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# Combining ability studies for fibre quality traits in intra (*G. arboreum* x *G. arboreum*) and interspecific (*G. herbaceum* x *G. arboreum*) crosses of desi cotton

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#### Abstract

The Line x Tester method of analysis was followed involving seven female lines viz., PA 810, PA 828, PA 837, PA 811, PAIG 380, G. Cot. 25 and G. Cot. 17 for study of heterosis for various fibre quality characters at three environments viz., Parbhani, Nanded & Badnapur. The  $F_1$  and their parents were evaluated in randomized block design with three replications, observations were recorded on Fibre length (mm), micronaire ( $\mu$ g/inch), Uniformity ratio (%) and Fibre strength (g/tex). The combining ability analysis was carried out in relation to GCA and SCA. Results were revealed that with regards to quality traits, PA 810 for UHML, PAIG. 380 for micronaire value & fibre strength and PA 811 for uniformity ratio found to be best general combiner for fibre quality traits. The cross PA 828 x Phule Dhanwantary had good specific combining ability effects for upper half mean length and fibre strength, PA 828 x JLA 794 for micronaire, whereas, G. Cot. 25 x AKA 7 for uniformity ratio.

Keywords: Line x Tester, crosses, combining ability, GCA & SCA

# Introduction

Cotton, popularly known as the "White Gold," has long been produced in India. Cotton fabric may be traced back to the Rigveda, which dates from around 4000 B.C. and is not only the birthplace of cotton, but also of the cotton industries. As a result, India holds the distinction of being the first country in the world to domesticate cotton and use its fibre for textile production. Cotton (*Gossypium* sp.) is the most widely grown fibre crop on the country. It is primarily produced as an industrial raw material for the textile and oilseed industries in more than 70 countries across the world. Cotton has a significant part in India's economy, both in terms of directly or indirectly employing about 60 million people and in terms of producing wealth and generating hard currency (Koutu *et al.*, 2012) <sup>[5]</sup>. It is crucial to evaluate a huge number of available germplasm in order to develop superior and heterotic hybrids in cotton. High volume instrument testing is universally acknowledged by the industry and is becoming a requirement in the context of quality assessment, allowing cotton to be marketed more directly on the needs of textile mills rather than the traditional grade, staple and micronaire. As a result, high-quality hybrids and varieties have been developed and accepted.

The analysis of general combining ability and specific combining ability helps in identifying potential parents or inbreds for the production of superior hybrids. The Line x Tester analysis (Kempthorne, 1957)<sup>[6]</sup> is one of the simplest and efficient methods of evaluating large number of inbred/parents for their combining ability. Based on the information from Line x Tester analysis production of commercially viable hybrids is possible. The combining ability studies provide information on the genetic architecture of the parents as well as crosses, which is useful in developing a specific breeding strategy.

# **Material and Methods**

The present investigation on "Combining ability studies for fibre quality traits in intra (*G. arboreum* x *G. arboreum*) and interspecific (*G. herbaceum* x *G. arboreum*) crosses of desi cotton" was conducted at the Department of Agricultural Botany, VNMKV, Parbhani. The experimental material for present investigation consisted of fifteen diverse genotypes. These selected fifteen genotypes possess good amount of variation for fibre length, micronaire value, uniformity ratio & fibre strength. The fifteen genotypes used in the present study were PA 810, PA 828, PA 837, PA 811, PAIG 380, G. Cot. 25 & G. Cot. 17 (Lines) and AKA 7, Phule Dhanwantary, JLA 794, PA 08, PA 402, DLSA 17, AKA 8 and JLA 505 (Testers).

Complete set of entries comprising of 56  $F_{1}$ 's, 7 lines, 8 testers and 3 checks (PKV Suvarna, PKVDH 1 & PA 255) were grown in Randomized Block Design with two replications. The experiment was conducted under rainfed condition at three locations *viz.*, Cotton Research Station, Mahboob Baugh Farm, Parbhani (L<sub>1</sub>), Cotton Research Station, Nanded (L<sub>2</sub>), and KVK, Badnapur (L<sub>3</sub>) during *kharif*, 2020. The sowing of trials was done on 1<sup>st</sup> July, 3<sup>rd</sup> July and 6<sup>th</sup> July, 2020 at L<sub>1</sub>, L<sub>2</sub> and L<sub>3</sub> locations, respectively.

# **Result and Discussion**

it would make more sense to compare mean squares for inferring the predictability ratio to assess the weightage of GCA and SCA effects for the particular character to know its gene action because significance of mean squares for line x tester provides a direct test of significance of dominance variance and additive variance is provided by significance of lines and testers mean squares.

The genotypes, cross, lines, testers and line x testers effects were found significant for the characters studied (Table 1). Similar results were obtained by Choudhary *et al.*, (2017) <sup>[2]</sup>, Chinchane *et al.*, (2018) <sup>[1]</sup>.

Pooled estimates of combining ability effects are tabulated in Table 2.

| Table 1: | Pooled | analysis | of | variance | for | combining | ability |
|----------|--------|----------|----|----------|-----|-----------|---------|
|          |        |          |    |          |     |           |         |

|                                | Df | Mean sum of squares |            |            |          |  |  |
|--------------------------------|----|---------------------|------------|------------|----------|--|--|
| Sr. No                         |    | UHML                | Micronaire | Uniformity | Fibre    |  |  |
|                                |    |                     | value      | ratio      | strength |  |  |
| Replication                    | 1  | 0.03                | 0.00       | 0.03       | 0.02     |  |  |
| Genotypes                      | 70 | 5.14**              | 0.14**     | 5.14**     | 10.68**  |  |  |
| Cross                          | 55 | 3.89**              | 0.11**     | 3.89**     | 10.67**  |  |  |
| Line(c)                        | 6  | 10.83**             | 0.23**     | 10.83**    | 13.80**  |  |  |
| Test(c)                        | 7  | 5.12**              | 0.09**     | 5.12**     | 32.12**  |  |  |
| LXT (c)                        | 42 | 2.69**              | 0.10**     | 2.69**     | 6.65**   |  |  |
| Parent                         | 14 | 10.03               | 0.19       | 10.03      | 6.12     |  |  |
| Line(p)                        | 6  | 17.16               | 0.26       | 17.16      | 6.23     |  |  |
| Test(p)                        | 7  | 3.48                | 0.06       | 3.48       | 3.32     |  |  |
| L(P)vT(P)                      | 1  | 13.07               | 0.64       | 13.07      | 25.06    |  |  |
| CrovsPAR                       | 1  | 5.45                | 0.98       | 5.45       | 75.11    |  |  |
| Error                          | 70 | 0.34                | 0.01       | 0.34       | 0.25     |  |  |
| σ <sup>2</sup> gca             |    | 0.31                | 0.04       | 1.01       | 0.90     |  |  |
| σ <sup>2</sup> sca             |    | 0.96                | 0.05       | 1.57       | 3.71     |  |  |
| $\sigma^2$ gca/ $\sigma^2$ sca |    | 0.32                | 0.80       | 0.63       | 0.26     |  |  |

Table 2: Pooled estimates of GCA effects of parents and SCA effects of crosses studied over three environments

| Sr. No. | Genotype                   | Upper half mean length | Micronaire | Uniformity ratio | Fibre strength |
|---------|----------------------------|------------------------|------------|------------------|----------------|
|         |                            | GCA Lines              |            |                  | <b>_</b>       |
| 1.      | PA 810                     | 1.29 **                | -0.16 **   | 0.72 **          | 1.01 **        |
| 2.      | PA 828                     | -0.58 **               | -0.00      | -1.02 **         | 0.08           |
| 3.      | PA 837                     | 0.56 **                | 0.08 **    | 0.23             | -0.59 **       |
| 4.      | PA 811                     | -0.01                  | 0.01       | 0.79 **          | 0.63 **        |
| 5.      | PAIG 380                   | 0.47 **                | -0.17 **   | 0.76 **          | 1.03 **        |
| 6.      | G. Cot. 25                 | -1.01 **               | 0.12 **    | -1.07 **         | -1.00 **       |
| 7.      | G. Cot. 17                 | -0.72 **               | 0.12 **    | -0.41            | -1.16 **       |
|         |                            | GCA Testers            |            |                  |                |
| 1.      | AKA 7                      | -0.32 *                | -0.05 *    | 0.34             | 1.11 **        |
| 2.      | JLA 794                    | -0.26                  | 0.04       | 0.45             | 0.77 **        |
| 3.      | PA 08                      | -0.27                  | -0.08 **   | 0.52 *           | 0.62 **        |
| 4.      | PA 402                     | -0.37 *                | -0.04      | 0.23             | 1.95 **        |
| 5.      | AKA 8                      | -0.82 **               | 0.01       | 0.17             | 0.70 **        |
| 6.      | Phule Dhanwantary          | 0.98 **                | -0.03      | -0.27            | -1.05 **       |
| 7.      | JLA 505                    | 0.53 **                | -0.02      | -0.89 **         | -1.95 **       |
| 8.      | DLSA 17                    | 0.53 **                | 0.18 **    | -0.55 *          | -2.15 **       |
|         |                            | SCA Crosses            |            |                  |                |
| 1.      | PA 810 X AKA 7             | -0.53                  | -0.06      | -0.41            | 0.57           |
| 2.      | PA 810 X JLA 794           | 0.76                   | 0.11       | 0.17             | -0.79 *        |
| 3.      | PA 810 X PA 08             | -0.43                  | 0.11       | -1.55 *          | -0.65          |
| 4.      | PA 810 X PA 402            | 1.22 **                | -0.12      | -0.35            | -1.18 **       |
| 5.      | PA 810 X AKA 8             | -0.73                  | 0.08       | 0.75             | 1.97 **        |
| 6.      | PA 810 X Phule Dhanwantary | 0.12                   | -0.25 **   | 2.20 **          | 1.38 **        |
| 7.      | PA 810 X JLA 505           | 0.02                   | 0.11       | 0.61             | -0.02          |
| 8.      | PA 810 X DLSA 17           | -0.43                  | 0.02       | -1.42 *          | -1.28 **       |
| 9.      | PA 828 X AKA 7             | 1.74 **                | -0.04      | 0.93             | -0.20          |
| 10.     | PA 828 X JLA 794           | -1.72 **               | -0.41 **   | -1.09            | -3.55 **       |
| 11.     | PA 828 X PA 08             | -2.31 **               | 0.30 **    | -0.76            | 0.39           |
| 12.     | PA 828 X PA 402            | -0.81 *                | -0.16 *    | 0.48             | -2.44 **       |
| 13.     | PA 828 X AKA 8             | 1.04 *                 | 0.21 **    | 0.19             | -0.59          |
| 14.     | PA 828 X Phule Dhanwantary | 2.39 **                | -0.29 **   | 0.58             | 3.37 **        |
| 15.     | PA 828 X JLA 505           | 0.49                   | 0.34 **    | -0.80            | 1.02 **        |
| 16.     | PA 828 X DLSA 17           | -0.81                  | 0.05       | 0.46             | 2.01 **        |
| 17.     | PA 837 X AKA 7             | 0.50                   | 0.29 **    | -0.52            | -5.33 **       |
| 18.     | PA 837 X JLA 794           | 0.69                   | -0.17 *    | 0.86             | 2.41 **        |
| 19.     | PA 837 X PA 08             | 0.56                   | 0.20 **    | 2.24 **          | 1.75 **        |
| 20.     | PA 837 X PA 402            | -2.10 **               | 0.20 **    | 0.43             | 0.77 *         |
| 21.     | PA 837 X AKA 8             | 0.05                   | -0.31 **   | -0.31            | -0.43          |
| 22.     | PA 837 X Phule Dhanwantary | 0.16                   | 0.12       | -1.57 *          | 0.53           |
| 23.     | PA 837 X JLA 505           | -0.00                  | -0.09      | 0.05             | -0.87 *        |

| 24. | PA 837 X DLSA 17               | 0.16     | -0.23 ** | -1.19    | 1.17 **  |
|-----|--------------------------------|----------|----------|----------|----------|
| 25. | PA 811 X AKA 7                 | 0.12     | 0.03     | -1.89 ** | -0.05    |
| 26. | PA 811 X JLA 794               | 0.71     | -0.04    | -0.40    | 2.49 **  |
| 27. | PA 811 X PA 08                 | -1.83 ** | -0.05    | -0.17    | -1.32 ** |
| 28. | PA 811 X PA 402                | 0.52     | 0.18 *   | 0.92     | 0.35     |
| 29. | PA 811 X AKA 8                 | 1.52 **  | -0.04    | -0.12    | -1.45 ** |
| 30. | PA 811 X Phule Dhanwantary     | -1.88 ** | 0.04     | 0.52     | -0.84 *  |
| 31. | PA 811 X JLA 505               | 0.62     | -0.15 *  | -0.21    | 0.96 **  |
| 32. | PA 811 X DLSA 17               | 0.22     | 0.03     | 1.35 *   | -0.15    |
| 33. | PAIG 380 X AKA 7               | -0.46    | -0.15 *  | -0.05    | 0.65     |
| 34. | PAIG 380 X JLA 794             | 0.53     | 0.27 **  | 0.33     | -0.30    |
| 35. | PAIG 380 X PA 08               | 1.90 **  | -0.19 ** | 1.71 **  | 1.44 **  |
| 36. | PAIG 380 X PA 402              | -0.76    | -0.04    | -0.50    | -0.49    |
| 37. | PAIG 380 X AKA 8               | -1.26 ** | 0.24 **  | -1.54 *  | 1.56 **  |
| 38. | PAIG 380 X Phule Dhanwantary   | -0.40    | 0.44 **  | 1.05     | -1.53 ** |
| 39. | PAIG 380 X JLA 505             | -0.06    | -0.30 ** | -0.98    | -1.28 ** |
| 40. | PAIG 380 X DLSA 17             | 0.50     | -0.27 ** | -0.02    | -0.04    |
| 41. | G. Cot. 25 X AKA 7             | -1.08 ** | 0.12     | 2.48 **  | 2.33 **  |
| 42. | G. Cot. 25 X JLA 794           | 0.16     | 0.17 *   | -0.59    | 0.97 **  |
| 43. | G. Cot. 25 X PA 08             | 1.67 **  | -0.09    | -0.16    | -1.64 ** |
| 44. | G. Cot. 25 X PA 402            | 0.52     | -0.16 *  | -1.77 ** | 0.58     |
| 45. | G. Cot. 25 X AKA 8             | 0.47     | -0.21 ** | 0.34     | -0.07    |
| 46. | G. Cot. 25 X Phule Dhanwantary | -0.38    | 0.09     | -1.07    | -2.71 ** |
| 47. | G. Cot. 25 X JLA 505           | -1.13 ** | -0.04    | 1.05     | 0.79 *   |
| 48. | G. Cot. 25 X DLSA 17           | -0.23    | 0.12     | -0.29    | -0.27    |
| 49. | G. Cot. 17 X AKA 7             | -0.28    | -0.19 ** | -0.53    | 2.04 **  |
| 50. | G. Cot. 17 X JLA 794           | -1.13 ** | 0.05     | 0.71     | -1.22 ** |
| 51. | G. Cot. 17 X PA 08             | 0.43     | -0.27 ** | -1.32 *  | 0.03     |
| 52. | G. Cot. 17 X PA 402            | 1.42 **  | 0.11     | 0.78     | 2.40 **  |
| 53. | G. Cot. 17 X AKA 8             | -1.08 ** | 0.04     | 0.68     | -1.00 ** |
| 54. | G. Cot. 17 X Phule Dhanwantary | -0.02    | -0.14 *  | -1.72 ** | -0.20    |
| 55. | G. Cot. 17 X JLA 505           | 0.07     | 0.13     | 0.29     | -0.60    |
| 56. | G. Cot. 17 X DLSA 17           | 0.58     | 0.27 **  | 1.11     | -1.45 ** |
|     | SE±                            |          |          |          |          |
|     | Lines                          | 0.2      | 0.03     | 0.32     | 0.17     |
|     | Tester                         | 0.22     | 0.04     | 0.35     | 0.19     |
|     | Crosses                        | 0.58     | 0.1      | 0.91     | 0.49     |

#### Upper half mean length (mm)

The highest positively significant GCA among lines for improving fibre UHML was observed in PA 810 (1.29). Next highest GCA for bestowing UHML was reported in PA 837 (0.56). Amongst the testers the tester *i.e.* Phule Dhanwantary (0.98) showed significantly positive GCA for contributing towards the progeny. The combination of this highest combiners *i.e.* PA 810 x Phule Dhanwantary (0.12) possessed non-significant positive SCA.

Amongst the crosses highest SCA was found in cross PA 828 x Phule Dhanwantary (2.39). Next highest positive significant SCA was observed in PAIG 380 x PA 08 (1.90). Among the interspecific group, cross G. Cot. 25 x PA 08 (1.67) exhibited significant and positive SCA effects. This cross was followed by G. Cot. 17 x PA 402 (1.42). The predictability ratio for this character was 0.32 indicating the importance of non-additive gene action for improvement of the trait.

The highest SCA effects resulted from poor x good and good x poor general combiners resulted in superior cross combinations due to complementary gene action which has arisen out through both additive and non-additive gene action and these crosses may likely develop through pedigree or heterosis breeding, these results confirmed the findings of Solanke *et al.*, (2015) <sup>[11]</sup>, Patel *et al.*, (2018) <sup>[8]</sup> and Chinchane *et al.*, (2018) <sup>[1]</sup>.

# Micronaire (µg/ inch)

The highest significant GCA in desirable direction among

lines was observed in PAIG 380 (-0.17). Among testers, highest negative significant GCA was observed in PA 08 (-0.08).

Among crosses, highest significant SCA in desirable direction was observed in PA 828 x JLA 794 (-0.41). Cross PA 837 x AKA 8 (-0.31) possesses the second highest significant SCA effect.

Out of 14 interspecific crosses, five exhibited significant and negative SCA effects. The maximum SCA effect was registered by G. Cot. 17 x PA 08 (-0.27) followed by G. Cot. 25 x AKA 8 (-0.21). Predictability ratio for this trait was 0.80 which was very close to unity indicating the equal importance of both additive and non-additive gene action for this trait.

Non additive type of gene action was observed for fibre fineness. Above cited crosses were the combinations of poor x poor general combiners indicating that, selection is not only based on mean performance and GCA effects but also on SCA effects of cross combinations. Similar results were shown by Solanke *et al.*, (2015) <sup>[11]</sup>, Reddy *et al.*, (2016) <sup>[10]</sup> and Patel *et al.*, (2018) <sup>[8]</sup>.

# Uniformity index (%)

Among lines highest positively significant GCA for bestowing fibre uniformity was imparted by PA 811 (0.79). PAIG 380 (0.76) was the second largest line with high GCA. Among the testers, highest positive significant GCA for fibre uniformity was reported in PA 08 (0.52). The combination of two highest combiners *i.e.* PA 811 x PA 08 (-0.17) showed non-significant negative SCA.

Among crosses, highest positively significant SCA was reported in G. Cot. 25 x AKA 7 (2.48). Next highest SCA was observed in PA 837 x PA 08 (2.24) and PA 810 x Phule Dhanwantary (2.20). Among the interspecific crosses, only one cross G. Cot. 25 x AKA 7 (2.48) exhibited significant and positive SCA effects in pooled analysis.

The predictability ratio for this trait was 0.63 which indicate the importance of non-additive gene action for the improvement of this character.

The highest SCA effects resulted from poor x poor, poor x good and good x poor parents reporting that additive and non-additive gene action is responsible for uniformity index, which substantiate the operation of non-additive gene action be explored in one, that indiacated the choice of parents for crossing programme should not based only on the per se performace and GCA effects but also on the SCA effects of cross combinations and these crosses may likely develop through pedigree or heterosis breeding, These findings were in agreement with Rajamani *et al.*, (2014) <sup>[9]</sup>, Reddy *et al.*, (2016) <sup>[10]</sup> and Naik *et al.*, (2019) <sup>[7]</sup>.

#### Fibre strength (g/tex)

Among lines highest positive significant GCA for improving fibre strength was bestowed by PAIG 380 (1.03). It was accompanied by PA 810 (1.01). Among testers, highest positive significant GCA was observed in PA 402 (1.95). It was followed by AKA 7 (1.11) and JLA 794 (0.77). Among the crosses, highest positive significant SCA was reported in PA 828 x Phule Dhanwantary (3.37). Next highest SCA was observed in PA 811 x JLA 794 (2.49).

Another cross with significantly positive SCA was reported by PA 837 x JLA 794 (2.41). Among the interspecific group, out of 14 crosses, five crosses recorded significantly positive SCA in pooled analysis. Cross G. Cot. 17 x PA 402 (2.40), G. Cot. 25 x AKA 7 (2.33) and G. Cot. 17 x AKA 7 (2.04) exhibited highly significant and positive SCA effects for this trait in all the locations as well as in pooled analysis. The predictability ratio for this trait was 0.26 which indicate the importance of non-additive gene action in the improvement of this trait.

The good general combining parents when crossed do not always result into crosses having high SCA effect. Similar findings have been reported by Khokar *et al.*, (2018) <sup>[4]</sup>, Patel *et al.*, (2018) <sup>[8]</sup> and Gnanasekaran *et al.*, (2020) <sup>[3]</sup>. Above cited crosses were the combinations of poor x poor, good x good and poor x good general combiners and could be exploited for practical breeding which is expected to throw stable performing transgressive segregants carrying fixable genes. The SCA effects represent the dominance and epistatic effects and can be related to heterosis.

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