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Genetics of fiber quality, oil content, seed-cotton yield and its allied traits in cotton: A review

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Abstract
Present review was directed to define the role of genetic studies viz. genetic potential, variability, heritability, genetic advance, gene action and association of seed-cotton yield and yield contributing traits among parents and their F1 cross combinations. Such knowledge can practically be subjected to devise an efficient selection procedure to develop commercial hybrid cultivars with improved yield, oil % and fiber quality traits; possessing broad genetic base.

Keywords: Seed-cotton yield, genetic potential, fiber quality

Introduction

Cotton being grown in more than 70 countries, worldwide, is the most important economical field crop in Pakistan. Role of cotton and its by-product in economy of developing and developed countries have dominated both the Old and New World. In Pakistan, excavations depict that cotton plant history ink back to Mohen Jo Daro's civilization (Khan, 2003) [20]. Cotton is chiefly grown for its fiber but it is also a vital source of edible cooking oil, protein and cotton-seed meal for livestock animals. It is an important commercial cultivated crop generally grown in Sindh and Punjab provinces of Pakistan (Pakistan economic survey, 2016-17) [8]. Healthy cotton crop is a sign of prosperity and strength for a nation. In Pakistan, cotton (*Gossypium hirsutum* L.) as a major cash crop covers textile industry, oilseed, food and livestock feed production to lift up the economy. It earns 45-60% foreign exchange depending upon the production and consumption. Along with its great economic importance as a fiber crop, it contributes 65-70% share in provision of edible oil to the oil industry and feed/seed cake for livestock (Khan *et al*., 2003; Khan, 2010; Khan *et al*., 2011) [20, 21, 22].

Cotton crop has 1.0 % and 5.2 % share in GDP and agriculture value addition, respectively. Pakistan is the 4th in cotton production with 1.68 (million tonnes) having an area of 2.5 (million hectare) under cultivation and 3rd largest consumer with 2.23 (million tonnes) consumption. Still our yield/ha averages 730 (kgs/ha) which is very low when compared with other countries (Pakistan economic survey, 2016-17) [8]. The yield in cotton is a very complex trait and is directly or indirectly influenced by the different yield contributing and morpho-physiological character. For breeders, comprehensive knowledge of the inheritance pattern of yield and other morpho-physiological traits is prerequisite in order to tackle problems causing low yield (Aaliya 2016; Ali et al., 2016; Ahmad *et al*., 2008; Ahmad *et al*., 2011; Khan *et al*., 2010) [1, 7, 5, 4, 21]. Genetic improvement of morpho-physiological traits in cotton is of substantial interest; comprehensive understanding on mode of inheritance help determine the relative purity of hybrids and selection of promising lines to use in breeding. Development of cotton cultivars having acceptable fiber quality by exploiting the cotton germplasm remained the main focus of cotton breeders. The fiber quality, yield and its contributing traits are transmissible in nature. Thus, these quantitative and qualitative characters can be improved through developing the novel crosses (variation) by exploiting suitable breeding programs. To serve the cause, breeders were keen to devise the breeding strategies in accordance to their breeding objectives by gathering ample knowledge of genetic components such as heritability, genetic variability, genetic advance and coefficient of variation (Abbas et al., 2016a, b; Ali and Khan, 2007; Dhamayanathi *et al*., 2010; Rashid et al., 2016a, b) [2, 3, 6, 16, 28, 29]. Existence of genetic variability is considered as the preliminary requirement to screen the available genetic material against diverse range of biotic and abiotic stresses which is further exploited by using different statistical tools. Heritability estimate is an effective statistical tool; helps the breeder to evaluate the influence of environment on various traits and determines the extent of trait that is transmitted from one generation to another. Thus, incorporation of heritability, genetic variability and genetics advance at once could be powerful tool to select appropriate breeding program (Chandio *et al*., 2003; Baloch *et al*., 2004; Baloch *et al*., 2014; Rehman et al., 2017) [15, 12, 13].

Literature

Ehsan *at el*., (2008) [17] used five elite cotton cultivars i.e. FH-207, FH-901, MNH-786, FH-115 and FH-113 that wer tested for growth and seed yield performance in a field experiment. Results depicted significant differences for plant height (cm), no. of bolls/plant, average boll weight (g), ginning out turn (%), fiber fineness, fiber length, no. of sympodial branches/plant and seed-cotton yield among these cultivars. The standout cultivar FH-115 with more no. of bolls/plant, higher ginning out turn (GOT %), and no. of sympodial branches/plant, statistically produced maximum yield. Batool *at el*. (2010) [14] in genetic variability and heritability studies on *Gossypium hirsutum L.* cultivars; CIM-446, SLH-284, CIM-496, CIM-499, CIM-473, CIM-506, CIM-707 and CIM-554 manifested highly significant variances (p<0.01) for seed-cotton yield/plant, plant height, monopodia/plant and sympodia/plant. Days to first flower emergence and boll weight were significant (p<0.05) while 1st internode length presented non-significant variances among the cultivars. CIM-506 (short stature and early maturing type) was top performer for boll weight, no. of sympodia/plant, seed-cotton yield/plant than others. This was followed by CIM-707 and CIM-554 with comparable seed yield and yield contributing traits. Broad sense heritability (bs) was having sequence; boll weight (0.97), days to first flower emergence (0.96), plant height (0.95), seed cotton yield/plant (0.91), sympodia/plant (0.89), monopodia/plant (0.88) and internode length (0.36). Presence of high heritability and greater genetic variances than environmental variances suggested that breeding material has potential to improve morpho-yield characters in future cotton breeding.

Khan *at el*., (2010) [21] while computing genetic gain, genetic variability, correlation and heritability for cotton fiber, seed and oil content (%) in American cotton lines manifested highly significant differences for no. of seeds/locule, no. of seeds/boll, seed index, seed lint %, lint index, oil content % and cotton-seed yield while, no. of seeds/locule had non-significant results. Genetic variances were reported greater as compared to environmental variances for all the characters except seed index and no. of seeds/locule. Selection response and broad sense heritability were; (0.84 g, 0.67), (0.47 g, 0.77), (0.33 g, 0.96), (1.66 %, 0.96), (643.16 kg, 0.98) and (1.28 %, 0.87) for seeds/boll, seed index, lint index, lint %, seed-cotton yield and cotton-seed oil % respectively. All the studied characters were positively correlated to yield except oil % and seeds/locule. Further, Highest seed-cotton yield was noted in CIM-499 followed by CIM-496, CIM-473 and CIM-506. No. of seeds/boll, seed index, lint % and cotton-seed oil % was also good. Cultivar SLH-279 had better results for lint %, lint index, and oil %. Even small genetic gain in lint, oil % and seed characters are appreciable.

Ashokkumar *at el*., (2010) [9] calculated general combining ability (GCA) of the parents and specific combining ability (SCA) for eleven parents (4 lines & 7 testers) and their 28 first generation hybrids mated in line × tester fashion. L × T analysis showed significant general and specific combining ability effects for each character except earliness. Amongst the genotypes studied, MCU-12 for boll weight (g), no. of bolls/plant and seed cotton yield/plant (g), F-1861 for no. of bolls/plant, SURABHI for no. of sympodia, SOCC-17 for earliness and TCH-1641 for GOT % and lint index had maximum GCA effects while F-776 and F-1861 together were good combiners in fiber quality. Hybrid combinations were selected with significant SCA effects for seed-cotton yield and fibre characteristics. Khan *at el*., 2015 [19] tested six parental genotypes; CIM-446, CIM-499, CIM-554, CIM-496, CIM-506 and CIM-707 and resulting 30 F_1 progenies for General and specific combining ability in 6 × 6 diallel. Significant differences ($p \leq 0.01$) among genotypes were evident for seed cotton yield/plant, no. of bolls/plant, no. of bolls/sympodia, boll weight (g), lint index and lint %. Even, mean squares were highly significant and F1 hybrids also had significant means over parents. High mean suare for GCA than SCA showed additive gene action. CIM-554 and CIM-446 being best general combiners produced; CIM-446 × CIM-496, CIM-446 × CIM-554 and CIM-506 × CIM-554, cross combinations for yield and fiber characters.

Results established that low × high, high × low and often high × high GCA parents exhibited best results for major economic traits. Significant correlation of seed cotton yield with all yield traits was positive except for lint %. Hence, hybrid cotton production is possible. Kumar *at el*., (2014) [24] in a study on seven parents and their 42 hybrids, additive gene action was dominant for all character except bundle strength, sympodial/plant and plant yield. Best performer; BW4-1 for plant yield, bolls/plant, boll weight, seed index, micronaire and lint index while 2nd best; MCU-13 for plant yield, lint index, seed index and sympodial/plant. Significantly positive GCA for plant height, ginning %, sympodial/plant and boll weight was recorded in TCH-1726. MCU-13 with greater gca effects for plant yield, sympodial/plant, seed and index was best general combiner. TCH-1705 × MCU-3 and KC-2 × TCH-1726 showed better sca for plant yield, bolls/plant and sympodia/plant while KC 2 × TCH 1726 for plant yield and sympodia/plant.

Salahuddin et al., (2010) [31] in his correlation studies on *Gossypium Hirsutum* L. reported significant positive correlation (r=0.567) between sympodia/plant and seed-cotton yield as coefficient of determination (r2=0.321) shown 32.1% variation in the seed-cotton yigeld/plant due to sympodia/plant. Regression coefficient (b=5.66) showed 5.66 g increase in seed-cotton yield/plant with a unit increase in sympodia/plant while seed cotton yield exhibited good positive association (r=0.959) with bolls/plant. The coefficient of determination (r2=0.92) and regression coefficient (b=3.37) revealed that for a unit increase in bolls/plant, seed-cotton yield will increase by 3.37 g, proportionally. Highly positive significant correlation (r=0.597) and regression coefficient (b=53.479) revealed 53.48 g boost in seed-cotton yield/plant with single unit increase in boll. However, the monopodia/plant and plant height had non-significant association with the yield/plant. Patel *at el*., (2014) [27] completed the experiments of combining ability and heterosis for yield and fiber characters involving ten parents (5-lines, 5-testers) revealed significant diversity for majority of the characters that was non-additive in nature for seed-cotton yield, GOT %, lint yield and fiber strength while additive for fiber fineness, 2.5 % span length, uniformity % and maturity %. GISV-185 (line) was good general combiners for lint yield, seed-cotton yield and 2.5% span length while GSHV-99/307 (tester) was the best general combiner for fiber fineness, maturity %, lint yield, GOT % and seed-cotton yield. Crosses, GISV-103 × GSHV-99 /307 followed by; GISV-185 × GSHV-97/59, GISV-105 × GSH-2, GISV-185 × GSH-2, GISV-216 × GSHV-99/307, GISV-185 × GSHV-01 /1338, GISV-216 × GSB-39 and GISV-197 × GSB-39 performed better in terms of heterosis in anticipated direction for yield. Moreover, hybrid breeding to improve seed-cotton yield, lint yield, GOT %, and fiber strength while recombination breeding for fiber quality character improvement was recommended.

Babu *at el*., (2011) [11] worked to create variability in *Gossypium hirsutum* L. by crossing three lines; RAH-100(A), RAH 20 (B) & RAH-10 (C) to develop two hybrids; RAHH-92 (A × B) and RAHH-102 (A × C), also included 12 random lines from F_5 generation in this study. This was followed by combining ability assessment of these two sets of lines by incorporating four testers (male). The consequent F1 hybrids obtained were then compared with initial cross hybrids (RAHH-92 & RAHH-102). The variability and combining ability among F_5 lines of one set were assessed and compared with second and found remarkable potential of F_1 hybrid as compared to their benchmark crosses (RAHH-92 & RAHH-102). Khan *at el*., (2015) [23] carried out the combining ability studies by incorporating parents (7 lines & 8 testers) and their 56 hybrids developed by line x tester analysis. The greater gca variance than to sca variance for seed-cotton yield, ginning %, micronaire value and 2.5% span length showed additive dominance while, non-additive dominance was observed for bundle strength and uniformity ratio. For yield and at least one fiber quality character BC-68-2, HAG-1055, Galama, LRA-5166, CPD-420 and LK-861 were good general combiners. Whereas, NA-1325 × 4084 and NA-1325 × L-604 were good specific combiners for seed-cotton yield. Additionally, desirably significant sca effects were recorded in IC-357063 × L-761, IC-357063 × JK-344, CPD-420 × L-761 and IC-357063 × LRA-5166 for fiber quality characters. Mendez *at el*., (2012) [25] examined the six commercial cultivars of upland cotton, viz., Acala 90-1, Cabuyare, Deltapine 16, Tamcot-SP-21, Ospino and Stoneville and their fifteen 1st generation hybrids using Griffing's model-I, method-II. All the traits were significantly different excluding no. of bolls/plant and no. of seeds/boll. Excluding fiber %, seed-cotton yield/ha, seed yield, fiber % and boll set, all the traits revealed significant GCA and SCA variance; both additive and non-additive gene action. Cabuyare for seed yield, blooming initiation and fiber fineness, Stoneville for no. of fruiting branches, no. of flowers/plant, plant height, stem diameter, and boll weight, Tamcot-SP-21 for fiber fineness and boll set, Ospino for fiber strength, Deltapine-16 for plant height, had good general combining ability. Further, significantly positive associations of fruiting branches/plant with plant height and negative associations of no. of flowers, plant height and boll weight with boll set was evident. Parsad *at el*., (2016) [26] reported highly significant mean squares owing to parents and crosses for almost all the studied traits; considerable gca variance for parents and sca variance for hybrids was present. Both additive and non-additive gene action were present in combing ability analysis. Three crosses; G.Bhv-305 × G.Shv-280/11 (20.73), G.Bhv-287 × G.Shv-233/09 (22.76) and G.Cot.-23 × G.Shv-433/08 (24.90), had high sca effects for seed-cotton yield/plant, while physiological parameters and yield contributing characters were also good. Govindbhai (2015) [18] carried out research to gather the genetic information on gene effects for seed cotton yield and its component traits in cotton by using twelve generations viz., P-1, P-2, F-1, F-2 , B-1 , B-2 , B-11, B-12, B-21, B-22, B-1s and B-2s of crosses; G.Cot-10 × MR-78 and G.Cot-12 × GTHV-95/145. Special scaling tests (X and Y) showed presence of epistasis as they were significant for all the four traits studied. At the six degrees of freedom, X_2 (2) value was significant for all the traits; presence of higher order epistasis in both crosses. In cross-1, X_2 (3) value was non-significant for bolls/plant, boll weight and seed-cotton yield/plant at two degrees of freedom; best fit model (ten parameter model). Whereas, the significant value of X2 (3) in cross-2, at two degrees of freedom for all the traits specified the existence of either linkage or higher order epistasis or both.

Summary

Existence or creation of ample genetic variability is prerequisite to screen the available genetic material. Consequently, integration of heritability, variability, gene action and traits association studies at once could be powerful tool to select appropriate breeding program.

References

1. Aaliya K, Qamar Z, Nasir IA, Ali Q, Munim AF. Transformation, evaluation of gtgene and multivariate genetic analysis for morpho-physiological and yield attributing traits in Zea mays. Genetika. 2016; 48(1):423-443.
2. Abbas GH, Shahid MR, Mahmood A, Ali Q. Characterization of plant spacing best fit for economic yield, fiber quality, whitefly and CLCuV disease management on upland cotton. Nature and Science. 2016a; 14(5):12-16.
3. Abbas HG, Mahmood A, Ali Q. Zero tillage: a potential technology to improve cotton yield. Genetika (0534-0012), 2016b; 48(2).
4. Ahmad M, Khan NU, Mohammad F, Khan SA, Munir I, Bibi Z *et al*. Genetic potential and heritability studies for some polygenic traits in cotton (*G. hirsutum* L.). Pak. J Bot. 2011; 43(3):1713-1718.
5. Ahmad W, Khan NU, Khalil MR, Parveen A, Aiman U, Saeed M *et al*. Genetic variability and correlation analysis in upland cotton. Sarhad. J Agric. 2008; 24:195-201.
6. Ali MA, Khan IA. Assessment of genetic variation and inheritance mode of some metric traits in cotton (*Gossypium hirsutum* L.). J Agric. Soc. Sci. 2007; 3:112-116.
7. Ali Q, Ahsan M, Kanwal N, Ali F, Ali A, Ahmed W, Saleem M. Screening for drought tolerance: comparison of maize hybrids under water deficit condition. Advancements in Life Sciences. 2016; 3(2):51-58.
8. Anonymous. Pakistan Economic Survey, Ministry of Finance, Economic Advisor's Wing, Islamabad, 2016-17.
9. Ashokkumar K, Ravikesavan R, Prince KSJ. Combining ability estimates for yield and fiber quality traits in line × tester crosses of upland cotton. Int. J Biol. 2010; 2(1):179-183.
10. Ashokkumar K, Ravikesavan R. Genetic studies of combining ability estimates for seed oil, seed protein and fiber quality traits in upland cotton (*G. hirsutum* L.). Res. J Agric. Biol. Sci. 2008; 4(6):798-802.
11. Babu DH, Patil SS, Maralappanavar MS, Ranganatha HM, Swathi P, Rajeev S *et al*. Estimation of variability and heritability for combining ability in heterotic populations of cotton (*Gossypium hirsutum*). World Cotton Res. Conference Techn. Prosperity, 2011, 112.
12. Baloch MJ. Genetic variability and heritability estimates of some polygenic traits in upland cotton.

Pak. J Sci. Ind. Res. 2004; 42(6):451-454.

13. Baloch MJ, Khan NU, Rajput MA, Jatoi WA, Gul S, Rind IH *et al*. Yield related morphological measures of short duration cotton genotypes. J Anim. Pl. Sci. 2014; 24(4):1198-1211.
14. Batool S, Khan NU, Makhdoom K, Bibi Z, Hassan G, Marwat KB *et al*. Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. Pak. J Bot. 2010; 42(6):1057-1064.
15. Chandio MA, Kalwar MS, Baloch GM. Gene action for some quantitative characters in upland cotton (*Gossypium hirsutum* L.). Pak. J Sci. Ind. Res. 2003; 46:295-299.
16. Dhamayanathi KPM, Manickam S, Rathinavel K. Genetic variability studies in *Gossypium barbadense* L. genotypes for seed cotton yield and its yield components. El. J Pl. Breed. 2010; 1(4):961-965.
17. Ehsan F, Ali A, Nadeem MA, Tahir M, Majeed A. Comparative yield performance of new cultivars of cotton (*Gossypium hirsutum* L.). Pak. J Life Soc. Sci. 2008; 6:1-3.
18. Govindbhai VM. Genetics of seed cotton yield and its component traits in cotton (*Gossypium hirsutum* L.). Thesis. Genet. Pl. Breed, 2015. http://krishikosh.egranth.ac.in/handle/1/79219
19. Khan SA, Khan NU, Gul R, Bibi Z, Khan IU, Gul S *et al*. Combining ability studies for yield and fiber traits in upland cotton (*Gossypium hirsutum* L.). J Anim. Pl. Sci. 2015; 25(3):698-707.
20. Khan NU. Genetic analysis, combining ability and heterotic studies for yield, its components, fibre and oil quality traits in upland cotton (*G. hirsutum*). Ph.D thesis, Sindh Agric. Uni., Tandojam, Pak, 2003.
21. Khan NU, Marwat KB, Hassan G, Farhatullah S, Batool K, Makhdoom W *et al*. Genetic variation and heritability for cottonseed, fiber and oil traits in *G. hirsutum* L. Pak. J Bot. 2010; 42(1):615-625.
22. Khan SA, Khan NU, Mohammad F, Ahmad M, Khan IA, Bibi Z *et al*. Combining ability analysis in intraspecific F_1 diallel crosses of upland cotton. Pak. J Bot. 2011; 43(3):1719-1723.
23. Khan SA, Khan NU, Gul R, Bibi Z, Khan IU, Gul S *et al*. Combining ability studies for yield and fiber traits in upland cotton. The J Anim. Plant Sci. 2015; 25(3):698-707.
24. Kumar SK, Ashokkumar K, Ravikesavan R. Genetic effects of combining ability studies for yield and fibre quality traits in diallel crosses of upland cotton (*Gossypium hirsutum* L.). African J Biotech. 2014; 13(1):119-126.
25. Mendez NJR, Rondon A, Hernandez J, Pinto JFM. Genetic Studies in Upland Cotton (*Gossypium hirsutum* L.) II. J Agric. Sci. Tech. 2012; 14:617-627.
26. Parsad I, Naik MR, Patel HN. Combining Ability Studies in desi Cotton (*G. herbaceum* L.) in vertisols of Gujarat. Int. J Appl. pure Sci. Agric. 2016; 7(2):91-95.
27. Patel DH, Patel DU, Kumar V. Heterosis and combining ability analysis in tetraploid cotton (*G. hirsutum* L. and *G. barbadense* L.). Ele. J Pl. Breed. 2014; 5(3):408-414.
28. Rashid BHT, Yousaf I, Rasheed Z, Ali Q, Javed F, Husnain T. Roadmap to sustainable cotton production. Life Science Journal. 2016a; 13(11):41-48.
29. Rashid B, Kousar S, Yousaf M, Ali Q, Fatima F, Parveen S *et al*. Biotechnology: Future Tools for Stable Insect Pest and Weed Control in Cotton. Cotton Genomics and Genetics, 2016b, 7.
30. Rehman I, Aftab B, Bilal Sarwar M, Rashid B, Ali Q, Majid MU *et al*. gene expression in response to cotton leaf curl virus infection in Gossypium hirsutum under variable environmental conditions. Genetika (0534-0012). 2017; 49(3).
31. Salahuddin S, Abro S, Kandhro MM, Salahuddin L, Laghari S. Interrelation and path coefficient analysis of yield components of upland cotton (*Gossypium hirsutum* L.). World Appl. Sci. J. 2010; 8:71-75.
32. Salahuddin S, Abro S, Rehman A, Iqbal K. Correlation analysis of seed cotton yield with some quantitative traits in upland cotton (*gossypium hirsutum* L.). Pak. J Bot. 2010; 42(6):3799-3805.
33. Srinivas B, Bhadru D, Rao MVB, Gopinath M. Genetic studies in yield and fiber quality traits in American cotton (*Gossypium hirsutum* L.). Agric. Sci. Digest. 2014; 34(4):285-288.