*BinBee Arı ve Doğal Ürünler Dergisi, 2025: 34-49*
*Journal of BinBee-Apicultural and Natural Products (JBANP)*

# Heterosis studies in upland cotton for seed cotton yield and yield related components

Sana Khan[1], Azeem Iqbal Khan[1], Asad Azeem[2], Muhammad Abu Bakar Zia[3*], Sami ul ALLAH[4], Zeshan Hassan[2]

**Article info**
Received:05.26.2025
Accepted: 06.26.2025

**Article type:** Research

**Keywords:** Gossypium hirsutum L, seed cotton yield, Heterosis, Heritability

**Abstract**

Cotton belongs to the Malvaceae family, is one of the major fiber crops of the world popularly known as "White Gold". Cotton and its by-products play a crucial role in the economy of developed and developing countries. Several biotic and abiotic factors are responsible for low yield and poor fiber quality in cotton. Heterosis studies provide basis for development of hybrid combinations and their commercial consumption. The current research was conducted to investigate the degree of heterosis for seed cotton yield and yield related components under RCBD design having four parents and six hybrids with three replications. Data were collected for plant height, sympodia/plant, monopodia/plant, number of fruiting nodes/plant, seed cotton yield/plant, node ratio, boll weight, GOT percentage, seed index, micronaire, fiber length, fiber strength and number of bolls/ plant. Analysis of variance showed significant differences between parents and hybrids. The parents Debel and VH-330 demonstrated as the most effective for cross combination for the traits viz. plant height, boll weight and number of monopodial branches, seed cotton yield/plant, micronaire, fiber length, fiber strength, Got% and number of sympodial branches. The hybrids VH-330 x Debel, VH-330 x MS-DK and FH-444 x VH-330 exhibited significant and highest heterotic effects for yield and yield related traits and fiber quality parameter. The estimates of broad sense heritability exposed that moderate heritability was observed between all traits. The value of GCV was less than the value of PCV which means the influence of environment is more on all traits. These hybrids can be utilized for exploitation of yield and fiber quality parameters in future breeding programmes.

**Citation:** Khan, S., Azeem, A., Zia, MA.B., Hasan, Z. (2025). Heterosis studies in upland cotton for seed cotton yield and yield related components. Journal of BinBee - Apicultural and Natural Products (JBANP), 5(1), 34-49.

# Yüksek verimli pamukta tohum pamuk verimi ve verimle ilgili bileşenler üzerine heterozis çalışmaları

**Makale bilgileri**
Geliş Tarihi:26.05.2025
Kabul Tarihi: 26.06.2025

**Makale türü: Araştırma**

**Anahtar kelimeler;** Gossypium hirsutum L, tohum pamuk verimi, Heterosis, Kalıtım

**Özet**

Pamuk, Malvaceae familyasına aittir ve dünya çapında "Beyaz Altın" olarak bilinen başlıca lif bitkilerinden biridir. Pamuk ve yan ürünleri, gelişmiş ve gelişmekte olan ülkelerin ekonomisinde önemli bir rol oynamaktadır. Pamukta düşük verim ve düşük lif kalitesinden çeşitli biyotik ve abiyotik faktörler sorumludur. Heterosis çalışmaları, melez kombinasyonların geliştirilmesi ve ticari tüketimine temel oluşturur. Mevcut araştırma, dört ebeveyn ve altı melez ile üç tekrarlı RCBD tasarımında tohum pamuğu verimi ve verimle ilgili bileşenler için heterozis derecesini araştırmak amacıyla gerçekleştirilmiştir. Bitki boyu, simpodya/bitki, monopodia/bitki, meyve veren düğüm sayısı/bitki, tohum pamuğu verimi/bitki, düğüm oranı, koza ağırlığı, GOT yüzdesi, tohum indeksi, mikroner, lif uzunluğu, lif mukavemeti ve koza sayısı/bitki için veriler toplanmıştır. Varyans analizi, ebeveynler ve melezler arasında önemli farklılıklar olduğunu göstermiştir. Debel ve VH-330 ebeveynleri, bitki boyu, koza ağırlığı ve monopodyal dal sayısı, tohum pamuğu verimi/bitki, mikronaire, lif uzunluğu, lif mukavemeti, Got% ve simpodyal dal sayısı özellikleri için en etkili çapraz kombinasyon olarak gösterilmiştir. VH-330 x Debel, VH-330 x MS-DK ve FH-444 x VH-330 melezleri, verim ve verimle ilgili özellikler ile lif kalitesi parametresi için önemli ve en yüksek heterotik etkiler sergilemiştir. Geniş anlamlı kalıtım tahminleri, tüm özellikler arasında orta düzeyde kalıtım gözlemlendiğini ortaya koymuştur. GCV değeri PCV değerinden daha düşüktü, bu da çevrenin tüm özellikler üzerinde daha fazla etkiye sahip olduğu anlamına gelir. Bu melezler, gelecekteki ıslah programlarında verim ve lif kalitesi parametrelerinin geliştirilmesi için kullanılabilir.

Atıf: Khan, S., Azeem, A., Zia, MA.B., Hasan, Z. (2025). Yüksek verimli pamukta tohum pamuk verimi ve verimle ilgili bileşenler üzerine heterozis çalışmaları. Journal of BinBee - Apicultural and Natural Products (JBANP), 5(1), 34-49.

---

[1] * Corresponding Author Email Address: abziathebest@gmail.com

## Introduction

Cotton (*Malvaceae: Malvales*) is one of the most crucial natural fiber producing crop. Cotton has four domestic species viz *G. hirsutum and G. barbadence* (American) *G. herbarium and G. arboreum* [1] which are commercially cultivated for household use [2]. *G. arboreum* and *G. herbaceum* are diploid while *G. hirsutum & G. barbadense* consisted of allotetraploid genomes, and belongs to family Malvaceae [3]. Cotton is vital crop that is grown in more than 80 countries because of its products and socioeconomic importance. The top five countries India, China, the USA, Brazil, and Pakistan produce 80% of the world's cotton production [4]. Our World's population is increasing day by day, so appropriate cotton production is needed to encounter the increasing demand of fiber [5]. Pakistan's economy is based on cotton production, which is regarded as a cash crop [6]. Cotton crop is the backbone of Pakistan's economy and is considered as a main earning commodity by providing 0.3% to gross domestic product (GDP) and 1.4% to cost added in agriculture (Economic survey of Pakistan, 2022-2023). The area of cotton that was grown in the 2022–2023 season increased to 2,144 thousand hectares, an increase of 10.7% from the 1,937 thousand hectares of the previous year (Economic survey of Pakistan, 2022-2023). Cotton is referred to as a king of fiber occupies a huge and crucial position as a cash crop that has a substantial influence on the world economy and social dynamics [7].It is known as "White gold" because it gives excessive profit and exported in almost 111 countries of the world [2]. Cotton and its by-products play significant role in the economy of developed and developing countries [8]. The cotton crop provides the raw materials for a wide range of industries, allowing for the manufacture of edible oil, textiles, seed cakes for use as livestock feed, organic matter, and a number of other goods [9]. It employs millions of people globally in activities like cultivation, seed production, marketing, industry utilization, and research as the primary raw material (representing 85% of the textile industry's needs) [10].

Cotton is exposed to several biotic and abiotic stresses that causes to produce less cotton production. Cotton is susceptible to several diseases, including Fusarium wilt, Verticillium wilt (Bardak et al., 2021; Çelik et al., 2017; Çelik et al., 2019; Çelik et al., 2022) bacterial blight, and fungal blight [11]. Whiteflies and thrips caused substantial damage to the cotton crop in the cotton belts of Punjab and Sindh. The CLCV Disease repeatedly and persistently present produced a detrimental effect on the cotton crop [12]. Several ecological factors, including temperature variations, rainfall distribution and intensity, relative humidity, and winds all indicators of climate change have an impact on the growth and development of cotton [13]. Since cotton is more susceptible to environmental challenges, temperatures above the optimum will gradually reduce yield. Additionally, in most cotton belts during the flowering stage and the production of the bolls, the temperature is already above the ideal threshold temperature is 60°F, and an increase will reduce the crop's yield [13]. Farmers and the textile industry are seeking enhancements in both fiber quality and seed cotton yield [12; 14].

Considering the tendency towards diminishing yields and the rising demand from the textile sector, it is crucial to develop breeding programmes that can significantly increase cotton production in the country. Pakistan has the potential to become a large global producer of cotton [12]. The development of commercial hybrid varieties (both interspecific and intraspecific) is a crucial strategy to fulfil the current cotton demand among the many tactics used to improve yield and quality in grown cotton [1]. According to [15] heterosis has constantly distinguished itself as a noteworthy accomplishment in cotton breeding processes. Heterosis refers to the enhancement in a hybrid's performance compared to the average of its parents, and this can manifest as either positive or negative values. Breeders of cotton have become more interested in heterosis during the past few decades [16]. Heterosis involves assessing the performance of an F1 hybrid resulting from the crossbreeding of two varieties or pure lines, although its effective utilization in cotton breeding has not yet reached its full potential [17]. According to [7; 18] genetic traits relating to economic and fiber properties in cotton cultivars were improved through heterosis breeding. The heritability signify the genetic variance transmitted to offspring, holds a substantial role in the improvement of quantitative traits [19]. The aim of this research was to investigate heterosis and heritability analysis for various yield and yield related components in upland cotton that can be employed in future cotton breeding programme.

## Materials and Methods

The experiment was conducted in the field area of Department of Plant breeding and Genetics, University of Agriculture, Faisalabad during 2020-2021. During November 2020, seeds of four cotton genotypes viz. FH-444, MS-DK, Debel, VH-330 were planted in pots in a glasshouse. At flowering, these varieties were crossed in complete diallel fashion to develop $F_1$ seed. Only six $F_1$ hybrids viz. FH-444 × VH-330, FH-444 × Debel, FH-444 × MS-DK, VH-330 × Debel, VH-330 × MS-DK and Debel × MS-DK were developed. There were 5 pots for each variety. The temperature in the glasshouse was kept at 35°C. Selective crossing was made at the time of flowering. All preventive measures were adopted to avoid any genetic contamination at the time of flowering. The parental seeds and $F_1$ hybrids of these varieties were treated with sulphuric acid after harvesting to eliminate fuzz before sowing. The seeds of six hybrids along with their parents was field planted in randomized complete block design (RCBD) design with three replications. The space between rows and plants was kept at 75cm and 30cm respectively. Standard and uniform cultural practices was followed to each genotype. At the maturity stage, five plants per replication of each genotype was chosen for collecting data of Plant height(cm), Number of monopodial branches, Number of sympodial branches, Number of fruiting nodes per plant, Number of bolls/plant, Boll weight (g), Seed cotton yield/plant (g), Ginning out turn (%), Seed index (g), Fiber length (mm), Fiber strength (g/tex), Micronaire (µg/inch) and node ratio.

$$\mathrm{GOT\%} = \frac{\mathrm{Lint\ weight(g)}}{\mathrm{Seed\ cotton\ yield\ (g)}} \times 100$$

## Statistical Analysis

The recorded data was examined for the analysis of variance (ANOVA) suggested by [20] Heterosis were estimated by following [21]. The values of GCV, PCV, and broad sense heritability were calculated by using method [22].

MP and BP heterosis of these $F_1$ hybrids were estimated by given formulas;

$$\mathrm{Mid\ Parent\ Heterosis} = \frac{(\mathrm{F_1 - MP})}{(\mathrm{MP})} \times 100$$

$$\mathrm{Better\ Parent\ Heterosis} = \frac{(\mathrm{F_1 - BP})}{(\mathrm{BP})} \times 100$$

Heritability $h^2$ was estimated as following;

$$h^2 = Vp/Vg$$

## Test for significance of mid and better parent heterosis

The t-test was utilized to examine whether the $F_1$ hybrid's mid and better parent heterosis was statistically significant. The t value was calculated using the following formula by [23].

**t- test for heterosis**

$t = (F_1\text{-}MP)/\ 3/2rEMS)^{0.5}$

**t- test for heterobeltiosis**

$t = (F_1\text{-}BP)/\ 2/rEMS)^{0.5}$

## 3. Results and discussion

### 3.1. Heterosis

Statistical analysis for all parameters revealed significant differences among genotypes. It revealed that all genotypes differ from one another exhibited in table (3.1). The estimation of heterosis and heterobeltiosis for plant height are exhibited in table (3.2). VH-330 × Debal exhibited maximum heterosis (-26.74) followed by Debal × MS-DK (-9.73). The crosses FH-444 × VH-330, FH-444 × Debal and FH-444 × MS-DK showed non-significant mid parent heterosis. The hybrid VH-330 × Debal revealed highest significant and negative heterobeltiosis (-27.92) followed by Debal × MS-DK (-19.60), VH-330 × MS-DK (-13.59), FH-444 × Debal (-11.29) and FH-444 × VH-330 (-10.97). The estimation of heterosis and heterobeltiosis for monopodial branches are exhibited in table (3.2). The hybrid FH-444 × VH-330 showed the highest heterosis (43.07) followed by FH-444 × Debel (-18.07), VH-330 × MS-DK),(-21.05) and Debel × MS-DK (-31.91). The hybrid FH-444 ×VH-330 revealed the highest heterobeltiosis (40.90) followed by FH-444 × Debel (-32), VH-330 × MS-DK (-31.81) and Debel × MS-DK (-36). For sympodial branches, the estimation of heterosis and heterobeltiosis are given in table (3.2). The hybrid VH-330 × Debel showed the highest heterosis (-39.89) following VH-330 × MS-DK (-29.73), Debel × MS-DK (-15.33) and FH-444 × VH-330 (-12.80). The highest heterobeltiosis (-45.73) was exhibited by VH-330 × Debel. Five crosses FH-444 × VH-330, FH-444 × Debel, Debel × MS-DK, VH-330 × Debel and VH-330 × MS-DK revealed significant and negative (-13.56, -17.85, -22.53, -45.731 and -30.76).

For number of bolls/plant, the estimation of heterosis and heterobeltiosis are shown in (3.3). VH-330 × MS-DK revealed maximum heterosis (-23.24) following VH-330 × Debel (-22.06). The hybrid VH-330 × MS-DK revealed highest heterobeltiosis (-27.58) following VH-330 × Debel -24.34) while remaining four crosses revealed nonsignificant and negative heterobeltiosis and heterosis. For number of fruiting nodes/plant, the estimation of heterosis and heterobeltiosis are shown in table (3.3). The hybrid FH-444 ×VH-330 revealed highest heterosis (20.16) followed by Debel × MS-DK (19.11). All hybrids revealed nonsignificant positive and negative heterobeltiosis. For seed index, the estimation of heterosis and heterobeltiosis are shown in table (3.3). The hybrid Debel × MS-DK showed significant and positive heterosis (20.77) following VH-330 × Debel (19.20) and FH-444×VH-330 (17.85). The hybrid Debel × MS-DK showed maximum heterobeltiosis (19.23) followed by VH-330 × Debel (18.42) while remaining four crosses showed nonsignificant positive and negative heterobeltiosis.

For boll weight, the estimation of heterosis and heterobeltiosis are exhibited in table (3.4). The hybrid VH-330 × MS-DK exhibited the highest heterosis (36.44) followed by VH-330 × Debel (22.14) and FH-444 × VH-330 (19.10). The hybrid VH-330 × MS-DK showed the maximum (33.24) heterobeltiosis followed by FH-444 × Debel (-21.14) while remaining four crosses showed nonsignificant heterobeltiosis. For ginning outturn, the estimation of heterosis and heterobeltiosis are shown in table (3.4). The cross VH-330 × MS-DK exhibited highest heterosis (-11.99) followed by VH-330 × Debel (-10.24) and FH-444 × Debel (9.60) while remaining three crosses FH-444 × VH-330, FH-444 × MS-DK and Debel × MS-DK exhibited nonsignificant positive and negative heterosis. The cross VH-330 × MS-DK exhibited maximum heterobeltiosis (-14.72) followed by FH-444 × Debel (9.46), VH-330 × Debel (-12.58). For fiber strength, the estimation of heterosis and heterobeltiosis are shown in table (3.4). The hybrid FH-444 × MS-DK showed maximum heterosis (17.46) followed by VH-330 × Debel (-9.59) and Debel × MS-DK (-9.04). The hybrid FH-444 × MS-DK showed significant and highest heterobeltiosis (14.51) followed by FH-444 × VH-330 (-11.03), VH-330 × Debel (-13.58), Debel × MS-DK (-10.75) and VH-330 × MS-DK (-9.16).

For micronaire value, the estimation of heterosis and heterobeltiosis are shown in table (3.5). Debel × MS-DK revealed significant and negative heterosis (-13.54) while the remaining five crosses FH-444 × Debel, FH-444 × VH-330, FH-444 × MS-DK, VH-330 × MS-DK and VH-330 × Debel revealed nonsignificant heterosis. Debel × MS-DK revealed significant and negative heterobeltiosis (-14.43) while the remaining five crosses revealed nonsignificant heterobeltiosis.

For fiber length, the estimation of heterosis and heterobeltiosis are shown in table (3.5). The hybrid FH-444 × Debel revealed highest heterosis (-20.55) followed by Debel × MS-DK (18.07) and VH-330 × Debel (-13.51). The hybrid FH-444 × Debel revealed significant and negative heterobeltiosis (-21.41) following VH-330 × Debel (-16.43), Debel × MS-DK (11.50) and FH-444 × VH-330 (-10.72). The estimation of heterosis and heterobeltiosis for node ratio are shown in table (3.5). The hybrid VH-330 × MS-DK exhibited highest heterosis (-25.75) while the remaining crosses showed nonsignificant heterosis. The hybrid VH-330 × MS-DK showed maximum heterobeltiosis (-25.75) followed by Debal × MS-DK (-21.35), VH-330 × Debal (17.51) and FH-444 × MS-DK (-9.07). For seed cotton yield/plant, the estimation of heterosis and heterobeltiosis are shown in (3.5). The cross FH-444 × VH-330 exhibited maximum heterosis (30.95) followed by FH-444 × MS-DK (23.52) and VH-330 × Debel (-19.15). The hybrid FH-444 × VH-330 showed significant and positive heterobeltiosis (30.33) followed by VH-330 × Debel (-29.98), FH-444 × MS-DK (20.86) and Debel × MS-DK (-16.33).

Table 3.1. Analysis of variance for yield and fiber parameters in upland cotton

| SOV | PH | MB | SB | SI | NB | NFN | BW |
|---|---|---|---|---|---|---|---|
| Replication | 76.69 | 0.09 | 11.08 | 0.96 | 9.03 | 122.21 | 0.3 |
| Genotypes | 319.56** | 0.38* | 55.98** | 2.25** | 23.45** | 421.70** | 0.74** |
| Error | 59.19 | 0.09 | 4.99 | 0.46 | 4.22 | 119.93 | 0.17 |

| SOV | GOT% | FS | MIC | FL | NR | SCY | |
|---|---|---|---|---|---|---|---|
| Replication | 10.64 | 2.7 | 0.002 | 0.08 | 0.01 | 122.21 | |
| Genotypes | 17.89** | 12.86** | 0.002* | 20.77** | 0.061** | 421.70** | |
| Error | 5.27 | 3.07 | 0.055 | 5.16 | 0.015 | 119.93 | |

Table 3.2. Mid and better parent heterosis (%) for Plant height, number of monopodial branches and number of sympodial branches in $F_1$ of upland cotton

| Crosses | Plant height (cm) | | Number of monopodial branches | | Number of sympodial branches | |
|---|---|---|---|---|---|---|
| | MP (%) | BP (%) | MP (%) | BP (%) | MP (%) | BP (%) |
| FH-444 × VH-330 | -6.76 ns | -10.97* | 43.07* | 40.90* | -12.80* | -13.56* |
| FH-444 × Debal | -5.64 ns | -11.29* | -18.07* | -32* | -9.74ns | -17.85* |
| FH-444 × MS-DK | 7.513 ns | 1.46 ns | 9.09ns | -4.54ns | 1.55ns | 0.95ns |
| VH-330 × Debal | -26.74* | -27.92* | 3.65ns | -15ns | -39.89* | -45.73* |
| VH-330 × MS-DK | -4.39 ns | -13.59* | -21.05* | -31.81* | -29.73* | -30.76* |
| Debal × MS-DK | -9.73* | -19.60* | -31.91* | -36* | -15.339* | -22.53* |

Table 3.3. Mid and better parent heterosis (%) for number of bolls, number of fruiting nodes and seed index in $F_1$ of upland cotton

| Crosses | Number of bolls | | Number of fruiting nodes/plant | | Seed index (g) | |
|---|---|---|---|---|---|---|
| | MP (%) | BP (%) | MP (%) | BP (%) | MP (%) | BP (%) |
| FH-444 × VH-330 | 7.20ns | -0.85ns | 20.16* | 2.65ns | 17.85* | 6.45ns |
| FH-444 × Debal | -3.36ns | -8.08ns | 12.52ns | 10.78ns | 6.50ns | -3.22ns |
| FH-444 × MS-DK | -7.41ns | -9.36ns | 8.29ns | 0.76ns | 5.26ns | -3.22ns |
| VH-330 × Debal | -22.06* | -24.34* | 0.71ns | -6.94ns | 19.20* | 18.42* |
| VH-330 × MS-DK | -23.24* | -27.58* | 6.88ns | -6.29ns | -9.80ns | -11.53ns |
| Debal × MS-DK | -4.68ns | -7.43ns | 19.11* | 12.46ns | 20.77* | 19.23* |

Table 3.4. Mid and better parent heterosis (%) for boll weight, ginning outturn and fiber strength in $F_1$ of upland cotton

| Crosses | Boll weight (g) | | Ginning Outturn (%) | | Fiber strength (g/tex) | |
|---|---|---|---|---|---|---|
| | MP (%) | BP (%) | MP (%) | BP (%) | MP (%) | BP (%) |
| FH-444 ×VH-330 | 19.10* | 19.04ns | -5.93ns | -8.27ns | -6.34ns | -11.03* |
| FH-444 × Debal | -8.49ns | -21.14* | 9.60* | 9.46* | 5.15ns | 4.46ns |
| FH-444 × MS-DK | -1.05ns | 14.65ns | 4.30ns | 3.62ns | 17.46* | 14.51* |
| VH-330 × Debal | 22.14* | 5.26ns | -10.24* | -12.58* | -9.59* | -13.58* |
| VH-330 ×MS-DK | 36.44* | 33.24* | -11.99* | -14.72* | -6.71ns | -9.16* |
| Debal × MS-DK | 10.10ns | -3.15ns | -6.36ns | -6.84ns | -9.04* | -10.75* |

Table 3.5. Mid and better parent heterosis (%) for micronaire, fiber length, node ratio and seed cotton yield/plant in $F_1$ of upland cotton

| Crosses | Micronaire (µg/inch) | | Fiber length (mm) | | Node ratio | | Seed cotton yield/plant | |
|---|---|---|---|---|---|---|---|---|
| | MP (%) | BP (%) | MP (%) | BP (%) | MP (%) | BP (%) | MP (%) | BP (%) |
| FH-444 × VH-330 | -3.22ns | -4.25ns | -8.59* | -10.72* | 1.90ns | 1.90ns | 30.95* | 30.33* |
| FH-444 × Debal | 3.66ns | 2.06ns | -20.55* | -21.41* | -6.14ns | -6.14* | 1.08ns | -12.10ns |
| FH-444 ×MS-DK | -3.70ns | -4.21ns | 1.16ns | -5.44ns | -9.07ns | -9.07* | 23.52* | 20.86ns |
| VH-330 × Debal | -0.52ns | -3.09ns | -13.51* | -16.43* | -17.51ns | -17.51* | -19.15* | -29.98* |
| VH-330 × MS-DK | 0.53ns | -1.05ns | 9.93* | 0.51ns | -25.75* | -25.75* | -9.27ns | -11.63ns |
| Debal × MS-DK | -13.54* | -14.43* | 18.07* | 11.50* | -21.35ns | -21.35* | -5.57ns | -16.33ns |

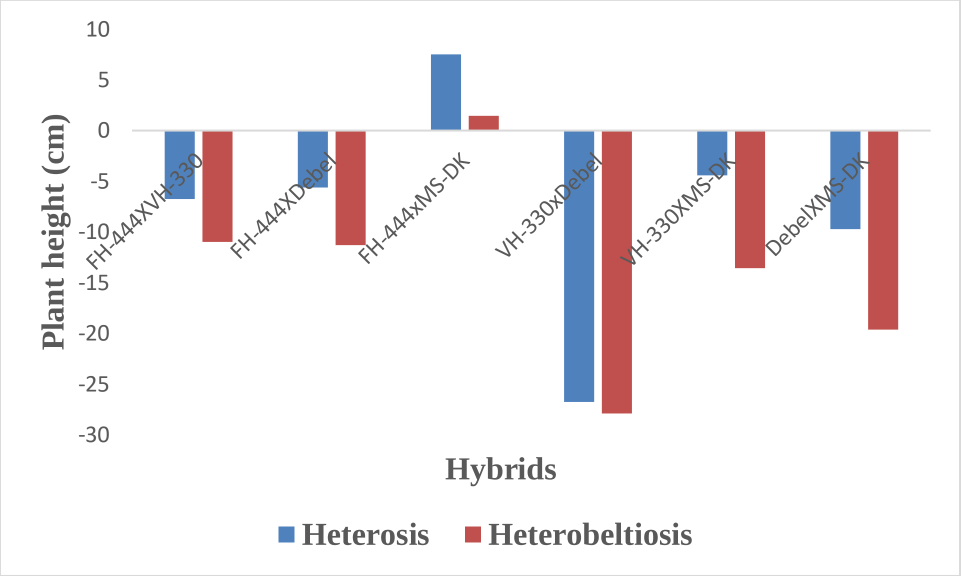

Fig. 3.1.1: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for plant height in upland cotton

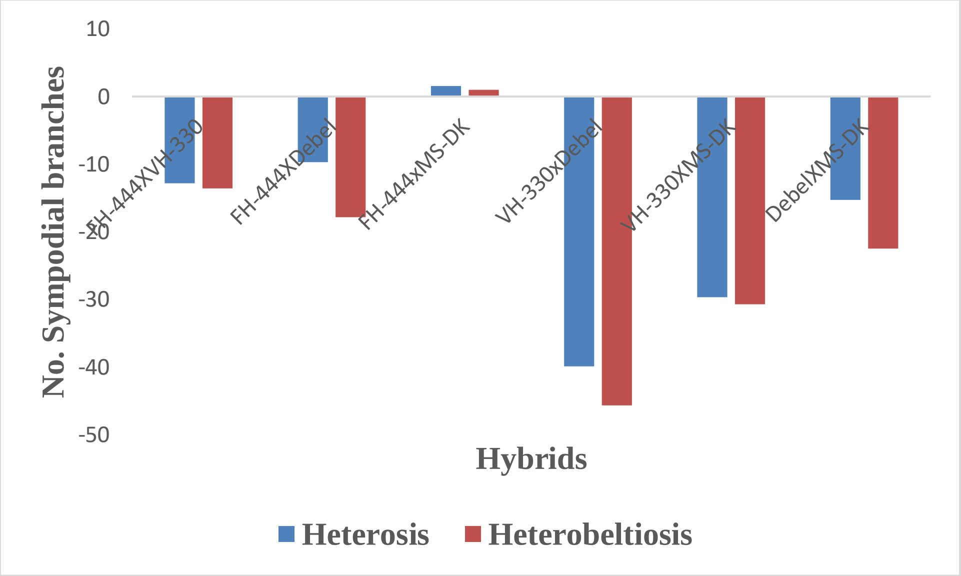

Fig. 3.1.2: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for number of sympodial branches in upland cotton

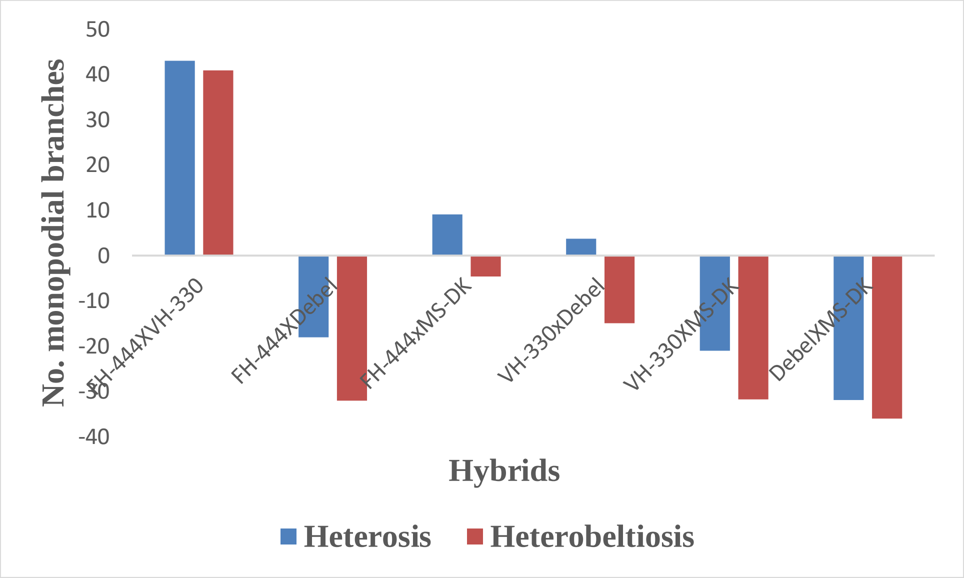

Fig. 3.1.3: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for number of monopodial branches in upland cotton

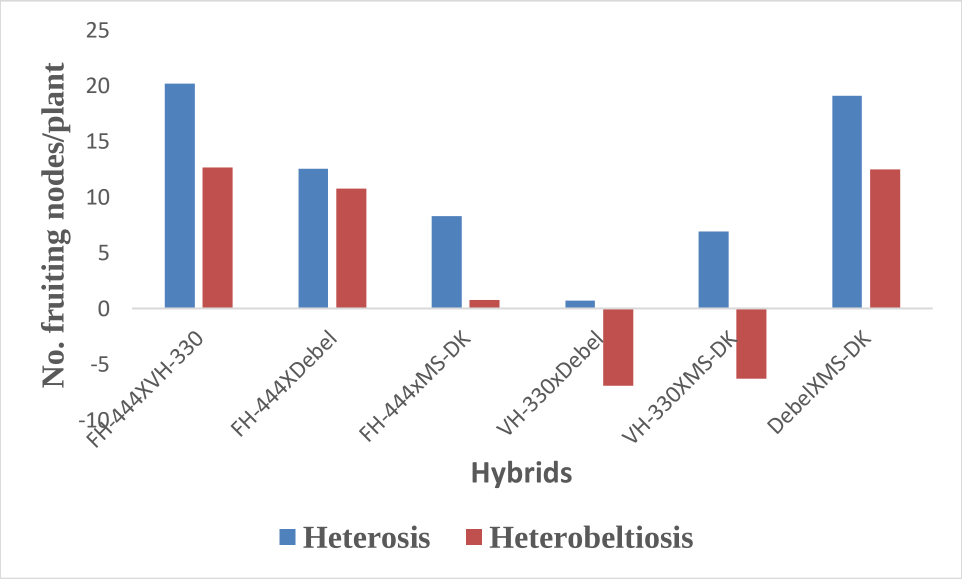

Fig 3.1.4: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for number of fruiting nodes/plant in upland cotton

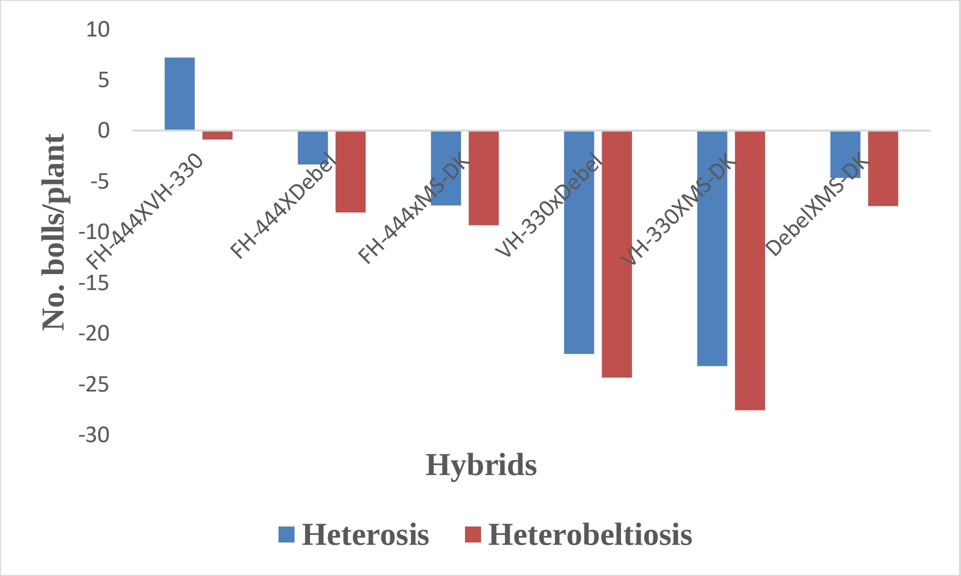

Fig. 3.1.5: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for number of bolls in upland cotton

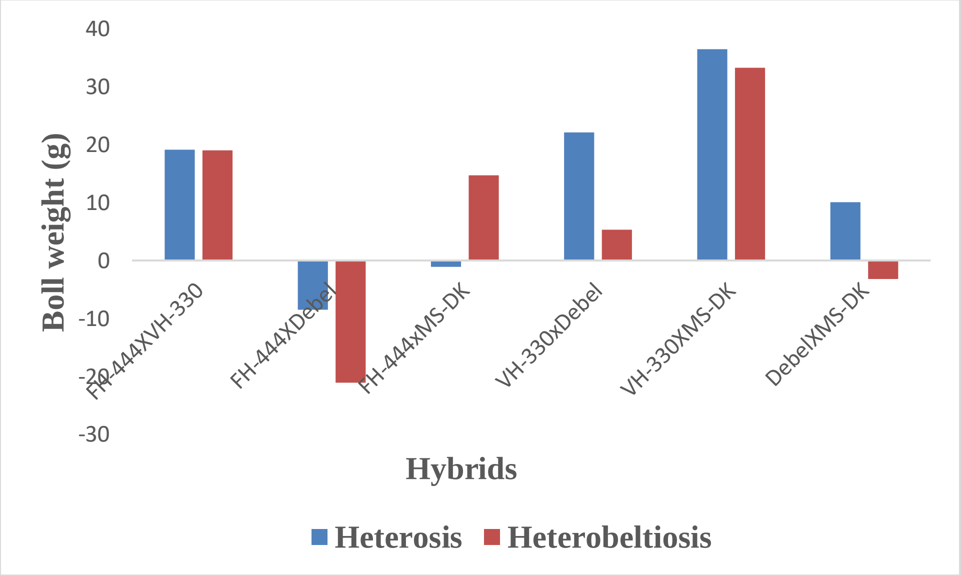

Fig. 3.1.6: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for boll weight in upland cotton

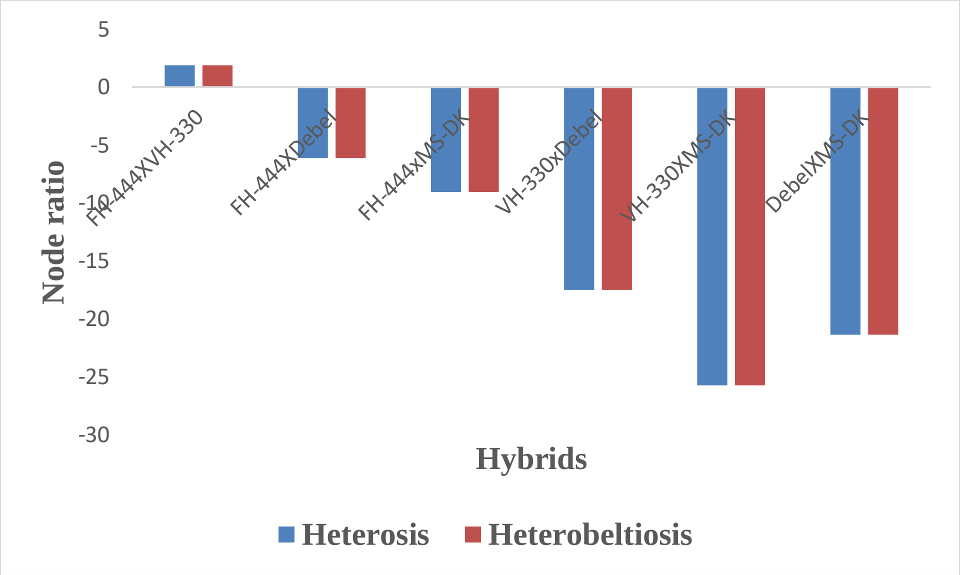

Fig. 3.1.7: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for node ratio in upland cotton

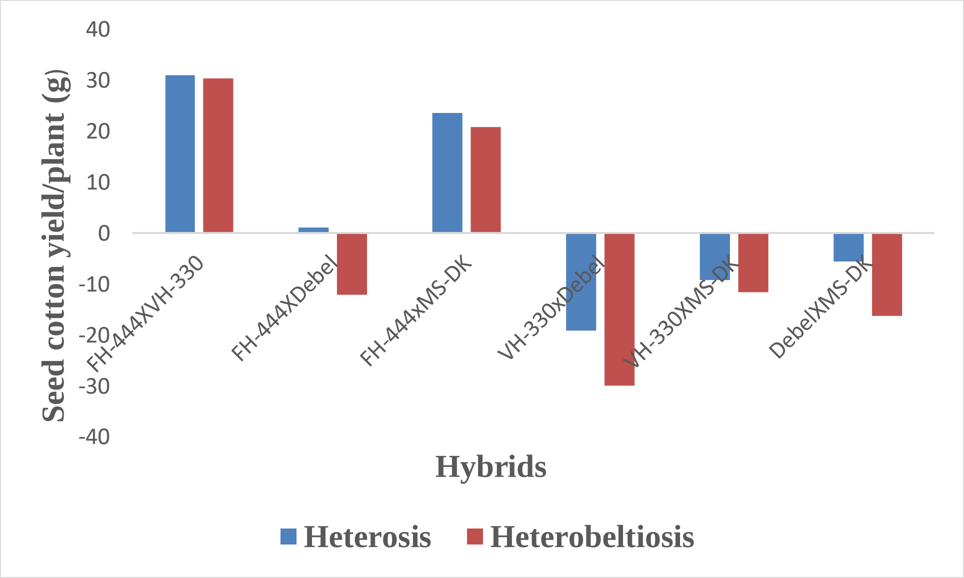

Fig 3.1.8: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for seed cotton yield/plant in upland cotton

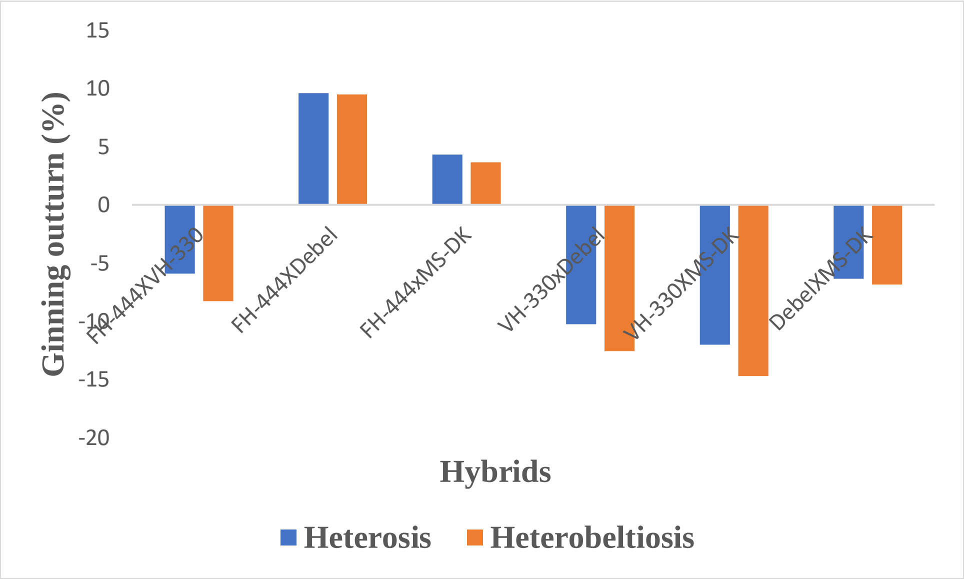

Fig. 3.1.9: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for ginning outturn in upland cotton

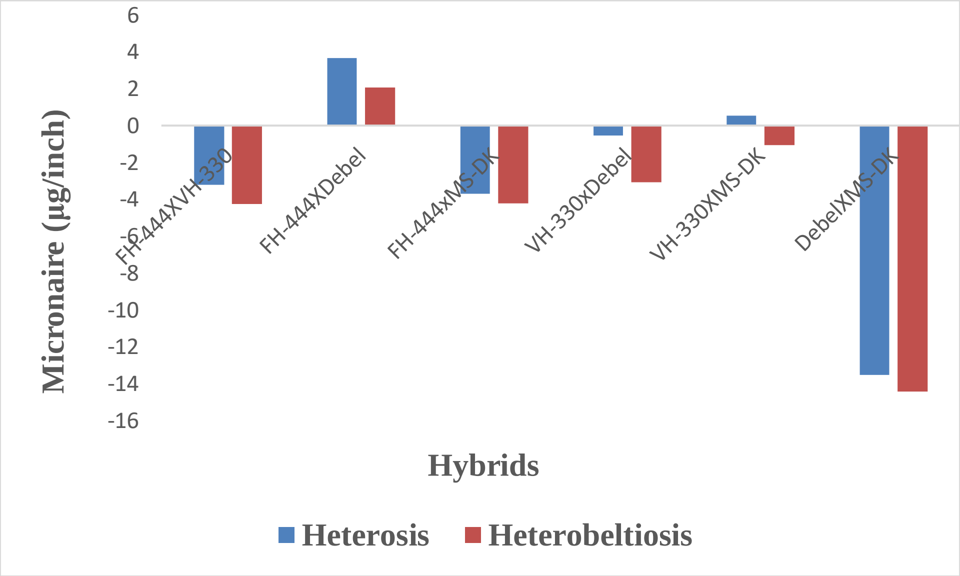

Fig. 3.1.10: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for micronaire in upland cotton

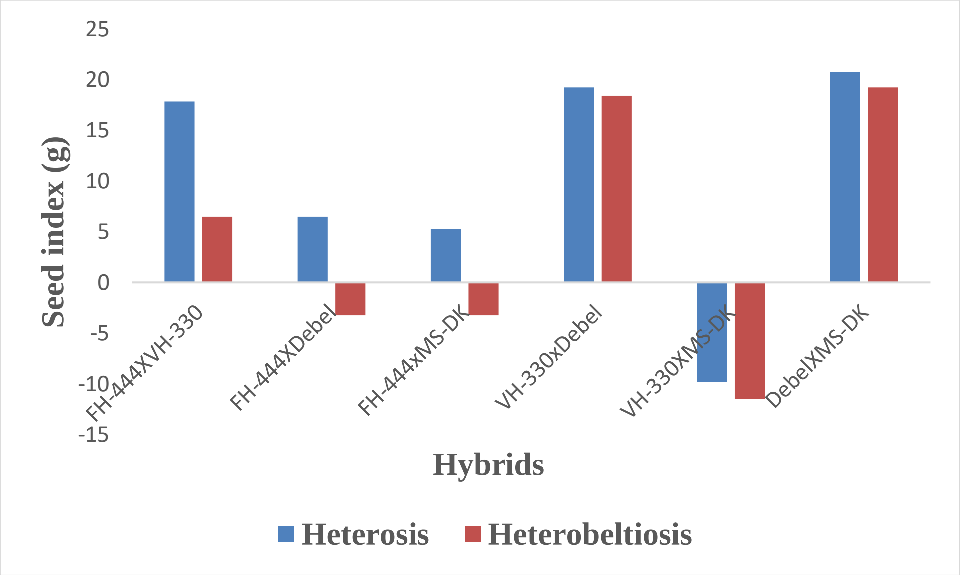

Fig. 3.1.11: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for seed index in upland cotton

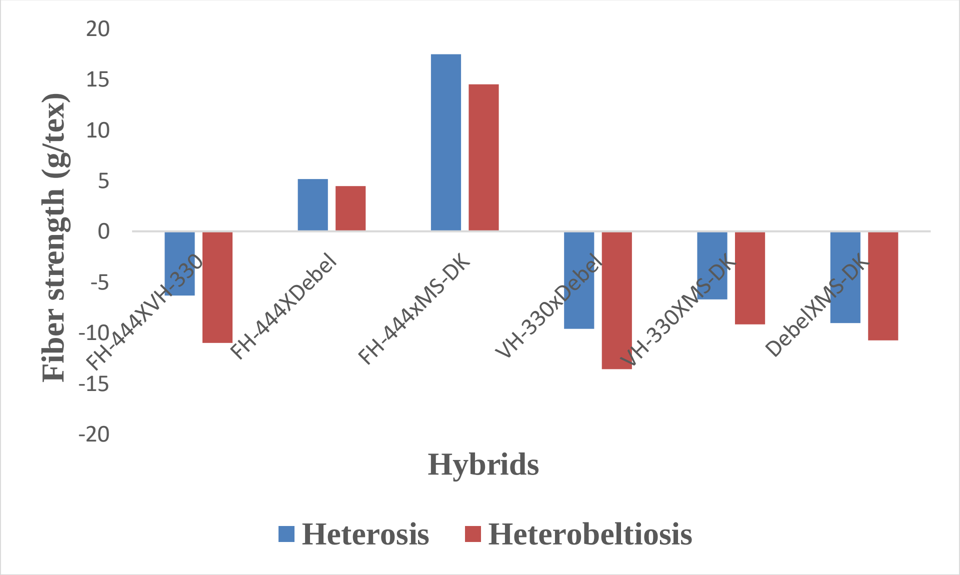

Fig. 3.1.12: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for fiber strength in upland cotton

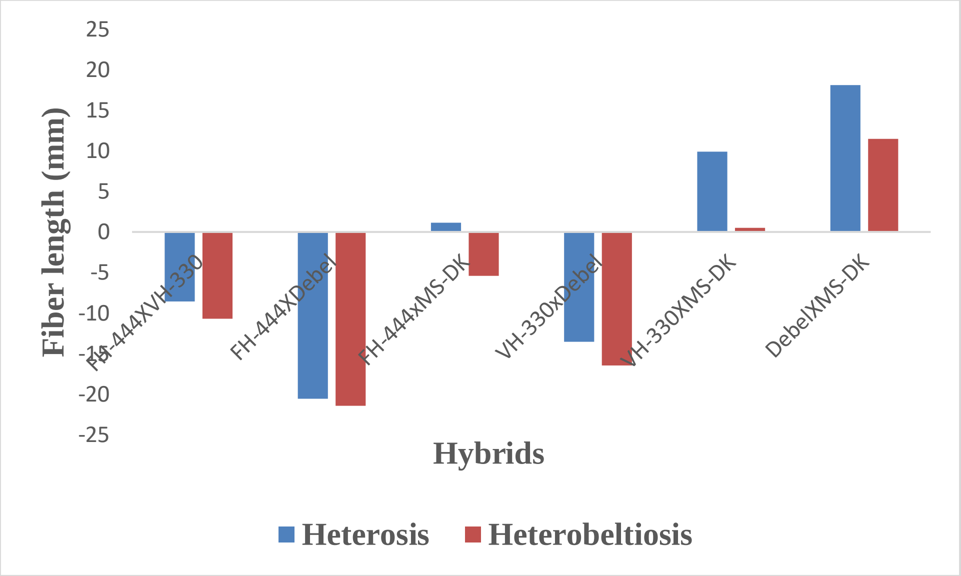

Fig. 3.1.13: Percent increase (+) or decrease (-) of $F_1$ hybrids over MP and BP for fiber length in upland cotton

## 3.2. Heritability

The evaluation of genetic variability revealed a strong association between phenotypic and genotypic variations for all parameters. The value of heritability for plant height recorded (0.59 or 59%) with genetic advance (13.85%). The value of GCV (8.72%) was less than the value of PCV (22.58%) which means the influence of environment is more on this trait. For number of monopodia the heritability (0. 51 or 51%) was observed with genetic advance (23.84%). The value of GCV (16.17%) was less than the value of PCV (22.58%), which means the influence of environment is more on this trait. The value of broad sense heritability for number of sympodial branches (0.77 or 77%) was estimated with genetic advance (31.15%). The estimated heritability value (0.35 or 35%) was observed for number of bolls with genetic advance (11.79%). The GV was less in comparison to PV for number of sympodial branches and number of bolls. For number of fruiting nodes/plant estimated value of broad sense heritability (0.34 or 34%) with genetic advance (10.73%). The estimated value of heritability for seed index (0.38%) was recorded with genetic advance (8.27%). The broad sense heritability for boll weight (0.51 or 51%) was observed with genetic advance (18.53%). The value of GCV was less than the value of PCV which means the influence of environment is more on number of fruiting nodes/plant, seed index and boll weight. The estimated value of broad sense heritability for ginning outturn % (0.37 or 37%) was observed with genetic advance (6.66%). For fiber strength the estimated heritability value (0.51 or 51%) was observed. The assessed value of broad sense heritability for micronaire (0.34 or 34%) was recorded with genetic advance (4.48%). The estimated value of broad sense heritability for fiber length (0.39%) with genetic advance (6.36%). For node ratio the assessed value of heritability was (0.48%) with genetic advance (18.68%). The value of GCV was less than the value of PCV which means the influence of environment is more on ginning outturn %, fiber strength, micronaire, fiber length and node ratio. For seed cotton yield the estimated heritability (0.45 or 45%) value was observed with genetic advance (16.44%). The phenotypic variance observed more than genotypic variance. It means seed cotton yield not only influenced by genotypes also affected by environment.

3.2.1. The range of heritability for yield and fiber quality parameters

| Traits | PCV | GCV | Heritability ($H^2$) | GAM% |
|---|---|---|---|---|
| Plant height | 11.31 | 8.72 | 0.59 | 13.85 |
| Number of monopodial branches | 22.58 | 16.17 | 0.51 | 23.84 |
| Number of sympodial branches | 19.56 | 17.20 | 0.77 | 31.15 |
| Number of bolls | 16.12 | 9.60 | 0.35 | 11.79 |
| Number of fruiting nodes/plant | 15.13 | 8.88 | 0.34 | 10.73 |
| seed index | 10.50 | 6.49 | 0.38 | 8.27 |

| | | | | |
|---|---|---|---|---|
| Boll weight | 17.36 | 12.49 | 0.5182 | 18.53 |
| Ginning Outturn % | 8.52 | 5.25 | 0.3797 | 6.66 |
| Fiber strength | 9.18 | 6.5942 | 0.5150 | 9.74 |
| Micronaire | 9.7482 | 3.6976 | 0.3467 | 4.4844 |
| Fiber length | 7.8443 | 4.9241 | 0.394 | 6.3675 |
| Node ratio | 18.5563 | 12.9728 | 0.4887 | 18.6876 |
| Seed cotton yield/plant | 17.5022 | 11.8205 | 0.4561 | 16.4454 |

## Discussion

The genetic technique of heterosis commonly called hybrid vigor, has become essential for raising the yield of both self- and cross-pollinated crops. It is recognized as a ground-breaking accomplishment in the field of crop improvement. Heterosis can have a positive or negative effect depending on how much the hybrid's average value differs. The significant increase in agricultural plant yield is the primary goal of heterosis breeding. Similar results were also showed by [16] who reported that medium tall plants may be chosen for further selection in cotton and negative heterosis is useful for discourage the highest plant height. Similar results were also found by [24], [25],[26], [27] and [28] were also reported the same results in their experiment. Similar outcomes were also found by [29] who said that negative heterosis for the number of monopodia is very desired because more monopodia make the plant bushier and more resistant, which wastefully increases the amount of space the plant occupies. Therefore, it is desirable to reduce the number of monopodia. The results were also supported by [27], [28] and [30]. Similar findings was also found by [31] who stated that number of sympodial branches are the primary component which directly reflects the seed cotton yield/plant and proposed as suitable selection criteria for high yielding hybrids. Results showed similarities with the results of [32], [2] and [27]. [33] found similar results and described that number of bolls per plant is crucial yield-attributing trait and generally positively linked with seed cotton yield. This demonstrated that an increase in the number of bolls also correlates to an increase in the yield of seed cotton. Similar results were also corroborated by [28], [14], [34] and [26]. The results are supported by [35] who described that number of fruiting nodes was positively linked with seed cotton yield and fruiting bolls. Therefore, by rising the number of fruiting nodes also rise the chance of producing more fruiting bolls. Similar results were also described by [18], and [29]. The results are corroborated by [36] who reported that significant heterosis and heterobeltiosis exhibited in their experiment and ranged varies from (17.26% and 14.17%) for seed index. Similar results were also showed by [27] and [16]. [30] found similar results and reported that boll weight is an important yield attributing character and positively correlated with seed cotton yield. Boll weight was the primary contributor towards increased the heterotic effect for seed cotton yield/ plant. Similar results were also found by [37], [26] and [38] in their research. The findings are corroborated by [27] who stated that GOT % is important economic trait and considered as a secondary contributor to increase the heterotic effect toward seed cotton yield/plant. Thus, positive heterosis for GOT% was desirable and positively associated with seed cotton yield/plant. The results are corroborated by [39], [36] and [40]. Fiber strength is important fiber quality parameter and quantitively inherited. Stronger, finer, longer and more uniform fiber is preferred by textile industry thus positive heterosis for fiber strength is desirable. Similar outcomes were also showed by [27], [17], and [41] also found same results in his experiment. Similar results were also showed by [28] who reported that micronaire value is important fiber quality trait in assessing the lint quality of cotton. Minimum micronaire value is always into consideration as it shows good fiber fineness. Therefore, negative heterosis is required for good micronaire value. Similar findings were also found [27], [39; 41], and [42]. High fiber length is stronger and finer then shorter ones thus positive heterosis for fiber length is desirable. Modernized spinning mills today require the identification hybrids with high fibre length. The results are supported by [17], [41] and [16]. The results are supported by [28] for node ratio trait.

The combination of heritability estimations and genetic advancement holds greater significance in predicting yield through phenotypic selection, as proposed by [43] and [44] as opposed to depending solely on heritability estimates. The results were similar to the previous results (Gnanasekaran et al., 2020) for plant height and boll weight. Plant height and boll weight exhibited moderate heritability estimates. These results are similar with the findings described by [45] for plant height; [46] for boll weight. The results are supported by [47] for fiber length. [48], [49], [50] and [51] estimated 33%, 62%, 68% and 47.14% heritability for fiber strength trait. The results are supported by [52], [53] and [54] studied 79%, 43% and 79.17% broad sense heritability for parameter of number of sympodial branches/plant respectively. [53] and [55] assessed 34% and 56% broad sense heritability for of number of monopodial branches/plant. The findings are supported by [46] who observed broad sense heritability 0.26 for micronaire. The results are supported by [51; 56] estimated heritability 29.5 and 19.98 for ginning outturn% . The results are similar with the results of [51] estimated heritability 36.66 for Seed cotton yield/plant. The findings are supported by [19] who reported broad sense heritability 25.58% for seed index. The results are corroborated by [57] for number of bolls and number of fruiting nodes/plant. The results are similar with the findings [56] for number of bolls/plant trait. These results align with the findings described by [58] for node ratio. Seed cotton yield/plant were positively linked with number of bolls/plant, boll weight and sympodia/plant thus considered to the main yield contributing traits. Comparable findings also showed by [27], [36] and [39].

## Conclusion

The aim of this research was to investigate heterosis and heritability analysis for seed cotton yield and yield associated components in upland cotton that can be employed in future cotton breeding programme. The parents Debel and VH-330 were found to be the most effective for cross combination for the parameters viz. plant height, boll weight and number of monopodial branches, seed cotton yield/plant, micronaire, fiber length, fiber strength, Got% and number of sympodial branches. The hybrids VH-330 × Debel, VH-330 × MS-DK and FH-444 × VH-330 exhibited significant and highest heterotic effects for yield and yield associated parameters and fiber quality parameter. The estimates of broad sense heritability exposed that moderate heritability was observed between all traits. These hybrids can be utilized for exploitation of yield and fiber quality parameters in future breeding programmes.

## References:

1. Isong, A., Balu, A., Isong, C., & Bamishaiye, E. (2019). Estimation of heterosis and combining ability in interspecific cotton hybrids. *Electronic Journal of Plant Breeding*, *10*(2), 827-837. https://doi.org/10.5958/0975-928X.2019.00110.8
2. Chakholoma, M., Nimbal, S., Sangwan, O., Mor, V., & Jain, A. (2021). Studies on economic heterosis for yield and fibre quality traits in American cotton (Gossypium hirsutum L.). *Journal of Cotton Research and Development*, *35*(2), 185-192.
3. Khan, A. M., Khan, A. A., Azhar, M. T., Amrao, L., & Cheema, H. M. N. (2016). Comparative analysis of resistance gene analogues encoding NBS-LRR domains in cotton. *Journal of the Science of Food and Agriculture*, *96*(2), 530-538. https://doi.org/10.1002/jsfa.7120
4. Farooq, A., Shakeel, A., Saeed, A., Farooq, J., Rizwan, M., Chattha, W. S., Sarwar, G., & Ramzan, Y. (2023). Genetic variability predicting breeding potential of upland cotton (Gossypium hirsutum L.) for high temperature tolerance. *Journal of Cotton Research*, *6*(1), 1-17. https://doi.org/10.1186/s42397-023-00144-z
5. Bilwal, B., Vadodariya, K., Lahane, G., & Rajkumar, B. (2018). Heterosis study for seed cotton yield and its yield attributing traits in upland cotton (Gossypium hirsutum L.). *Journal of Pharmacognosy and Phytochemistry*, *7*(1), 1963-1967.
6. Rizwan, M., Farooq, J., Farooq, M., Sarwar, A., Ali, A., Ilahi, F., Asif, M., & Sarwar, G. (2021). Quantitative Studies in Upland Cotton (Gossypium hirsutum L.) using Multivariate Techniques. *Pakistan Journal of Agricultural Research*, *34*(1).
7. Gohil, S., Parmar, M., & Chaudhari, D. (2017). Study of heterosis in interspecific hybrids of cotton (Gossypium hirsutum L. x Gossypium barbadense L.). *Journal of Pharmacognosy and Phytochemistry*, *6*(4), 804-810.
8. Masood, S. A., Rehman, H. U., Yasin, M., Ali, M., Ahmad, S., Salman, S., & Ali, Q. (2019). Genetics of fiber quality, oil content, seed-cotton yield and its allied traits in cotton: A review. *Genetics*, *4*(3).
9. Khan, N., Han, Y., Xing, F., Feng, L., Wang, Z., Wang, G., Yang, B., Fan, Z., Lei, Y., & Xiong, S. (2019). Plant density influences reproductive growth, lint yield and boll spatial distribution of cotton. *Agronomy*, *10*(1), 14. https://doi.org/10.3390/agronomy10010014.
10. Vavdiya, P., Chovatia, V., Madariya, R., Mehta, D., & Solanki, H. (2019). Heterosis studies for seed cotton yield and its components over environments in cotton. *Journal of Pharmacognosy and Phytochemistry*, *8*(2), 2049-2053.
11. Hasan, I., Rasul, S., Malik, T. H., Qureshi, M. K., Aslam, K., Shabir, G., & Manzoor, H. (2019). Present status of cotton leaf curl virus disease (CLCUVD): A major threat to cotton production. *International Journal of Cotton Research and Technology*, *1*(1), 1-13. https://doi.org/10.33865/IJCRT.001.01.0240
12. Khokhar, E. S., Shakeel, A., Maqbool, M. A., Abuzar, M. K., Zareen, S., Syeda, S. A., & Asadullah, M. (2018). Studying combining ability and heterosis in different cotton (Gossypium hirsutum L.) genotypes for yield and yield contributing traits. *Pakistan Journal of Agricultural Research*, *31*(1).
13. Ullah, K., Khan, M. I., Mahmood, Z., Iqbal, T., Muhammad, S., Haq, H. A., Ahmad, A., & Hussain, S. (2017). Response of yield and related attributes of upland cotton to weather variables. *American Journal of Plant Sciences*, *8*(07), 1711. https://doi.org/10.4236/ajps.2017.87118
14. Richika, R., Rajeswari, S., Premalatha, N., & Thirukumaran, K. (2021). Heterosis and combining ability analysis for yield contributing traits and fibre quality traits in interspecific cotton hybrids (Gossypium hirsutum L. x Gossypium barbadense L.). *Electronic Journal of Plant Breeding*, *12*(3), 934-940.

15. Pheirim, R., Niyaria, R., & Singh, P. K. (2017). Heterosis prediction through molecular markers. *Rising A j. Res*, *1*(1), 45-50.
16. Baloch, A., Solangi, A., Baloch, M., Baloch, G., & Abro, S. (2015). Estimation of heterosis and heterobeltiosis for yield and fiber traits in F1 hybrids of upland cotton (Gossypium hirsutum L.) genotypes. *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences*, *31*(2), 221-228.
17. Aydın, Ü., ÖZBEK, N., & Cinar, V. M. (2019). Line x tester analysis for yield and fiber quality in cotton (Gossypium hirsutum L.). *Turkish Journal of Field Crops*, *24*(2), 215-220. https://doi.org/10.17557/tjfc.509134
18. Monicashree, C., Balu, P. A., & Gunasekaran, M. (2017). Combining ability and heterosis studies on yield and fibre quality traits in upland cotton (Gossypium hirsutum L.). *Int. J. Curr. Microbiol. App. Sci*, *6*(8), 912-927. https://doi.org/10.20546/ijcmas.2017.608.113
19. FaizaNizamani, M. J. B., Baloch, A. W., Buriro, M., Nizamani, G. S., Nizamani, M. R., & Baloch, I. A. (2017). Genetic distance, heritability and correlation analysis for yield and fibre quality traits in upland cotton genotypes. *Pakistan Journal of Biotechnology*, *14*(1), 29-36.
20. d Steel, R. G., & Torrie, J. H. (1986). *Principles and procedures of statistics: a biometrical approach*. McGraw-Hill New York, NY, USA.
21. Falconer, D. S. (1996). *Introduction to quantitative genetics*. Pearson Education India.
22. Singh, R. K., & Chaudhary, B. D. (1977). Biometrical methods in quantitative genetic analysis. *Biometrical methods in quantitative genetic analysis.*
23. Wynne, J., Emery, D., & Rice, P. (1970). Combining ability estimates in Arachis hypogaea L. II. field performance of F1 hybrids 1. *Crop Science*, *10*(6), 713-715.
24. Nirania, K., Kumar, A., & Pundir, S. (2017). Heterosis studies for seed cotton yield and other traits in upland cotton (Gossypium hirsutum L.). *Journal of Pharmacognosy and Phytochemistry*, *6*(6), 583-586.
25. Zapadiya, V., Valu, M., Madariya, R., & Katara, D. (2018). Estimation of heterobeltiosis and standard heterosis for seed cotton yield and its component traits in upland cotton (Gossypium hirsutum L.). *Journal of Pharmacognosy and Phytochemistry*, *7*(5), 2167-2172.
26. Naik, K. S., Satish, Y., & Babu, D. P. (2020). Studies on heterosis for yield and yield attributing traits in American cotton (Gossypium hirsutum L.). *Int. J. Chem. Stud*, *8*(1), 2064-2068. https://doi.org/10.22271/chemi.2020.v8.i1ae.8568
27. Udaya, V., Saritha, H., & Patil, R. S. (2023). Heterosis studies for seed cotton yield and fibre quality traits in upland cotton (Gossypium hirsutum L.). *Indian journal of agricultural research*, *57*(2), 150-154.
28. Monicashree, C., Amala Balu, P., & Gunasekaran, M. (2017). Heterosis studies for yield and fibre quality traits in upland cotton (Gossypium hirsutum L.). *Int. J. Pure App. Biosci*, *5*(3), 169-186.
29. Kencharaddi, H., Hanchinal, R., Patil, S., Manjula, S., Pranesh, K., & Rajeev, S. (2015). Studies on heterosis in inter heterotic group derived cotton hybrids for lint yield and its components. *Plant archives*, *15*(1), 323-333.
30. Rani, S., Chapara, M., & Satish, Y. (2020). Heterosis for seed cotton yield and yield contributing traits cotton (Gossypium hirsutum L.). *International journal of chemical studies*, *8*, 2496-2500. https://doi.org/10.22271/chemi.2020.v8.i3aj.9581
31. Saifullah, A., Sawan, L., Deho, Z., & Manjh, M. (2014). To estimates heterosis and heterobeltosis of yield and quality traits in upland cotton. *Journal of Biology, Agriculture and Healthcare*, *4*(6), 19-22.
32. Ranganatha, H., Patil, S., Manjula, S., & Patil, B. (2013). Studies on heterosis in cotton (Gossypium hirsutum L.) for seed cotton yield and its components. *Asian Journal of Bio Science*, *8*(1), 82-85.
33. Solanki, H., Mehta, D., & Valu, V. R. M. (2014). Heterosis for seed cotton yield and its contributing characters in cotton (GossypiumhirsutumL.). *Electronic Journal of Plant Breeding*, *5*(1), 124-130.
34. Vineela, N., Murthy, J., Ramakumar, P., & Kumari, S. (2013). Heterosis for morpho physiological studies in cotton. *J. Nat. Sci*, *1*(2), 53-64.
35. Munir, S., Hussain, S., Manzoor, H., Quereshi, M., Zubair, M., Nouman, W., Shehzad, A., Rasul, S., & Manzoor, S. (2016). Heterosis and correlation in interspecific and intraspecific hybrids of cotton. *Genet. Mol. Res*, *15*(10.4238). https://doi.org/10.4238/gmr.15028083
36. Soomro, A. W., Panhwar, F. H., Channa, A. R., Ahsan, M. Z., Majidano, M. S., & Sial, K. B. (2016). Study of heterosis and heterobeltiosis in upland cotton. *Int. J. Biol. Biotech*, *13*(1), 111-114.
37. Mastungi, S., & Ansari, B. (2015). Heterosis manifestation leading to hybrid development in upland cotton. *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences*, *31*(2), 240-248.
38. Patel, N., Patil, S., Patel, S., & Jadhav, B. (2015). Estimation of heterosis for seed cotton yield and its component characters in upland cotton (Gossypium hirsutum L.). *Trends in Biosciences*, *8*(4), 925-928.
39. Srinivas, B., & Bhadru, D. (2015). Heterosis studies for yield and fiber quality traits in intra hirsutum hybrids of cotton (Gossypium hirsutum L.). *Agricultural Science Digest-A Research Journal*, *35*(4), 295-299.

40. Tigga, A., Patil, S., Edke, V., Roy, U., & Kumar, A. (2017). Heterosis and inbreeding depression for seed cotton yield and yield attributing traits in intrahirsutum (G. hirsutum L. X G. hirsutum L.) hybrids of cotton. *International Journal of Current Microbiology and Applied Sciences*, *6*(10), 2883-2887. https://doi.org/10.20546/ijcmas.2017.610.339
41. Usharani, K., Vindhiyavarman, P., Balu, P. A., & Boopathi, N. (2015). Heterosis studies for fibre quality traits in diallel crosses of upland cotton (Gossypium hirsutum L.). *The Bioscan*, *10*(2), 793-799.
42. KAIPU, B. R. (2015). Heterosis for seed cotton yield and quality traits in cotton (Gossypium hirsutum L.). *Electronic Journal of Plant Breeding*, *6*(4), 1124-1131.
43. Johnson, H. W., Robinson, H., & Comstock, R. (1955). Estimates of genetic and environmental variability in soybeans 1. *Agronomy journal*, *47*(7), 314-318.
44. Swarup, V., & Chaugle, B. (1962). Studies on genetic variability in sorghum. Phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding*, *22*, 31-36.
45. Sunayana, R., Sangwan, S., & Nimbal, S. (2017). Studies on association, path analysis and genetic parameters for seed cotton yield and it's contributing characters in desi cotton (Gossypium arboreum L.). *Int J Curr Microbiol Appl Sci*, *6*(11), 104-111.
46. Reddy, R. Y., & Sarma, A. (2014). Genetic variability for yield components and fibre characters in cotton (Gossypium arboreum L.). *Plant archives*, *14*(1), 417-419.
47. Nawaz, B., Sattar, S., & Malik, T. A. (2019). Genetic analysis of yield components and fiber quality parameters in upland cotton. *International Multidisciplinary Research Journal*, *9*(9), 13-19.
48. Desalegn, Z., Ratanadilok, N., & Kaveeta, R. (2009). Correlation and heritability for yield and fiber quality parameters of Ethiopian cotton (Gossypium hirsutum L.) estimated from 15 (diallel) crosses. *Agriculture and Natural Resources*, *43*(1), 1-11.
49. Shahzad, M. T., Ijaz, F., Khan, O., Saleem, B., & Hassan, U. (2015). Correlation, Path Analysis & Heritability Among Some Yield and Fibre Related Traits of Gossypium hirsutum L. *Cotton Genomics and Genetics*, *6*. https://doi.org/10.5376/cgg.2015.06.0004
50. Khokhar, E. S., Shakeel, A., Maqbool, M. A., Anwar, M. W., Tanveer, Z., & Irfan, M. F. (2017). Genetic study of cotton (Gossypium hirsutum L.) genotypes for different agronomic, yield and quality traits. *Pakistan Journal of Agricultural Research*, *30*(4).
51. Komala, M., Ganesan, N. M., & Kumar, M. (2018). Genetic variability, heritability and correlation analysis in F2 populations of ratoon upland cotton hybrids. *International Journal of Agriculture, Environment and Biotechnology*, *11*(6), 815-827. https://doi.org/10.30954/0974-1712.12.2018.2
52. Joshi, H., Chovatia, P., & Mehta, D. (2006). Genetic variability, character association and component analysis in upland cotton. *Indian journal of agricultural research*, *40*(4), 302-305.
53. Farooq, J., Anwar, M., Riaz, M., Farooq, A., Mahmood, A., Shahid, M., Rafiq, M., & Ilahi, F. (2014). Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (Gossypium hirsutum L.). *JAPS: Journal of Animal & Plant Sciences*, *24*(3).
54. Baloch, M., Baloch, A., Baloch, M., Mallano, I., Baloch, A., Baloch, N., & Abro, S. (2015). Association and heritability analysis for yield and fiber traits in promising genotypes of cotton (Gossypium hirsutum L.). *Sindh University Research Journal-SURJ (Science Series)*, *47*(2).
55. Vineela, N., Samba Murthy, J., Ramakumar, P., & Ratna, K. (2013). Variability studies for physio morphological and yield components traits in American cotton (Gossypium hirsutum L.). *J. Agric. Vet. Sci*, *4*(3), 7-10.
56. Jarwar, A. H., Wang, X., Wang, L., Ma, Q., & Fan, S. (2018). Genetic advancement, variability and heritability in upland cotton (Gossypium hirsutum L.). *J Envir Agric Sci*, *6*, 24-31.
57. Dhamayanathi, K., Manickam, S., & Rathinavel, K. (2010). Genetic variability studies in Gossypium barbadense L. genotypes for seed cotton yield and its yield components. *Electronic Journal of Plant Breeding*, *1*(4), 961-965.
58. Dhivya, R., Amalabalu, P., Pushpa, R., & Kavithamani, D. (2014). Variability, heritability and genetic advance in upland cotton (Gossypium hirsutum L.). *African Journal of Plant Science*, *8*(1), 1-5. https://doi.org/10.5897/AJPS2013.1099