GENETICS OF EARLINESS IN *G. hirsutum* L. UNDER DIFFERENT NITROGEN LEVELS

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Development of earliness in cotton plant without sacrificing yield is a prime objective of cotton breeders. Early maturing genotypes provide more efficient wheat-cotton-wheat rotation, also provide escape mechanism from biotic and abiotic stresses, reduce the input resources and extend the period for harvesting and ginning operations. To examine the genetic diversity of earliness in *G. hirsutum* L., 45 diverse genotypes collected from different research institutes of Punjab, were screened for their earliness related traits and seed cotton yield (SCY) in field conditions. Index scores and principal component analysis separately generated three distinct groups on the basis of their maturity viz; late maturing and high yielding group 1, early maturing group 3, and group 2 had both types of genotypes. From these groups, six high yielding early maturing genotypes (FH-682, FH-2015, MALMAL, MNH-147, PB-900, VH-300) were selected as lines, and hybridized with five late maturing selected genotypes (B-557, BH-121, FH-941, MNH-93, MS-40) as male parents in line × tester fashion. General and specific combining ability effects of parents, on earliness related traits and SCY, were studied by planting the parents and their crosses in the field under three nitrogen levels (60, 120 and 180 kg/ha). The experimental design was a split plot arrangement. The L × T analysis of combining ability resulted significant variation among genotypes (parents and crosses) for all studied traits. The gca and sca variances and their ratio exhibited pre-dominance of non-additive gene action for almost all studied traits under all of three nitrogen levels, except for SCY (under 60 kg/ha). The GCA effects revealed the line, MNH-147 as best combiner for majority of earliness related traits and FH-682 was observed best general combiner for SCY and earliness index (EI) under all the three nitrogen levels. Best hybrid combinations identified were MALMAL × MS-40 for node number for first fruiting branch (NNFFB), FH-682 × MS-40 for days to flowering (DTF) and FH-682 × MNH-93 for EI. A few combinations, like FH-682 × MNH-93, FH-2015 × B-557, MNH-147 × MS-40, PB-900 × MNH-93 and VH-300 × FH-941, having harmonious combination of some earliness related traits along with yield traits, have also been identified under the three nitrogen levels. Higher proportion of dominance variance in all the studied traits suggested delayed selection or these crosses depicted remarkable potential to be exploited through heterosis breeding.
Keywords: Early maturing high yielding; PCA, index scoring, combining ability, cotton.

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is the mainstay of economy of Pakistan. It is a major cash crop of the country and fetches about 60 percent of total foreign exchange earnings through export of its fibre and finished products. It accounts for 4.1 percent of value added in agriculture and 0.8 percent of GDP (Govt. of Pakistan, 2020). It is grown on an extensive area in the province of Punjab with its optimum sowing time mid of April through May and stays in the field till the months of November and December. In this way it overlaps the proper sowing time of wheat (October and mid of November), the most important food crop of Pakistan. It is reported that sowing of wheat after November 10 results in a loss @ 42 kg/ha/day in grain yield (Khan, 2003). To avoid this negative effect of cotton crop on wheat, it is imperative to develop early maturing cotton varieties, which may vacate the fields for timely sowing of wheat. Therefore, development of early maturing varieties has become one of

the major objectives of cotton breeders these days (Azhar *et al.,* 2007), because early maturing cotton varieties will make wheat-cotton-wheat rotation system more efficient so that high yield of wheat may be obtained. Besides promoting production of wheat crop, the short duration cotton varieties have been observed to possess some good features, for example, they manage well to soil moisture stress, escape losses from the late season insect injuries (*Heliothis* species and whitefly) (Yonas *et al*., 2019; Wazeer *et al*., 2020) and extend the season for harvesting and ginning operations.
The previous work indicates that various morphological plant characters have been used as reliable indicators for determining earliness in cotton. Godoy and Palomo (1999a) have reported days to first square, vertical flowering interval and boll maturation period as important indicators for earliness in cotton whilst Panhwar *et al.,* (2002) observed number of node for first sympodial branch and days to first flower. Similarly, Iqbal *et al.,* (2003) mentioned less number

of monopodial branches and days taken to open first boll as reliable parameters for early maturity in cotton.

In addition, many physiological, agronomic, and management factors affect plant responses as reported by Pandey *et al*. (2017). But crop production can be improved through improving the metabolic activity and nutritional status of crop plants (Sawan *et al.,* 2006). Among them chemical fertilizers, particularly nitrogenous fertilizers, are one of the greatest production inputs. Nitrogen is essential nutrient in creating the plant dry matter as well as many energy rich compounds that regulate photosynthesis and plant protection. The plant genetic characters and their interaction with the environments affect crop maturity in cotton. It has been reported that plant maturity is affected by altering time and dosage of nitrogenous fertilizers (Pettigrew *et al.,* 1996), phosphorus (Saleem *et al.,* 2010) and potassium fertilizer (Kaleem *et al.,* 2009).

Different biometrical techniques, have been applied by the breeders to generate useful information for crop improvement programmes, for example, Principal component analysis (PCA) is a highly effective technique which works by comparing difference among the genotypes and one of the most frequently used multivariate data analysing method. Maitra and Yan (2008) reported that PCA is a traditional multivariate statistical method commonly used to reduce the number of predictive variables. PCA is used to reduce data for explaining the association between two or more characters. It can be used to summarize the data without losing too much information in the process. In crop breeding programs it is widely used to group the large scale of genotypes on the basis of different traits.

These analyses have been used successfully by different breeders to assess the variability in various crops. Saeed *et al*., (2013) used PCA and showed four PCs having eigen values >1, and cluster analysis grouped 79 cotton genotypes in four divergent groups. Ahmed *et al*., (2012) reported grouping of 39 cotton genotypes into five clusters to study their genetic diversity. Similarly, Yan (1999) used PCA to check genetic diversity in wheat. He also concluded that it is a very useful graphical technique for plant breeders.

To identify the best performing line and the lines which can be used as parents in future are two principal objectives considering in most of the crop breeding programs (Oakey, *et al.,* 2006). Selection of the best performing lines for required traits are based on conducting multi-environment trials following statistical analysis. A well-designed trial accompanied by statistical analysis discovers genetic and environmental influences. Line × tester mating designs (Sprague and Tatum, 1942) can be used to select the parental lines. It is used to partition the genetic influences into additive and non-additive components (Oakey *et al*., 2006).

Combining ability analysis provides information for the selection of parents as well as the nature and magnitude of gene action involved in the expression of traits. Parents showing a high average combining ability in crosses are considered to have good general combining ability (GCA) while if their potential to combine well is bounded to a particular cross, they are considered to have good specific combining ability (SCA). GCA is important for selection and hybridization programmes, whereas SCA is useful for hybrid crop development. Therefore, genetic information regarding the selected parents and their hybrids through combining ability analysis becomes an important objective of cotton breeders. Soomro (2007), and Zhen *et al*., (2012) found the significance of gca and sca variances, suggesting importance of additive as well as dominant genes. They reported predominance of additive gene action if the gca/sca ratio was greater than unity. Basbag *et al.,* (2007) indicated the importance of additive genes in the inheritance of days to flowering and node number for first fruiting branch. Whereas, Khan *et al.,* (2005) and Panhwar (2007) observed higher sca than gca indicating preponderance of non-additive (dominance type of) genes controlling yield related traits i.e., number of bolls, seed cotton yield and lint percentage. In contrast Soomro (2007) found additive type of gene actions controlling these traits. Godoy and Palomo, (1999a) and Chen *et al*., (1991) suggested DTF as an important determinant of earliness.

For this purpose, data regarding earliness related traits of 45 cotton genotypes were subjected to statistical analysis to estimate variability for early maturity in available germplasm and genetic basis of earliness related traits. The data of selected parents along with their l × t crosses (F_1) were subjected to line × tester analysis to find/assess their genetic control (combining abilities) under different nitrogen levels.

MATERIALS AND METHODS

The study was conducted in the experimental farm and green house of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during 2011-2014.

Seeds of 45 diverse cotton accessions/lines/varieties (Table 2) used in the study were collected from germplasm available at Cotton Research Station, Ayub Agricultural Research Institute, Faisalabad; Cotton Research Institute, Multan; Cotton Research station, Vehari; Central Cotton Research Institute, Multan and Department of Plant Breeding & Genetics, University of Agriculture, Faisalabad, to identify the early and late maturing parents for the experiment.

Seeds of each genotype were soaked in water for a night and sown in the field next morning keeping 30 cm plant to plant and 75 cm row to row distance in randomized complete block design having three replications. The crop was continuously monitored and all the recommended agronomic and protection measures were adopted for having a normal

crop. During the growing phase of the plants and at the time of maturity of the crop the data for the following traits were recorded on ten guarded plants as follows:

Days to squaring (DTS): It was determined by counting the number of days from sowing of seeds to appearance of first eye visible square on each plant.

Days to flowering (DTF): Number of days from planting to appearance of first flower on each plant was recorded, and then all plants data were averaged for each entry (row) in a replication.

Number of nodes for first fruiting branch (NNFFB): Average node number of first fruiting branch was determined by counting number of nodes above cotyledonary node (zero node) along main stem, till the one that gave rise to first fruiting branch on the plants. Recorded data were averaged for each accession (variety/line) in each replication.

Seed cotton yield (SCY): Cotton plant is indeterminate by nature, therefore, total seed cotton harvest of a plant was completed by making three picks, (first picking was done after 110 days, second 140 days and last 170 days of sowing), which were mixed and weighed with an electronic balance to obtain total produce of plant. The average yield of each variety/line in each replication was calculated.

Earliness index (EI): Earliness index was determined by weighing seed cotton of first pick (after 110 days) and expressing it as a percentage of total seed cotton harvested from all picks. This measurement was recorded in three replications for each entry.

$$\text{Earliness index} = \frac{\text{Wt. of seed cotton in first picking} \times 100}{\text{Wt. of seed cotton of all pickings}}$$

The mean data for all these attributes were subjected to analysis of variance (ANOVA) following Steel *et al.,* (1997), to test the significance of variation among the genotypes. The contribution of plant traits to genetic diversity and to select potential genotypes regarding maturity (Early and late), index scores (Anderson, 1957) and Principal Component Analysis as used by Yan (1999) were applied using Statistica (v8.0) software (http://www.statsoft.com).

Development of plant material for genetic studies: Through screening of germplasm, eleven parents were selected on the basis of agronomic plant characters, six high yielding early maturing genotypes were selected as female parents for crossing with five late maturing genotypes, which were selected as male parents.

Seeds of six early maturing lines/varieties i.e., FH-682, FH-2015, MALMAL, MNH-147, PB-900, VH-300 and five late maturing i.e. B-557, BH-121, FH-941, MNH-93 and MS-40, were soaked overnight and then sown in pots, which were placed in glass house during November 2011. At the start of flowering in Jan-Feb 2012, few early flowers of each parent were selfed to obtain genetic purity in parental stock. Parents were hybridized keeping early maturing cultivars as females (lines) and late maturing as male (testers). To produce sufficient quantity of F_1 seed, numerous pollinations were attempted.

Assessment of genetic material for early maturity: Genetic variability for early maturity in *G. hirsutum* L. was studied in field during May 2013. The seeds of 41 entries (30 F_1 hybrids along with their eleven parents (six lines and five testers)) were soaked overnight before sowing. Two seeds of each entry were sown in single chamber of seedling trays in peat moss. After seedling's hardening (7-10 days old seedlings), these were transplanted in field in split plot design replicated thrice. To check the response of early maturity to Nitrogen, this experiment was conducted under three different nitrogen levels i.e., Nitrogen supplement level $N_o = 60$ kg/ha, whereas, $N_1 = 120$ kg/ha and $N_2 = 180$ kg/ha. Nitrogen in the form of CH_4N_2O (urea) having 46% N was applied in three split doses, first at bed preparation, second at the onset of flowering and third at boll filling stage.

At Maturity, ten guarded plants per entry per replication were tagged for recording data. Data were recorded on individual plant basis, later means were computed for all the lines. Methodology for recording the data was same as taken for screening germplasm.

Statistical analysis: Means of collected data regarding all the characters in each replication under three nitrogen regimes were subjected to ANOVA (Steel *et al.,* 1997). L×T technique (Kempthorne, 1957) was used to figure out the gca and sca effects of parents and their crosses for plant characters under study.

RESULTS

Assessment of variation in germplasm for the traits: The mean squares of genotypes indicated the significant differences for all the traits (Table 1). In accordance to mean values detailed results of each of characters are given here:

Table 1. Mean square values of different plant traits.

Source of variation	Degree of freedom	Days to squaring	Days to flowering	Node number of first fruiting branch	Seed cotton yield	Earliness index
Replications	2	59.13	0.013	9.40	1796.59	284.88
Genotypes	44	3.83**	9.310**	1.91**	4693.19**	825.43**
Error	88	1.66	0.010	0.43	1926.62	216.98
Total	134	-	-	-	-	-

**, denotes differences significant at 1% probability level

Table 2. Mean values and index scores (parenthesis) of 45 genotypes of *Gossypium hirsutum* L. for different plant traits.

Sr.	Genotypes	Days to squaring	Days to flowering	Node no. of first fruiting branch	Seed cotton yield	Earliness index %	Total score
1	B-557	40.17 (4)	50.83 (18)	8.23 (7)	172.82 (43)	17.56 (13)	85
2	MS-40	40.00 (6)	52.83 (4)	9.72 (2)	103.33 (26)	0.00 (1)	39
3	GR-156	40.11 (5)	52.17 (5)	8.80 (3)	60.45 (6)	16.05 (9)	28
4	MNH-93	39.56 (11)	48.17 (28)	8.54 (5)	100.50 (23)	18.61 (15)	82
5	MNH-147	39.43 (14)	48.97 (26)	7.64 (16)	120.42 (33)	31.99 (25)	114
6	MNH-554	40.83 (2)	50.03 (21)	8.59 (4)	124.27 (34)	34.09 (30)	91
7	MNH-738	37.63 (37)	49.00 (25)	6.70 (33)	61.58 (7)	33.00 (26)	128
8	MNH-786	39.14 (17)	47.97 (32)	7.50 (19)	71.02 (10)	4.17 (3)	81
9	FH-207	39.61 (8)	51.90 (12)	7.71 (14)	186.15 (45)	43.44 (36)	115
10	FH-900	38.56 (25)	48.93 (27)	7.51 (18)	139.05 (37)	20.45 (17)	124
11	FH-901	37.72 (36)	51.07 (13)	6.96 (32)	82.98 (17)	6.27 (5)	103
12	FH-941	38.92 (19)	53.03 (2)	7.39 (21)	108.90 (29)	20.96 (18)	89
13	FH-2015	37.45 (39)	50.03 (21)	6.46 (38)	88.42 (20)	49.48 (38)	159
14	RED ACALA	37.79 (33)	52.96 (3)	7.11 (28)	91.30 (21)	23.83 (19)	104
15	VH-256	38.36 (29)	47.10 (33)	7.16 (27)	147.10 (39)	26.42 (23)	151
16	VH-281	38.56 (25)	49.03 (24)	7.10 (29)	80.18 (14)	34.18 (31)	123
17	VH-289	38.56 (25)	51.05 (14)	7.21 (24)	162.73 (41)	36.50 (33)	137
18	VH-297	43.00 (1)	48.07 (29)	10.00 (1)	47.20 (4)	16.95 (11)	46
19	VH-300	37.79 (34)	47.03 (34)	7.77 (11)	101.05 (24)	48.56 (37)	140
20	BH-121	40.25 (3)	52.02 (10)	8.50 (6)	180.50 (44)	0.00 (1)	64
21	BH-123	39.46 (12)	51.05 (15)	7.54 (17)	142.83 (38)	0.00 (1)	83
22	BH-147	39.83 (7)	50.07 (20)	8.03 (8)	69.93 (9)	23.97 (20)	64
23	BH-162	38.80 (20)	52.03 (8)	7.81 (10)	54.85 (5)	0.00 (1)	44
24	CIM-109	38.76 (22)	52.03 (9)	7.24 (23)	84.13 (18)	15.38 (8)	80
25	CIM-240	38.55 (26)	49.04 (23)	7.19 (26)	115.97 (32)	5.51 (4)	111
26	CIM-443	38.39 (28)	48.01 (31)	6.98 (31)	40.54 (3)	33.17 (27)	120
27	CIM-473	38.77 (21)	52.07 (6)	7.60 (16)	152.69 (40)	9.06 (6)	89
28	CIM-496	37.44 (40)	54.03 (1)	7.33 (22)	81.33 (15)	19.16 (16)	94
29	FH-87	38.28 (30)	52.07 (6)	7.21 (24)	102.48 (25)	1.64 (2)	87
30	FH-632	37.94 (32)	52.04 (7)	7.07 (30)	115.87 (31)	35.47 (32)	132
31	FH-682	39.59 (9)	51.04 (16)	7.96 (9)	136.12 (36)	43.36 (35)	105
32	MS-39	39.28 (15)	50.10 (19)	7.46 (20)	71.55 (11)	0.00 (1)	66
33	MS-84	39.58 (10)	50.10 (19)	7.69 (15)	170.35 (42)	27.17 (24)	110
34	MNH-506	39.20 (16)	49.03 (24)	7.33 (22)	130.12 (35)	16.52 (10)	107
35	MNH-700	38.12 (31)	50.02 (22)	7.20 (25)	78.10 (13)	26.14 (22)	113
36	NIAB-111	38.40 (27)	52.03 (8)	7.76 (12)	112.46 (30)	24.93 (21)	98
37	NIAB-999	39.44 (13)	48.03 (30)	6.58 (34)	93.10 (22)	18.16 (14)	113
38	PB-38	36.76 (42)	49.03 (24)	6.07 (39)	61.90 (8)	11.10 (7)	120
39	PB-39	37.47 (38)	49.03 (24)	6.70 (33)	87.68 (19)	0.00 (1)	115
40	PB-899	37.35 (41)	50.03 (21)	6.54 (36)	107.42 (28)	17.16 (12)	138
41	PB-900	38.76 (23)	48.07 (29)	7.50 (19)	72.60 (12)	64.95 (40)	123
42	CIM-506	38.61 (24)	49.03 (24)	7.10 (29)	22.73 (1)	33.33 (28)	106
43	CIM-573	37.44 (40)	48.93 (27)	6.52 (37)	104.38 (27)	58.23 (39)	170
44	CIM-608	39.01 (18)	52.00 (11)	7.74 (13)	27.63 (2)	33.33 (29)	73
45	MALMAL	37.73 (35)	51.02 (17)	6.56 (35)	82.58 (16)	41.49 (34)	137

***Days to squaring*:** Days to squaring in 45 lines ranged from 36.76 to 43.00 days with a mean value of 38.85 days (Table 2). In PB-38, first square appeared after 36.76 days indicating it as early maturing, followed by PB-899, CIM-573, CIM-496 and FH-2015 with 37.35, 37.44, 37.44 and 37.45 days respectively. The line VH-297 produced squares in 43.00 days thus indicated as late maturing and was followed by MNH-554, BH-121, B-557 and GR-156 taking 40.83, 40.25, 40.17 and 40.11 days in this connection.

According to index scoring technique of Anderson (1957), the highest score was allotted to the line showing lowest number of days to square, whereas, the one showing highest

number of days to square was given the lowest score. The scoring was stared from 1 which was given to the line taking maximum number of days and it increased as the average number of days to square decreases in the lines. In the present studies the line VH-297 which took maximum number of days to square was given 1 (late maturing). It was followed by MNH-554 which got 2, BH-121 received 3, GR-156 got 4 and so on. For similar values the scoring was kept the same. Similarly, the line PB-38 which took the minimum days to square scored 42 (earliest).

Days to flowering: Days to flowering in the genotypes ranged from 47.03 to 54.03 days with mean of 50.24, (Table 2). The varieties, VH-300, VH-256, MNH-786, CIM-443, NIAB-999 and PB-900 took relatively minimum number of days i.e., 47.03, 47.10, 47.97, 48.01, 48.03 and 48.07 for producing first flower on plant, therefore, considered as early maturing. In contrast, CIM- 496, FH-941, RED ACALA, MS-40, GR-156 and CIM-473 took 54.03, 53.03, 52.96, 52.83, 52.17 and 52.07 days respectively were, therefore, categorized in late maturing.

On the basis of average number of days to flowering, scoring was done similarly as in case of days to squaring. Genotypes were scored from 1-34. Score remained same for similar mean values. Line CIM-496 started flowering in maximum number of days, therefore, it was given 1, followed by FH-941 (2), RED ACALA (3), MS-40 (4) and so on. Whereas, VH-300 got 34 scoring value as it produced flower in minimum number of days.

Node for first fruiting branch: It ranged from 6.07 to 10 with a mean value of 7.49 (Table 2). Node number for first fruiting branch was minimum in PB-38 (6.07) indicating it as early maturing variety. Similarly, FH-2015, CIM-573, PB-899, MALMAL, NIAB-999 and PB-39 with 6.46, 6.52, 6.54, 6.56, 6.58 and 6.7 mean values respectively, found to be early maturing. Whilst VH-297 developed first fruiting branch on higher node (10.00) followed by MS-40, GR-156, MNH-554, MNH-93, BH-121 and B-557 with node number of 9.72, 8.80, 8.59, 8.54, 8.50 and 8.23 respectively, were observed as late maturing.

As the first fruiting branch developed on higher node number in VH-297, 1 score was given to it, followed by MS-40, GR-156, MNH-554, by allotting 2, 3, 4 and so on. The highest score number 39 was assigned to PB-38 (6.07) which produced first fruiting branch on lowest node number, indicating it as early maturing.

Seed cotton yield: The mean values for seed cotton yield ranged from 22.73 to 186.15 g (Table 2). FH-207 produced maximum seed cotton yield i.e., 186.15 g followed by BH-121, B-557, MS-84, VH-289, CIM-473 and VH-256 which produced 180.5, 172.82, 170.35, 162.33, 152.69, and 147.10 g respectively. However, CIM-506 and CIM-608 produced lowest weight of seed cotton i.e., 22.73 and 27.63 g, respectively.

In scoring a genotype for seed cotton yield, lowest score was allotted to a line having lowest seed cotton weight, it increased as the average weight increased in lines therefore highest score was given to a line having maximum SCY. In present studies, lowest score i.e., unity (1) was assigned to CIM-506 (22.73 g) for having lowest weight of seed cotton, followed by CIM-608 (2), CIM-443 (3), VH-297 (4) and so on. Whilst highest score i.e., 45 was allotted to FH-207 due to higher yield (186.15 g).

Earliness index: Earliness index in 45 varieties ranged from zero (0%) to 64.95% with a mean value of 23.15% (Table 2). Earliness index of BH-121, BH-123, BH-162, MS-39, MS-40 and PB-39 were lowest i.e., Zero percent (0%) followed by FH-87 which had 1.64 % earliness index, indicating that these were late maturing varieties. Whilst cultivar PB-900 (64.95 %) showed highest percentage of earliness index, revealing to be early maturing, followed by CIM-573, FH-2015, VH-300, FH-207, FH-682, and MALMAL with 58.23, 49.48, 48.56, 43.44, 43.36 and 41.49 % respectively.

On the basis of average earliness index, scoring was done similarly as in case of seed cotton yield. The lines BH-121, BH-123, BH-162, MS-39, MS-40, and PB-39 which showed zero (0%) earliness indices were scored as 1, followed by FH-87 (1.64%) which got 2, MNH-786 received 3, CIM-240 got 4 and so on. Similarly, the line PB-900 scored the value of 40 showing the highest earliness index.

Principal component analysis (PCA): To assess diversity and grouping pattern of the germplasm, mean data were subjected to PCA. The criterion established by Kaiser (1960) for significance of the eigenvalues, was used to select the statistically significant principal components (PCs). The principal components exhibiting the eigenvalues greater than one were considered as significant. Out of five principal components, the first two showed eigenvalues greater than one (significant) (Table 3). The first two PCs cumulatively showed 64.67% variation. The first PC accounted for 39.79% of the variance and second for 24.88%.

Table 3. Principal component analysis

	PC1	PC2	PC3	PC4	PC5
Eigen values	1.99	1.24	0.98	0.69	0.09
Variability	39.79	24.88	19.64	13.84	1.85
Cumulative %	39.79	64.67	84.31	98.15	100.00

Biplot: The PCA biplot (Fig. 1) based on 1st and 2nd component factors of five traits showed groupings of 45 genotypes, only few cultivars were grouped in the centre while the remaining scattered in all of four coordinates away from centre and gave different groups of cultivars. The cultivars which were located close to centre, showed less genetic diversity for example FH-900, MNH-700, CIM-506. In contrast, CIM-496, BH- 121, MNH-738, MS-40, PB-900

and VH-300 were found away from the origin showing their broad genetic base.

Principal component analysis is also helpful in selecting diverse parents for hybridization and other plant breeding techniques. Thus, PCA plot confirmed the information generated by scoring index.
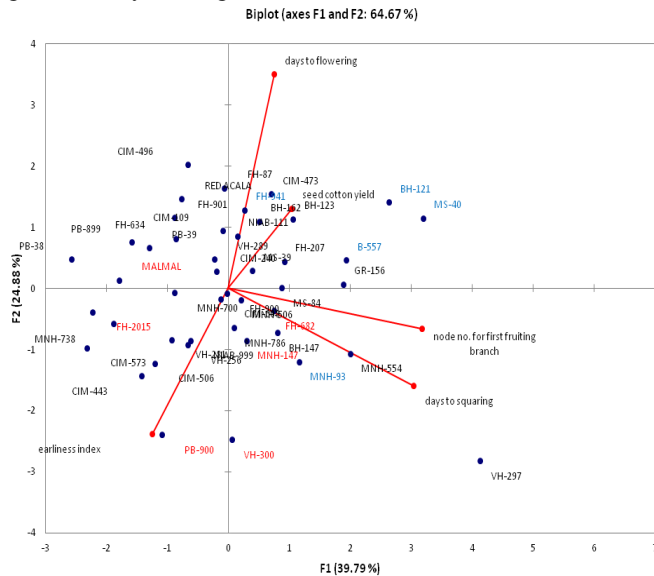

Figure 1. Principal Component's biplot of 45 cotton germplasm lines

Genetic analysis of the traits under different nitrogen levels

Pooled analysis of variance: The data for all the studied traits except days to squaring were subjected to pooled ANOVA and is presented in Table 4. Days to squaring was omitted as Basbag *et al.,* (2007) and Godoy and Palomo, (1999a), reported that it is not an authentic indicator to measure early maturity in cotton. Mean squares from ANOVA of four traits of 41 genotypes were evaluated under three levels of nitrogen, which showed highly significant differences (P≤ 0.01) among treatments effects and genotypes. However, the interactions effects were observed to be non significant in majority of the case except earliness index, where it was observed to be highly significant (P≤ 0.01). These results allowed to perform separate analysis for each environment (60 kg/ha, 120 kg/ha and 180 kg/ha of nitrogen) for each plant parameter. The analysis of variance following line × tester technique displayed significant variation among cotton genotypes (parents, crosses, l × t) for all traits (Table 5).

Under all of three Nitrogen levels, genotypes revealed highly significant (P≤ 0.01) differences for all the studied character except for SCY (under 60 kg/ha N) that showed significant differences. Mean squares of parents (due to gca effects) for all traits were highly significant (P≤0.01), whilst genotypes for SCY (under 120 kg/ha N) displayed significant (P≤0.05)

Table 4. Pooled analysis of variance

S.O.V.	d.f.	NNFFB	DTF	SCY	EI
Replications	2	1.20^{ns}	24.06^{ns}	50.03^{ns}	0.39^{ns}
Main effects					
Treatments (N)	2	64.45***	1103.67***	50679.44***	1728.19***
Genotypes	40	5.91***	144.52***	394.31***	581.52***
Interaction					
Treatment × Genotype	80	0.09^{ns}	38.94^{ns}	113.37^{ns}	7.64***
Error	244	0.42	31.13	98.59	4.05
Total	368				

Note: **: highly significant, *: significant , ^{ns} : non significant, NNFFB: node number for first fruiting branch, DTF: Days to flowering, SCY: Seed cotton yield and EI: earliness index

Table 5. Mean squares for different plant traits of *G. hirsutum* L. under different nitrogen levels.

Source of Variation	d.f.	NNFFB			DTF			SCY			EI		
		N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha
Replications	2	0.19ns	0.35ns	0.779^{ns}	20.35ns	5.60^{ns}	21.85^{ns}	31.66^{ns}	146.83^{ns}	168.38^{ns}	4.99^{ns}	5.18^{ns}	0.73^{ns}
Treatments	40	1.71**	2.05**	2.343**	58.28**	75.14**	88.98**	124.44*	212.65**	283.97**	224.93**	178.20**	193.78**
Parents$_{gca}$(P)	10	1.53**	1.86**	1.95**	44.75**	44.44^{ns}	50.08ns	256.16**	256.63*	405.54**	296.28**	256.83**	320.73**
P vs Crosses	1	0.24ns	1.24ns	1.84^{ns}	1.51^{ns}	1.23^{ns}	93.03ns	132.48^{ns}	99.11^{ns}	0.64^{ns}	171.71**	23.56**	53.65**
Crosses$_{sca}$	29	1.83**	2.15**	2.50**	64.90**	88.28**	102.25**	78.74**	201.40*	251.81**	202.16**	156.42**	154.84**
Lines (L)	5	5.41**	7.00**	8.05**	103.44**	42.30^{ns}	84.99**	171.98*	163.17^{ns}	136.03^{ns}	879.39**	617.65**	607.03**
Testers (T)	4	2.08**	2.39**	2.42**	17.26^{ns}	111.17*	150.24**	18.99^{ns}	85.42^{ns}	552.58**	4.05^{ns}	10.08*	3.19^{ns}
L × T	20	0.89**	0.89*	1.13*	64.79**	95.19**	96.07**	67.38^{ns}	234.16**	220.61*	72.48**	70.37**	72.13**
Error	80	0.31	0.45	0.53	16.05	35.59	42.71	68.02	105.79	119.46	4.59	3.11	4.41
Total	122												

**: highly significant, *: significant, ^{ns}: non significant, NNFFB: node number for first fruiting branch, DTF: Days to flowering, SCY: Seed cotton yield and EI: earliness index

differences, however, for DTF (under 120 kg/ha and 180 kg/ha N) were non-significant (P≥0.05). Parents vs. crosses, revealed highly significant differences for EI only, whilst mean squares due to parents vs. crosses were non-significant for all other traits.

The results revealed that mean squares of crosses (sca effects) for all of the earliness related traits were highly significant except SCY where it is significant at 120 kg/ha N and non-significant at 60 kg/ha N. Lines showed highly significant differences for NNFFB, DTF (under 60 kg/ha N only) and for EI, and similarly testers also differed significantly for NNFFB, DTF (under 120 and 180 kg/ha N), SCY (under 180 kg/ha N) and EI (under 120 kg/ha N). Interaction of lines and testers revealed highly significant differences for all the traits except NNFFB (under 120 kg and 180 kg nitrogen per ha) and SCY (under 180 kg/ha N) where the variation was significant differed, whist, non-significant (P≥ 0.05) for SCY (under 60kg/ha).

Estimation of Genetic Components of Variation: The variance due to specific combining ability (σ^2 sca) was greater than variance due to general combining ability (σ^2 gca) for all the traits except SCY under 60 kg/ha N only (Table 6). It indicated the preponderance of nonadditive genes under all the nitrogen levels. The negative sign

suggested the direction of dominance towards lower parent. The ratio of variance due to general to specific combining ability (σ^2 gca / σ^2 sca) was greater than unity for SCY (under 60 kg/ha N), signified the importance of additive genes for this trait only.

General Combining ability effects: For early maturity in *G. hirsutum* L., short stature plants with lower NNFFB and less DTF are important because plants with higher NNFFB were late maturing. Therefore, combining ability effects in negative direction are preferred. Accordingly, Under 60 kg/ha of nitrogen, comparison of combining ability estimates revealed that MNH-147 (-0.90) may, therefore, be the best general combiner for NNFFB followed by MALMAL (-0.55) (Table 7). Among testers, MNH-93 was good general combiner, followed by FH-941 for NNFFB having gca effect of -0.43 and -0.24 respectively. Under 120 and 180 kg/ha of nitrogen, MNH-147 was best general combiner. Similarly, among lines, FH-2015, FH-682 and PB-900 with negative values of -3.18, -2.52 and -.0.80 respectively were observed to be better female parents for DTF as compared to others. Among the testers, B-557 and BH-121 with the value -1.57 and -0.22 respectively had highest negative gca values. Whereas, MNH-147 (-2.21 and -3.36) was good general combiner line under 120 and 180 kg/ha of nitrogen, however

Table 6. Genetic components of variation for different plant traits in *G. hirsutum* L. under different nitrogen levels.

Genetic Components	NNFFB			DTF			SCY			EI		
	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha
$\sigma^2{}_{gca}$	0.26	0.35	0.38	0.0300	-1.90	1.45	3.12	-8.98	8.56	8.89	23.60	22.68
$\sigma^2{}_{sca}$	0.77	0.59	0.79	65.0000	79.47	72.35	-0.85	171.15	134.86	90.52	89.69	90.30
$\sigma^2{}_{A}$	0.52	0.69	0.75	0.0600	-3.79	2.90	6.23	-17.15	17.12	17.78	47.19	45.37
$\sigma^2{}_{D}$	0.77	0.59	0.79	65.0000	79.47	72.35	-0.85	171.17	134.86	90.52	89.69	90.30
$\sigma^2{}_{gca}/ \sigma^2{}_{sca}$	0.34	0.66	0.48	0.0004	-0.02	0.02	-3.65	-0.05	0.06	0.10	0.26	0.25

$\sigma^2{}_{gca}$ = general combining ability variance, $\sigma^2{}_{sca}$ = specific combining ability variance, $\sigma^2{}_{A}$ = additive variance, $\sigma^2{}_{D}$ = dominance variance, NNFFB: node number for first fruiting branch, DTF: Days to flowering, SCY: Seed cotton yield and EI: earliness index

Table 7. General combining ability effects of lines and testers for different plant traits in *G. hirsutum* L. under different nitrogen levels.

Parents	NNFFB			DTF			SCY			EI		
	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha
Lines												
FH-682	0.64	0.86	0.89	-2.52	2.24	3.11	6.16	5.36	-1.13	10.00	7.84	6.80
FH-2015	0.48	0.39	0.35	-3.18	-0.78	1.17	1.34	0.89	-0.46	0.34	0.46	1.45
MALMAL	-0.55	-0.51	-0.43	2.67	-0.04	-2.08	-2.25	-1.70	-4.51	-9.72	-7.87	-9.62
MNH-147	-0.90	-1.07	-1.19	0.72	-2.21	-3.36	2.74	-4.06	-0.28	-0.42	-0.31	-0.18
PB-900	0.11	0.19	0.41	-0.80	-0.88	-0.12	-0.27	1.39	1.94	-7.11	-6.47	-4.72
VH-300	0.22	0.14	-0.04	3.12	1.68	1.28	-2.23	-1.88	4.44	6.92	6.34	6.27
S.E. (Lines)	**0.14**	**0.17**	**0.19**	**1.03**	**1.54**	**1.69**	**2.13**	**2.66**	**2.82**	**0.55**	**0.46**	**0.54**
Testers												
B-557	0.07	0.12	0.16	-1.57	0.43	1.84	-1.29	-2.36	-6.75	0.31	0.39	-0.36
BH-121	0.44	0.47	0.41	-0.22	-1.17	-3.21	-0.84	-1.02	-1.64	0.33	0.46	-0.05
FH-941	-0.24	-0.34	-0.40	0.57	-3.14	-3.05	0.53	1.05	-2.13	-0.74	-1.19	0.66
MNH-93	-0.43	-0.39	-0.38	0.24	0.25	1.63	1.18	3.23	7.98	0.31	0.62	0.11
MS-40	0.17	0.15	0.21	0.98	3.64	2.79	0.41	-0.91	2.53	-0.22	-0.28	-0.36
S.E. (Testers)	**0.13**	**0.16**	**0.17**	**0.94**	**1.41**	**1.54**	**1.94**	**2.42**	**2.58**	**0.57**	**0.42**	**0.50**

S.E.: Standard error, NNFFB: node number for first fruiting branch, DTF: Days to flowering, SCY: Seed cotton yield and EI: earliness index

among testers, FH-941 (-3.14) was best general combiner under 120 kg/ha nitrogen and BH-121 (-3.21) under 180 kg/ha nitrogen.

For SCY, FH-682 (6.16 and 5.36) showed maximum gca effects among the female parents, whereas, the testers MNH-93 (1.18 and 3.23) expressed good and positive gca effects for the trait under 60 and 120 kg/ha nitrogen respectively. The line VH-300 (4.44) showed maximum gca for the respective trait Under 180 kg/ha nitrogen, and MNH-93 (7.98) remained best combiner among testers. The line FH-682, with the value of 10.00, 7.84 and 6.80 showed best gca effects for EI, followed by VH-300 with 6.92, 6.34, and 6.27 among lines under all the nitrogen levels. From testers, best and positive gca effects for EI were expressed by MNH-93 (0.31, 0.62 and 0.11).

Specific combining ability effects: Cross combinations showing negative values for NNFFB and DTF, whereas, positive SCA effects for SCY and EI will be desirable for the reason reported above in the case of GCA effects.

Under 60 kg/ha of nitrogen: The crosses MALMAL × MS-40, PB-900 × MNH-93, and FH-2015 × B-557, scored -0.96, -0.89 and -0.57, respectively which reflected good

combinations for NNFFB, whilst other combinations showed low or poor sca. For DTF, VH-300 × B-557 (-6.61), FH-682 × MS-40 (-5.82), and VH-300 × MNH-93 (-5.25) were the crosses which exhibited best combining ability effects (Table 8). Thirteen crosses gave positive sca effects for SCY with highest value scored by FH-682 × B-557 (7.30), followed by MALMAL × BH-121 (5.75), FH-2015 × FH-941 (5.26) and VH-300 × MNH-93 (5.07). In EI, the crosses having better specific combining ability effects were FH-682 × MNH-93 (8.03), FH-682 × MS-40 (7.16), FH-2015 × B-557 (4.49).

Under 120 kg/ha of nitrogen: For NNFFB, the top position was secured by the cross, MALMAL × MS-40 (-0.98) followed by PB-900 × MNH-93 (-0.85) and FH-682 × B-557 (-0.54), which attained low sca (Table 8). In case of DTF, the best combination was observed between FH-682 and MS-40 scoring highest negative significant estimate (-8.54) for sca effect. For SCY, top three crosses were MNH-147 × MS-40 (13.17), FH-682 × MNH-93 (11.76), and VH-300 × FH-941 (10.80) as far as sca is concerned. For the character, EI, best combination was observed between FH-682 and MNH-93 (7.06) and it was followed by VH-300 × MNH-93

Table 8. Specific combining ability effects of crosses for various earliness related traits in *G. hirsutum* L. under different nitrogen levels.

Crosses	NNFFB			DTF			SCY			EI		
	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha	N = 60 kg/ha	N = 120 kg/ha	N = 180 kg/ha
FH-682 × B-557	-0.37	-0.54	-0.18	1.19	0.10	2.38	7.30	4.38	5.60	-7.35	-5.28	-2.91
FH-682 × BH-121	-0.41	-0.46	-0.06	1.66	2.52	4.22	-2.64	-1.19	-0.58	-5.07	-5.70	-5.19
FH-682 × FH-941	0.50	0.47	0.33	1.47	3.02	0.93	-5.72	-9.76	0.10	-2.75	-1.25	-1.13
FH-682 × MNH-93	0.14	0.32	-0.09	1.55	2.90	1.49	2.21	11.76	3.46	8.03	7.06	4.20
FH-682 × MS-40	0.14	0.22	0.001	-5.87	-8.54	-9.03	-1.15	-5.19	-8.59	7.16	5.17	5.04
FH-2015 × B-557	-0.57	-0.38	-0.63	2.64	1.68	-2.27	1.87	6.66	17.20	4.49	3.16	4.41
FH-2015 × BH-121	-0.15	-0.19	-0.37	-1.43	0.12	0.57	-0.78	8.18	-1.50	2.46	3.49	0.46
FH-2015 × FH-941	0.17	0.19	0.15	-3.60	0.41	0.75	5.26	7.80	4.98	-5.51	-4.31	-4.11
FH-2015 × MNH-93	0.18	0.01	0.18	2.80	3.56	4.42	-0.69	-7.66	-5.04	-5.64	-7.48	-6.79
FH-2015 × MS-40	0.37	0.36	0.67	-0.40	-5.76	-3.47	-5.66	-14.98	-15.65	4.20	5.14	6.02
MALMAL × B-557	0.53	0.49	0.63	0.05	1.50	5.08	-3.88	-3.38	-9.67	1.05	1.33	0.65
MALMAL × BH-121	0.71	0.78	0.94	-2.99	0.89	-1.58	5.75	6.14	9.42	1.70	0.95	2.02
MALMAL × FH-941	-0.09	-0.18	-0.27	-1.50	0.98	-0.20	-3.20	-6.42	-6.92	-0.63	-1.39	-3.03
MALMAL × MNH-93	-0.18	-0.11	-0.12	4.30	-1.99	1.17	-0.38	-1.77	-4.89	-1.96	-0.72	-0.26
MALMAL × MS-40	-0.96	-0.98	-1.18	0.14	-1.38	-4.47	1.71	5.42	12.07	-0.16	-0.16	0.62
MNH-147 × B-557	-0.46	-0.43	-0.56	0.88	-4.80	-5.52	-3.30	-2.05	-9.32	2.19	3.63	3.46
MNH-147 × BH-121	-0.29	-0.28	-0.56	2.27	4.29	0.56	-3.75	-8.60	-3.23	3.42	4.13	4.17
MNH-147 × FH-941	-0.02	-0.02	-0.05	0.21	3.34	6.03	4.11	-2.15	-1.55	3.10	4.69	4.52
MNH-147 × MNH-93	0.92	0.86	1.08	0.45	-4.37	-7.44	-0.41	-0.37	1.62	-5.32	-6.88	-7.72
MNH-147 × MS-40	-0.15	-0.13	0.09	-3.81	1.54	6.37	3.35	13.17	12.48	-3.39	-5.57	-4.42
PB-900 × B-557	0.58	0.59	0.47	1.84	4.94	6.29	4.77	-0.86	-0.08	2.49	-0.65	0.01
PB-900 × BH-121	0.43	0.45	0.51	1.65	-0.59	0.60	1.63	-0.21	-2.54	-1.28	-0.04	-0.13
PB-900 × FH-941	-0.31	-0.25	-0.07	4.02	-1.90	-4.89	-5.52	-0.27	-0.31	3.65	2.08	1.62
PB-900 × MNH-93	-0.89	-0.85	-0.78	-3.85	-0.07	-0.03	2.10	8.17	6.41	-0.19	1.74	2.44
PB-900 × MS-40	0.19	0.06	-0.13	-3.66	-2.38	-1.98	-2.98	-6.83	-3.48	-5.12	-3.13	-3.94
VH-300 × B-557	0.30	0.28	0.26	-6.61	-3.42	-5.97	-6.76	-4.76	-3.73	-3.31	-2.18	-5.62
VH-300 × BH-121	-0.28	-0.30	-0.45	-1.16	-7.23	-4.37	-0.22	-4.31	-1.58	-1.22	-2.83	-1.32
VH-300 × FH-941	-0.25	-0.21	-0.09	-0.59	-5.85	-2.63	5.07	10.80	3.71	2.14	0.18	2.13
VH-300 × MNH-93	-0.17	-0.24	-0.28	-5.25	-0.03	0.39	-2.84	-10.14	-1.57	5.08	6.28	8.14
VH-300 × MS-40	0.41	0.46	0.55	13.60	16.52	12.58	4.74	8.41	3.17	-2.68	-1.45	-3.33
S.E. (Crosses)	**0.32**	**0.39**	**0.42**	**2.31**	**3.44**	**3.77**	**4.76**	**5.94**	**6.31**	**1.24**	**1.02**	**1.21**

S.E.: Standard error, NNFFB: node number for first fruiting branch, DTF: Days to flowering, SCY: Seed cotton yield and EI: Earliness index

(6.28).

Under 180 kg/ha of nitrogen: Crosses, MALMAL × MS-40, PB-900 × MNH-93 and FH-2015 × B-557 gave higher values i.e., -1.18, -0.78 and -0.63 for NNFFB respectively. The other crosses, either scored very low negative values or positive thus resulted to be poor combinations for this traits. For DTF, 14 crosses were observed having negative sca estimates. Out of these, three crosses, FH-682 × MS-40 (-9.03), MNH-147 × MNH-93 (-7.44), and VH-300 × B-557 (-5.97), exhibited good combining abilities for this trait. The crosses, FH-2015 × b-557 (17.20), MNH-147 × MS-40 (12.48) and MALMAL × MS-40(12.07) were observed to be the top three in the list as far as sca effects for SCY was concerned. For EI, the crosses observed having better specific combining ability effects were FH-682 × MS-40 (5.04), FH-2015 × MS-40 (6.02) and VH-300 × MNH-93 (8.14).

DISCUSSION

For the development of early maturing genotypes in *Gossypium hirsutum* L., genetic variability in plant characters must be present in the available germplasm. The workers like, Basbag *et al.,* (2007)*,* Shakeel *et al.,* (2011)*,* Godoy and Palomo, (1999a), had used phenological and morphological characters as effective selection criteria to screen-out early and late maturing cultivars in upland cotton based on the availability of genetic variability. In the present studies, 45 genotypes of upland cotton were evaluated for the assessment of earliness based on DTS, DTF, NNFFB and a ratio of weight of first picking of seed cotton to weight of seed cotton from all pickings i.e., earliness index, along with seed cotton yield. Anderson's index scoring on mean values, and principal component analysis of the germplasm revealed significant variation for all the traits and thus endorsed the findings of Rauf *et al*., (2006), Shakeel *et al*., (2000), and Godoy and Palomo (1999a) while working on cotton.

On the basis of mean performances, days to squaring showed significant variation ranging from 36.76 to 43.07 days. Jatoi *et al*., (2012), Shah *et al.,* (2010), and Ray and Richmond (1966), used less number of days to squaring as good indicator for early maturity in cotton. But Basbag *et al.,* (2007) and Godoy and Palomo, (1999a), reported days to squaring was not authentic indicator to measure early maturity in cotton. However, less number of days to flowering was considered authentic criterion for screening out early maturating genotypes by Shakeel *et al.,* (2012), Godoy and Palomo (1999a) and Basbag *et al.,* (2007). Rauf *et al.,* 2005 also reported that by reducing the days to flowering shortened the period of maturity of cotton crop as well as the period of boll formation.

Node number for first fruiting branch has been reported as basic criterion for measurement of earliness in cotton maturity by Shakeel *et al.,* (2008) and Iqbal *et al.,* (2010). In present studies significant variation was found among genotypes for this trait and the days ranged from 6.07 to 10. Genotypes PB-38, MNH-738, VH-281, and RED ACALA may be called as early maturing as they produced first fruiting branch at lower nodes i.e. 6.07, 6.70, 7.10 and 7,11 respectively, whilst VH-297, MS-40, GR-156 and MNH-554 which appeared to develop first fruiting branch at higher node i.e. 10.00, 9.72, 8.80 and 8.59 respectively so were considered as late maturing. Ahmed and Malik (1996) reported that cotton crop matures 4 - 7 days earlier just by decreasing a single node for sympodial branch. In similar studies Kairon and Singh (1996) observed that early maturing cotton genotypes set fruit at 4th or 5th node while late maturing set at 8th or 9th node.

Higher yield of seed cotton remained as primary consideration in breeding for early maturing genotypes in cotton (Godoy and Palomo, 1999b). Earliness index catches the interest of breeders in developing of early maturity in cotton (Hearn, 1969 and Azhar *et al.,* 2007) and in other crops having indeterminate growth habit like mung bean (Rehman *et al.,* 2010). Greater earliness index of PB-900, CIM-573, VH-300, and VH-207 suggested these as early maturing genotypes while, MS-40, BH-121, BH-123, BH-162, MS-39 and PB-39 with low percentage of SCY at first picking appeared to be late maturing.

From the above referred results and supporting observations of different researchers, it is concluded that early maturity is a complex trait and there is no single criterion for measuring earliness in cotton germplasm. Therefore, selection of a parent as early maturing on the basis of single parameter may not be a good suggestion. It has also been suggested by Shah e*t al.,* (2010), and Godoy and Palomo (1999a) that selection of more than one component for earliness could be used as an effective approach for early maturity in cotton.

Index scoring by Anderson (1957) has been used in present work for grouping accessions on the basis of morphological characters as suggested by Bhadra and Akhter (1991) and Shakeel *et al.,* (2012). This biometrical method is relatively simple and uses index score allotted to each character measured in each line/variety, and the available germplasm is classified into different groups on the basis of total index score. In the present case, total index score of 45 genotypes based upon the five characters varied from 28 to 180. It was found that the varieties namely CIM-573 (170), FH-2015 (156), VH-256 (151), VH-300 (140), PB-899 (138) and MALMAL (137) scored ≥100, and therefore, grouped as early and in contrast GR-156 (28), MS-40(39), BH-162 (44), VH-297 (46) and BH-121 (64) with lower score (≤100) were late maturing. Use of index scoring analysis has also been recommended by Du *et al.,* (2016) and Aslam *et al., (*2013) to generate distinct groups on the basis of variation present in germplasm in cotton. Singh and Narayanon (2011) recommended that the genotypes to be used as parents in hybridization programs, must be selected from different

groups staging the similar genetic variability existing in plant germplasm collection.

On the basis of variability and PCA, the germplasm was classified into three distinct groups. Group one having both early and late maturing, group two have late maturing and group three comprised of early maturing genotypes.

Different workers used PCA for categorising and grouping of their materials, e.g., Du *et al.*, (2016), and Aslam *et al.*, (2013), grouped as tolerant, susceptible and mixed genotypes while working on salinity tolerance in cotton and Abd-Elsalam *et al.*, (2014) on fusarium wilt. Solis *et al.*, (1989) classified cotton germplasm in early, late and intermediate groups on the basis of phenological and yield related parameter that suggested high degree of diversity in screened cotton genotypes.

Due to indeterminate nature of cotton plant, earliness is a complex phenomenon and is related with several physiological, morphological and phenological traits as well as with many cultural practices, that's why degree of earliness in cotton varies with macro and micro environments of the plants. Therefore, early maturity of the selected eleven genotypes along with their crosses was assessed under different macro-environmental regimes (nitrogen levels) to see their response for earliness coupled with Nitrogen level.

In almost all the traits the variance due to specific combining ability (σ^2_{sca}) was observed higher than variance due to general combining ability (σ^2_{gca}) under all the three nitrogen regimes revealing, thereby, predominance of non-additive type of gene action for these characters. However, for seed cotton yield under 60 kg nitrogen level, the gene action was that of additive type, where the gca variance were observed to be higher than sca variance. Both additive and non-additive genetic effects have been reported in the literature for different earliness related plant characters in cotton. For instance, Javaid *et al.*, (2014) and Saleem *et al.*, (2010) reported the involvement of non-additive, whereas, Basbag *et al.*, (2007) and Karademir *et al.*, (2009) narrated additive type of gene action. Griffing, (1956) and Sprague and Tatum, (1942) suggested that higher magnitude of sca signifies the importance of non-additive genes in controlling expression of plant parameters.

On individual basis comparison of gca among the eleven parents (six lines and five testers) revealed that MNH-147 performed best for node number for first fruiting branch under all the three nitrogen regimes. However, it additionally proved good for days to flowering under 120 and 180 kg/ha. The variety FH-682 gave highest gca effect for earliness index and seed cotton yield under 60 and 120 kg nitrogen and for earliness index under 180 kg nitrogen level. The Parent FH-2015 performed good for days to flowering under 60 kg/ha nitrogen.

In cross combinations it was generally observed that the genotypes having high gca effects did not, necessarily, make good combinations with the ones having good gca but it was otherwise. The behaviour of the genotypes was quite variable in their specific combining ability with other genotypes. For instance, the cross, MALMAL × MS-40 was best combination for node number for first fruiting branch under all the three nitrogen levels. This cross involved MALMAL with good gca and MS-40 had poor gca effects for the trait. The contribution of taller plants to increase SCY has been reported due to having more fruiting branches and ultimately more fruiting points, nonetheless due to delayed maturity and high water requirement, tallness has become an undesirable feature (Baloch *et al.*, 2011) for incorporating early maturity in upland cotton. Therefore, for NNFFB, parents having negative gca may be considered better as has been proposed by Rauf *et al.*, (2006). Similar is the choice of the breeders is for other plant traits like days to flowering where negative performance of the parents is desirable. For the trait i.e., DTF, under 60 kg/ha of nitrogen level, the cross VH-300 × B-557 gave better results, in which VH-300 was poor and B-557 was the best performer as far as gca effects are concerned. It reflects that parents having poor gca effect may produce good combinations. Whereas, under 120 kg and 180 kg nitrogen, the cross FH-682 × MS-40 gave good results for the trait. In the cross the parents were poor as far as their gca was concerned.

In other traits (EI and SCY) where positive and higher values are required, the cross FH-682 × MNH-93 have good sca effects for earliness index under 60 and 120 kg/ha of nitrogen level, and for SCY under 60 kg/ha of Nitrogen, however VH-300 with MNH-93 gave best sca for EI under 180 kg/ha nitrogen. The crosses, MNH-147 × MS-40 and FH-2015 × B-557 for seed cotton yield have good sca effects under the 120 kg/ha and 180 kg/ha nitrogen levels respectively. In all these crosses, the parents FH-682, MNH-147, MS-40 and MNH-93 were observed to be involved more frequently, whether they were good or poor as far as their gca effects were concerned. Again a different behaviour of the parents, regardless of their gca effects, was observed in combinations. Best crosses resulting from the parents possessing contrasting gca had been narrated in cotton by Soomro *et al.*, (2010) and Naeem and Azhar (2007).

Variation in performance of parents and hybrids could be justified on the basis of differences in genetic makeup and environmental conditions prevailing during trials (Bernier *et al.*, 1993; Peterson *et al.*, 2006).

Conclusion: All the crosses showing high sca effects in favourable direction which are indicated in above paras are, therefore, recommended for heterosis breeding. The GCA effects revealed the line, MNH-147 as best combiner for majority of earliness related traits and FH-682 for SCY and earliness index under all the three nitrogen levels. Best hybrid combinations identified were MALMAL × MS-40 for

node number for first fruiting branch, FH-682 × MS-40 for days to flowering and FH-682 × MNH-93 for EI. A few combinations, like FH-682 × MNH-93, FH-2015 × B-557, MNH-147 × MS-40, PB-900 × MNH-93 and VH-300 × FH-941, having harmonious combination of some earliness related traits along with yield traits, have also been identified under the three nitrogen levels. The predominance of sca effects in all the characters in general suggest that their improvement may not be achieved in early generations, and therefore, the material may be used advantageously for exploitation of hybrid vigor or the selection may be delayed till later generations.

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