genotypes for seed cotton yield and its yield components. *International Journal of Current Microbiology and Applied Sciences*, **9**(6), 01-12.

Pujer, S., Siwach, S. S., Deshmukh, J., Sangwan, R. S., and Sangwan, O. (2014). Genetic variability, correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, **5**(2), 284-289.

Punitha, D., Gunasekaran, M., Balu, P. A., Vinodhana, N. K., and Vindhiyavarman, P. (2013). Genetic studies of variability, correlation and path coefficient analysis in cotton. *Advances in Plant Sciences*, **26**(2), 331-334.

Ranganatha, H. M., Patil, S. S., Manjula, S. M., and Arvindkumar, B. N. (2013). Genetic variability studies in segregating generation of upland cotton (*Gossypium hirsutum* L.). *Molecular Plant Breeding*, 4.

Rao, P. J. M., and Gopinath, M. (2013). Association analysis of yield and fibre quality characters in upland cotton (*Gossypium hirsutum* L.). *Australian Journal of Basic and Applied Sciences*, **7**(8), 787-790.

Reddy, K. B., Reddy, V. C., Ahamed, M. L., Naidu, T. C. M., and Srinivasarao, V. (2015). Correlation and path coefficient analysis in upland cotton (*Gossypium hirsutum* L.). *Journal of Research ANGRAU*, **43**(1/2), 25-35.

Reddy, K. S., Balakrishna, B., and Reddy, V. C. (2019). Study of cause and effect relationship among yield, yield contributing and quality traits in cotton (*Gossypium hirsutum* L.). *International Journal of Current Microbiology and Applied Sciences*, **8**(6), 1798-1807.

Robinson, H. F. (1966). Breeding on the centennial of Mendelism. *Environment and Ecology*. **8**(1A): 236-238.

Sahar, A., Zafar, M. M., Razzaq, A., Manan, A., Haroon, M., Sajid, S., and Youlu, Y. U. A. N. (2021). Genetic variability for yield and fiber related traits in genetically modified cotton. *Journal of cotton research*, **4**(1), 1-10.

Salahuddin, S., Abro, S., Kandhro, M. M., Salahuddin, L., and Laghari, S. (2010). Correlation and path coefficient analysis of yield components of upland cotton (*Gossypium hirsutum* L.) sympodial. *World Applied Sciences Journal*, **8**, 71-75.

Saritha, H. S., and Patil, R. S. (2020). Genetic studies in colour-cotton (*Gossypium hirsutum* L.) genotypes for seed cotton yield and fibre quality traits. *Electronic Journal of Plant Breeding*, **11**(01), 30-35.

Shruti, H., Sowmya, C. H., Nidagundi, J. M., Lokesha, R., Arunkumar, B., and Murthy, M. S. (2019). Genetic variability studies for yield, yield attributing and fibre quality traits in cotton (*Gossypium hirsutum* L.). *International Journal of Current Microbiology and Applied Sciences*, **8**(10), 2677-2687.

Shivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agriculture Journal*. **60**(7): 1139-1140.

Simpson, D. M. (1954). Natural crossing in upland cotton. U. S. Department of Agriculture. *Tech Bull*. 1094.

Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi. pp. 215-218.

Sunayana, R., Sangwan, S., and Nimbal, S. (2017). Studies on association, path analysis and genetic parameters for seed cotton yield and it's contributing characters in desi cotton (*Gossypium arboreum* L.). *International Journal of Current Microbiology and Applied Sciences*, **6**(11), 104-111.

Swarup and Chaugle, B. S. (1962). Studies on genetic variability in sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding*. **22**: 31-36.

Tulasi, J., Lal, M. A., Murthy, J. S. V., and Rani, Y. A. (2012). Correlation and path analysis in American cotton. *Electronic Journal of Plant Breeding*, **3**(4), 1005-1008.

Wadeyar, B. S., and Kajjidoni, S. T. (2015). Genetic variability estimation and frequency of superior progenies in advance breeding lines in desi cotton at two locations. *Current World Environment*, **10**(1), 313.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*, **20**, 557-580.

APPENDICES

Appendix A: Mean weekly meteorological data recorded during experimental period (June 2020 – January 2021) at Talod

Month	Std. Week No.	Rainfall (mm)	Temperature (°C)		Relative Humidity (%)
			Max.	Min.	
June-2020	25	1.2	37.2	29.4	86.3
	26	9.0	38.1	30.6	81.9
	27	11.0	37.3	29.5	93.4
July-2020	28	45.0	36.5	26.0	94.3
	29	9.0	35.3	29.4	90.0
	30	118.0	36.7	27.9	89.6
	31	2.0	36.5	27.5	88.6
Aug-2020	32	61.0	34.6	26.3	87.0
	33	151.0	32.3	19.7	94.4
	34	280.0	29.4	21.4	96.6
	35	91.0	28.1	22.4	85.7
Sept-2020	36	32.0	30.9	19.3	92.1
	37	116.0	30.0	23.3	93.1
	38	28.0	29.0	22.7	91.0
	39	0.0	30.3	22.1	90.9
Oct-2020	40	0.0	31.6	21.6	87.7
	41	0.0	35.7	18.4	90.6
	42	6.4	32.3	21.3	91.6
	43	0.0	33.4	22.4	87.4
	44	0.0	36.9	19.1	85.0
Nov-2020	45	0.0	35.1	17.7	78.1
	46	0.0	33.4	16.4	80.1
	47	0.0	31.6	22.3	84.0
	48	0.0	26.6	16.4	89.7
Dec-2020	49	0.0	29.3	20.1	88.3
	50	1.0	28.6	20.4	86.6
	51	0.0	20.0	12.0	88.0
	52	0.0	18.6	11.3	88.6
	53	0.0	19.6	11.3	86.7
Jan-2021	1	0.0	23.3	12.3	85.3
	2	0.0	24.8	12.7	76.9
	3	0.0	25.3	11.6	82.0

Total rainfall: 961.6 mm
Average maximum temperature: 30.88 °C
Average minimum temperature: 20.77 °C
Average relative humidity: 87.85%

Source: Weather Data Book, Cotton Research Station, S.D.A.U., Talod. Dist.: Sabarkantha

Appendix B: Mean values of thirty five genotypes of cotton for different characters

Sr. No.	Genotypes	DF	PH	MP/P	SP/P	B/P	SCY/P	BW
1	**GSHV 234**	53.67	119.89	2.22	15.34	20.01	52.71	3.56
2	**GSHV 235**	52.67	132.12	1.98	17.43	30.08	65.44	3.98
3	**GSHV 236**	54.33	120.01	2.62	16.87	24.22	59.23	3.41
4	**GSHV 238**	54.67	120.39	1.81	17.98	23.36	61.70	3.48
5	**GISV 328**	51.67	124.49	1.81	18.26	16.89	47.90	3.64
6	**GISV 342**	54.33	126.64	1.42	17.15	15.55	47.57	3.58
7	**GSHV 191**	51.67	106.94	1.64	14.76	18.61	50.31	**3.02**
8	**GBHV 217**	52.33	110.07	2.13	12.13	16.11	**73.22**	4.49
9	**GBHV 218**	51.33	116.86	1.71	15.69	14.40	56.69	4.10
10	**GBHV 234**	52.00	129.13	2.03	**11.39**	18.47	52.69	3.78
11	**GBHV 241**	**49.33**	119.56	1.16	16.15	17.96	72.17	4.45
12	**GBHV 242**	50.00	119.29	1.73	12.62	18.80	48.16	3.46
13	**GHHV 34/2013**	50.67	119.00	2.07	16.52	23.37	61.88	4.25
14	**GJHV 562**	50.67	126.79	1.58	17.32	22.47	52.57	**4.63**
15	**GJHV 567**	54.67	109.16	1.42	16.31	20.64	46.70	3.89
16	**GJHV 584**	54.00	115.53	1.19	16.65	25.19	48.42	3.40
17	**GJHV 560**	51.00	119.83	1.81	19.24	25.19	70.18	3.76
18	**GTHV 19/6**	**55.33**	99.96	1.43	17.43	**11.75**	38.53	3.22
19	**GTHV 19/7**	51.33	125.68	1.30	16.42	16.58	42.29	4.57
20	**GTHV 18/6**	54.33	126.71	2.86	17.80	25.64	59.97	3.81
21	**GN. Cot. 32 (CC)**	55.00	119.45	1.90	15.59	17.82	38.14	3.62
22	**G. Cot. 38 (CC)**	51.00	104.53	1.91	17.31	24.14	45.20	4.15
23	**GSHV 223**	51.00	120.62	1.77	16.12	20.75	42.75	4.54
24	**GSHV 224**	51.00	119.43	2.60	14.80	16.04	**29.59**	3.20
25	**GISV 332**	52.67	121.87	**1.08**	15.58	18.16	35.85	3.67
26	**GSHV 208**	53.33	111.61	1.56	17.56	21.06	39.17	3.39
27	**GJHV 548**	51.33	111.91	**3.10**	16.34	20.56	46.63	3.25
28	**GJHV 568**	52.67	**96.43**	1.78	14.44	12.20	49.48	3.96
29	**GJHV 534**	50.67	108.30	1.72	13.49	18.64	38.44	3.39
30	**GHHV 60/2013**	52.67	114.11	2.61	15.57	20.19	37.00	4.00
31	**GTHV 18/17**	54.00	124.34	2.60	15.49	20.65	46.30	3.49
32	**GTHV 18/19**	51.33	120.81	2.34	17.84	20.66	38.11	3.60
33	**GTHV 15/34**	51.33	128.81	1.71	18.34	23.32	47.46	4.30
34	**GTHV 15/220**	53.00	119.22	1.46	12.00	16.84	41.48	3.55
35	**GN. Cot. 22 (CC)**	54.67	**133.56**	1.91	**19.49**	**33.09**	69.77	4.00
	Mean	52.45	118.37	1.89	16.10	20.27	50.11	3.79
	Minimum	49.33	96.43	1.08	11.39	11.75	29.59	3.02
	Maximum	55.33	133.56	3.10	19.49	33.09	73.22	4.63
	S. Em. ±	1.10	4.64	0.12	0.94	1.30	2.94	0.18
	C.D. at 5%	3.12	13.08	0.34	2.66	3.66	8.31	0.51
	C.V.%	3.65	6.78	11.08	10.15	11.08	10.18	8.24

Where, DF= Days to flowering, PH= Plant height, MP/P= No. of monopodia/plant, SP/P= No. of sympodia/plant, B/P= No. of boll per plant, SCY/P= Seed cotton yield/plant, BW= Boll weight

Appendix B cont…

Sr. No.	Genotypes	SI	LI	GOT	UHML	FF	FS	UI
1	**GSHV 234**	8.34	5.83	41.20	25.63	4.30	27.5	83.33
2	**GSHV 235**	8.80	5.97	40.20	26.67	4.73	26.8	83.33
3	**GSHV 236**	9.15	6.30	40.99	27.20	4.77	26.5	81.33
4	**GSHV 238**	8.99	5.83	39.35	27.40	4.30	27.6	83.67
5	**GISV 328**	7.21	5.17	41.98	24.17	4.67	25.8	81.00
6	**GISV 342**	7.66	5.77	**43.09**	**23.83**	4.63	24.8	81.67
7	**GSHV 191**	7.68	**3.57**	**31.75**	**27.87**	3.87	27.5	82.33
8	**GBHV 217**	7.89	4.60	37.01	26.07	4.47	25.7	81.33
9	**GBHV 218**	7.31	4.17	36.44	24.87	4.53	25.9	**80.33**
10	**GBHV 234**	7.05	3.97	35.69	26.17	4.53	26.4	83.00
11	**GBHV 241**	8.36	4.67	35.88	26.33	4.23	**28.2**	82.00
12	**GBHV 242**	8.51	5.30	38.66	24.83	**5.33**	26.3	82.00
13	**GHHV 34/2013**	8.15	5.03	38.20	25.63	4.70	26.2	83.00
14	**GJHV 562**	8.26	4.73	36.65	25.80	4.53	25.2	81.00
15	**GJHV 567**	7.71	4.77	37.15	25.90	4.63	25.9	82.67
16	**GJHV 584**	8.52	4.80	36.01	25.60	4.63	24.8	82.00
17	**GJHV 560**	7.40	4.30	36.86	25.73	4.53	24.5	81.33
18	**GTHV 19/6**	8.17	4.33	34.88	26.00	4.53	25.6	83.33
19	**GTHV 19/7**	7.34	4.97	40.48	24.03	4.77	24.6	83.33
20	**GTHV 18/6**	8.00	4.67	36.80	23.93	4.97	24.6	82.67
21	**GN. Cot. 32 (CC)**	9.15	**6.57**	41.71	26.30	5.07	27.0	**84.00**
22	**G. Cot. 38 (CC)**	8.46	5.13	37.90	24.47	5.23	24.9	81.33
23	**GSHV 223**	7.33	4.97	40.63	25.00	4.60	26.1	83.33
24	**GSHV 224**	9.06	5.70	38.95	26.87	4.80	25.9	82.67
25	**GISV 332**	7.10	4.60	39.04	25.17	4.83	24.2	81.00
26	**GSHV 208**	7.49	4.70	38.66	26.87	**3.60**	26.9	83.33
27	**GJHV 548**	7.93	4.43	36.13	25.33	4.40	**24.0**	81.33
28	**GJHV 568**	8.14	5.07	38.16	25.73	4.83	26.1	81.00
29	**GJHV 534**	7.88	4.17	34.55	26.20	4.73	25.7	82.00
30	**GHHV 60/2013**	8.00	5.00	38.57	25.00	5.30	24.5	81.00
31	**GTHV 18/17**	**9.38**	5.20	35.76	26.17	4.53	25.8	80.67
32	**GTHV 18/19**	8.15	4.53	35.71	26.40	4.03	27.5	81.33
33	**GTHV 15/34**	**6.50**	4.00	37.95	26.30	4.33	25.9	**80.33**
34	**GTHV 15/220**	7.74	4.83	38.66	26.73	4.70	26.7	80.67
35	**GN. Cot. 22 (CC)**	7.18	4.20	36.91	25.67	5.13	26.9	82.33
	Mean	8.00	4.91	37.96	25.77	4.62	26.0	82.03
	Minimum	6.50	3.57	31.75	23.83	3.60	24.0	80.33
	Maximum	9.38	6.57	43.09	27.87	5.33	28.2	84.00
	S. Em. ±	0.32	0.27	1.24	0.54	0.19	0.60	0.64
	C.D. at 5%	0.90	0.75	3.51	1.51	0.53	1.69	1.80
	C.V.%	6.87	9.37	5.67	3.60	7.05	4.00	1.35

Where, SI= Seed index, LI= Lint index, GOT= Ginning out-turn, UHML= Upper half mean length, FF= Fibre fineness, FS= Fibre strength, UI= Uniformity index

CERTIFICATE

This is to certify that I have no objection for supplying to any scientist only one copy or any part of this thesis at a time through reprographic process, if necessary for rendering reference service in a library or documentation centre.

(VARMA KEVAN N.)

Place : SARDARKRUSHINAGAR
Date : 24th DECEMBER, 2021